

# Sequence Kernel Association Tests for the Combined Ef

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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.	1.8	30
2	The Next-Generation Sequencing Revolution and Its Impact on Genomics. <i>Cell</i> , 2013, 155, 27-38.	13.5	856
3	Quantifying Missing Heritability at Known GWAS Loci. <i>PLoS Genetics</i> , 2013, 9, e1003993.	1.5	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.	1.1	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.	1.1	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.	1.1	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.	2.6	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.	1.5	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.	1.8	2
10	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. <i>Nature Communications</i> , 2014, 5, 3983.	5.8	81
11	Generalized Functional Linear Models for Gene-Based Case-Control Association Studies. <i>Genetic Epidemiology</i> , 2014, 38, 622-637.	0.6	22
12	Kernel-Machine Testing Coupled with a Rank-Truncation Method for Genetic Pathway Analysis. <i>Genetic Epidemiology</i> , 2014, 38, 447-456.	0.6	12
13	Greater power and computational efficiency for kernel-based association testing of sets of genetic variants. <i>Bioinformatics</i> , 2014, 30, 3206-3214.	1.8	35
14	Common variation at PPARCC1A/B and change in body composition and metabolic traits following preventive interventions: the Diabetes Prevention Program. <i>Diabetologia</i> , 2014, 57, 485-490.	2.9	29
15	Dynamic Bayesian Testing of Sets of Variants in Complex Diseases. <i>Genetics</i> , 2014, 198, 867-878.	1.2	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.	0.6	28
17	How important are rare variants in common disease?. <i>Briefings in Functional Genomics</i> , 2014, 13, 353-361.	1.3	76
18	A Powerful and Adaptive Association Test for Rare Variants. <i>Genetics</i> , 2014, 197, 1081-1095.	1.2	150

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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.	0.4	46
22	Detecting association of rare and common variants by adaptive combination of P-values. <i>Genetical Research</i> , 2015, 97, e20.	0.3	3
23	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. <i>Human Heredity</i> , 2015, 80, 126-138.	0.4	9
24	The Use of the Linear Mixed Model in Human Genetics. <i>Human Heredity</i> , 2015, 80, 196-206.	0.4	18
25	A combination of targeted enrichment methodologies for whole-exome sequencing reveals novel pathogenic mutations. <i>Scientific Reports</i> , 2015, 5, 9331.	1.6	14
26	SNP Set Association Testing for Survival Outcomes in the Presence of Intrafamilial Correlation. <i>Genetic Epidemiology</i> , 2015, 39, 406-414.	0.6	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.	1.1	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.	0.8	3
29	SPS: A Simulation Tool for Calculating Power of Set-Based Genetic Association Tests. <i>Genetic Epidemiology</i> , 2015, 39, 395-397.	0.6	3
30	Exome Analysis of Patients with Concurrent Pediatric Inflammatory Bowel Disease and Autoimmune Disease. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1.	0.9	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.	1.1	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.	1.1	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.	0.9	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.	3.5	34
36	Phenome-Wide Association Studies: Embracing Complexity for Discovery. <i>Human Heredity</i> , 2015, 79, 111-123.	0.4	20

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37	Contribution of Large Region Joint Associations to Complex Traits Genetics. <i>PLoS Genetics</i> , 2015, 11, e1005103.	1.5	10
38	A review of study designs and statistical methods for genomic epidemiology studies using next generation sequencing. <i>Frontiers in Genetics</i> , 2015, 6, 149.	1.1	48
39	The Genetics of Neuropsychiatric Diseases: Looking In and Beyond the Exome. <i>Annual Review of Neuroscience</i> , 2015, 38, 47-68.	5.0	27
40	Genomic approaches for understanding the genetics of complex disease. <i>Genome Research</i> , 2015, 25, 1432-1441.	2.4	75
41	Empirical Bayes Scan Statistics for Detecting Clusters of Disease Risk Variants in Genetic Studies. <i>Biometrics</i> , 2015, 71, 1111-1120.	0.8	6
42	The role of SHANK2 rare variants in schizophrenia susceptibility. <i>Molecular Psychiatry</i> , 2015, 20, 1486-1486.	4.1	16
43	Sequencing rare and common APOL1 coding variants to determine kidney disease risk. <i>Kidney International</i> , 2015, 88, 754-763.	2.6	30
44	GWAS of longitudinal amyloid accumulation on <sup>18</sup> F-florbetapir PET in Alzheimer's disease implicates microglial activation gene <i>IL1RAP</i> . <i>Brain</i> , 2015, 138, 3076-3088.	3.7	117
45	The contribution of rare and common variants in 30 genes to risk nicotine dependence. <i>Molecular Psychiatry</i> , 2015, 20, 1467-1478.	4.1	64
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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. <i>PLoS Computational Biology</i> , 2016, 12, e1004993.	1.5	11
49	The MKK7 p.Glu116Lys Rare Variant Serves as a Predictor for Lung Cancer Risk and Prognosis in Chinese. <i>PLoS Genetics</i> , 2016, 12, e1005955.	1.5	14
50	Genetic Evaluation of Schizophrenia Using the Illumina HumanExome Chip. <i>PLoS ONE</i> , 2016, 11, e0150464.	1.1	12
51	A Data Fusion Approach to Enhance Association Study in Epilepsy. <i>PLoS ONE</i> , 2016, 11, e0164940.	1.1	4
52	Beyond Rare-Variant Association Testing: Pinpointing Rare Causal Variants in Case-Control Sequencing Study. <i>Scientific Reports</i> , 2016, 6, 21824.	1.6	17
53	A genome-wide analysis in cluster headache points to neprilysin and PACAP receptor gene variants. <i>Journal of Headache and Pain</i> , 2016, 17, 114.	2.5	38
54	Local Joint Testing Improves Power and Identifies Hidden Heritability in Association Studies. <i>Genetics</i> , 2016, 203, 1105-1116.	1.2	9

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55	Circadian gene variants influence sleep and the sleep electroencephalogram in humans. <i>Chronobiology International</i> , 2016, 33, 561-573.	0.9	24
56	Genetic Associationâ€“Guided Analysis of Gene Networks for the Study of Complex Traits. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 179-184.	5.1	9
57	Clinical and Genetic Risk Factors for Acute Pancreatitis in Patients With Acute Lymphoblastic Leukemia. <i>Journal of Clinical Oncology</i> , 2016, 34, 2133-2140.	0.8	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. <i>Nature Neuroscience</i> , 2016, 19, 1433-1441.	7.1	427
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62	Small Sample Kernel Association Tests for Human Genetic and Microbiome Association Studies. <i>Genetic Epidemiology</i> , 2016, 40, 5-19.	0.6	45
63	Test for Rare Variants by Environment Interactions in Sequencing Association Studies. <i>Biometrics</i> , 2016, 72, 156-164.	0.8	68
64	A Wâ€“test collapsing method for rareâ€“variant association testing in exome sequencing data. <i>Genetic Epidemiology</i> , 2016, 40, 591-596.	0.6	6
65	<i>genipe</i>: an automated genome-wide imputation pipeline with automatic reporting and statistical tools. <i>Bioinformatics</i> , 2016, 32, 3661-3663.	1.8	22
66	Poisson Approximationâ€“Based Score Test for Detecting Association of Rare Variants. <i>Annals of Human Genetics</i> , 2016, 80, 221-234.	0.3	1
67	A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. <i>Genetic Epidemiology</i> , 2016, 40, 702-721.	0.6	10
68	Variation of 46 Innate Immune Genes Evaluated for their Contribution in Pneumococcal Meningitis Susceptibility and Outcome. <i>EBioMedicine</i> , 2016, 10, 77-84.	2.7	11
69	RNF213 Is Associated with Intracranial Aneurysms in the French-Canadian Population. <i>American Journal of Human Genetics</i> , 2016, 99, 1072-1085.	2.6	49
70	Exome Array Analysis of Susceptibility to Pneumococcal Meningitis. <i>Scientific Reports</i> , 2016, 6, 29351.	1.6	7
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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.	3.0	56
78	GWASeq: targeted re-sequencing follow up to GWAS. BMC Genomics, 2016, 17, 176.	1.2	7
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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.	2.9	17
81	Comparison of haplotype-based statistical tests for disease association with rare and common variants. Briefings in Bioinformatics, 2016, 17, 657-671.	3.2	19
82	Identification of rare variants in TNNI3 with atrial fibrillation in a Chinese GenelD population. Molecular Genetics and Genomics, 2016, 291, 79-92.	1.0	13
83	Multi-marker linkage disequilibrium mapping of quantitative trait loci. Briefings in Bioinformatics, 2017, 18, 195-204.	3.2	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.	1.8	72
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87	Selection Probability for Rare Variant Association Studies. Journal of Computational Biology, 2017, 24, 400-411.	0.8	3
88	De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. Genome Medicine, 2017, 9, 8.	3.6	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.	3.3	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
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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.	1.4	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.	6.5	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.	1.8	12
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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.	0.6	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.	1.4	4
100	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017, 205, 939-953.	1.2	39
101	Multiple linear combination (MLC) regression tests for common variants adapted to linkage disequilibrium structure. <i>Genetic Epidemiology</i> , 2017, 41, 108-121.	0.6	14
102	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. <i>Cell</i> , 2017, 170, 1164-1174.e6.	13.5	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.	1.1	0
104	Analysis of population-specific pharmacogenomic variants using next-generation sequencing data. <i>Scientific Reports</i> , 2017, 7, 8416.	1.6	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.	2.1	29
106	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017, 7, 6037.	1.6	12
107	Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits. <i>Genetics</i> , 2017, 206, 1779-1790.	1.2	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.	1.5	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.	2.4	11

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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.	1.6	4
111	Genetics of Spontaneous Intracerebral Hemorrhage. <i>Stroke</i> , 2017, 48, 3420-3424.	1.0	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.	1.1	18
113	Kernel-Based Measure of Variable Importance for Genetic Association Studies. <i>International Journal of Biostatistics</i> , 2017, 13, .	0.4	1
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115	Bayesian nonparametric clustering and association studies for candidate SNP observations. <i>International Journal of Approximate Reasoning</i> , 2017, 80, 19-35.	1.9	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.	3.5	89
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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.	1.1	8
123	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. <i>Genome Medicine</i> , 2017, 9, 97.	3.6	23
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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.	1.9	13
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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.	0.8	3



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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.	1.4	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.	0.9	6
131	Kernel machine methods for integrative analysis of genome-wide methylation and genotyping studies. <i>Genetic Epidemiology</i> , 2018, 42, 156-167.	0.6	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.	1.1	12
133	Insights of Acute Lymphoblastic Leukemia with Development of Genomic Investigation. <i>Methods in Molecular Biology</i> , 2018, 1754, 387-413.	0.4	1
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135	Probabilistic natural mapping of gene-level tests for genome-wide association studies. <i>Briefings in Bioinformatics</i> , 2018, 19, 545-553.	3.2	6
136	Power and sample size calculations for high-throughput sequencing-based experiments. <i>Briefings in Bioinformatics</i> , 2018, 19, 1247-1255.	3.2	32
137	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , 2018, 154, 719-722.e3.	0.6	38
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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.	1.1	1
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142	Linear mixed models for association analysis of quantitative traits with next-generation sequencing data. <i>Genetic Epidemiology</i> , 2019, 43, 189-206.	0.6	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.	1.5	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.	1.2	16
146	Genetic Determinants of IgA Nephropathy: Western Perspective. <i>Seminars in Nephrology</i> , 2018, 38, 443-454.	0.6	23

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148	A Survey of SNP Data Analysis. <i>Big Data Mining and Analytics</i> , 2018, 1, 173-190.	7.5	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.	1.4	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.	1.2	5
151	Frequency of Loss of Function Variants in <i>LRRK2</i> in Parkinson Disease. <i>JAMA Neurology</i> , 2018, 75, 1416.	4.5	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.	3.6	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.	1.1	3
154	Associations of MAP2K3 Gene Variants With Superior Memory in SuperAgers. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 155.	1.7	22
155	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid- $\beta$ accumulation in Alzheimer's disease. <i>Human Genetics</i> , 2018, 137, 521-533.	1.8	22
156	<i>CHCHD10</i> variants in amyotrophic lateral sclerosis: Where is the evidence?. <i>Annals of Neurology</i> , 2018, 84, 110-116.	2.8	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.	1.2	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.	0.3	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.	1.7	2
160	Mutation profiles and clinical characteristics of Chinese males with isolated hypogonadotropic hypogonadism. <i>Fertility and Sterility</i> , 2018, 110, 486-495.e5.	0.5	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.	1.4	13
162	Examining the role of common and rare mitochondrial variants in schizophrenia. <i>PLoS ONE</i> , 2018, 13, e0191153.	1.1	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.	2.7	35
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