Taesung Park

List of Publications by Citations

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

195 papers	6,767 citations	27 h-index	80 g-index
249 ext. papers	7,937 ext. citations	4.5 avg, IF	5.17 L-index

#	Paper	IF	Citations
195	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
194	A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. *Nature Genetics*, **2009**, 41, 527-34	36.3	822
193	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
192	Large-scale genome-wide association studies in East Asians identify new genetic loci influencing metabolic traits. *Nature Genetics*, **2011**, 43, 990-5	36.3	229
191	Statistical tests for identifying differentially expressed genes in time-course microarray experiments. *Bioinformatics*, **2003**, 19, 694-703	7.2	136
190	Odds ratio based multifactor-dimensionality reduction method for detecting gene-gene interactions. *Bioinformatics*, **2007**, 23, 71-6	7.2	132
189	Evaluation of normalization methods for microarray data. *BMC Bioinformatics*, **2003**, 4, 33	3.6	102
188	Log-linear model-based multifactor dimensionality reduction method to detect gene gene interactions. *Bioinformatics*, **2007**, 23, 2589-95	7.2	72
187	HNF4 is a therapeutic target that links AMPK to WNT signalling in early-stage gastric cancer. *Gut*, **2016**, 65, 19-32	19.2	69
186	Personalized identification of altered pathways in cancer using accumulated normal tissue data. *Bioinformatics*, **2014**, 30, i422-9	7.2	64
185	Joint identification of multiple genetic variants via elastic-net variable selection in a genome-wide association analysis. *Annals of Human Genetics*, **2010**, 74, 416-28	2.2	64
184	Large-scale genome-wide association study of Asian population reveals genetic factors in FRMD4A and other loci influencing smoking initiation and nicotine dependence. *Human Genetics*, **2012**, 131, 1009-21	6.3	48
183	A genome-wide scan for signatures of directional selection in domesticated pigs. *BMC Genomics*, **2015**, 16, 130	4.5	47
182	Associations of variants in CHRNA5/A3/B4 gene cluster with smoking behaviors in a Korean population. *PLoS ONE*, **2010**, 5, e12183	3.7	47
181	Clinical implication of serum carcinoembryonic antigen and carbohydrate antigen 19-9 for the prediction of malignancy in intraductal papillary mucinous neoplasm of pancreas. *Journal of Hepato-Biliary-Pancreatic Sciences*, **2015**, 22, 699-707	2.8	43
180	Molecular subtypes of pancreatic cancer based on miRNA expression profiles have independent prognostic value. *Journal of Gastroenterology and Hepatology (Australia)*, **2016**, 31, 1160-7	4	37
179	A novel method to identify high order gene-gene interactions in genome-wide association studies: gene-based MDR. *BMC Bioinformatics*, **2012**, 13 Suppl 9, S5	3.6	37

178	Enhancing inhibitory synaptic function reverses spatial memory deficits in Shank2 mutant mice. *Neuropharmacology*, **2017**, 112, 104-112	5.5	37
177	Caryophyllene potently inhibits solid tumor growth and lymph node metastasis of B16F10 melanoma cells in high-fat diet-induced obese C57BL/6N mice. *Carcinogenesis*, **2015**, 36, 1028-39	4.6	34
176	Combining multiple microarrays in the presence of controlling variables. *Bioinformatics*, **2006**, 22, 1682-9	7.2	33
175	Circulating Microbiota-Based Metagenomic Signature for Detection of Hepatocellular Carcinoma. *Scientific Reports*, **2019**, 9, 7536	4.9	31
174	Gene-gene interaction analysis for the survival phenotype based on the Cox model. *Bioinformatics*, **2012**, 28, i582-i588	7.2	31
173	Serum fibronectin distinguishes the early stages of hepatocellular carcinoma. *Scientific Reports*, **2017**, 7, 9449	4.9	30
172	Comprehensive Metabolomic Search for Biomarkers to Differentiate Early Stage Hepatocellular Carcinoma from Cirrhosis. *Cancers*, **2019**, 11,	6.6	29
171	Covariance models for nested repeated measures data: analysis of ovarian steroid secretion data. *Statistics in Medicine*, **2002**, 21, 143-64	2.3	29
170	Association between mutations of critical pathway genes and survival outcomes according to the tumor location in colorectal cancer. *Cancer*, **2017**, 123, 3513-3523	6.4	27
169	Definition of smad3 phosphorylation events that affect malignant and metastatic behaviors in breast cancer cells. *Cancer Research*, **2014**, 74, 6139-49	10.1	27
168	Relationship between thyroid-stimulating hormone levels and risk of depression among the general population with normal free T4 levels. *Psychoneuroendocrinology*, **2015**, 58, 114-9	5	26
167	Clinical Characteristics and Outcomes of COVID-19 Cohort Patients in Daegu Metropolitan City Outbreak in 2020. *Journal of Korean Medical Science*, **2021**, 36, e12	4.7	25
166	Pathway-based approach using hierarchical components of collapsed rare variants. *Bioinformatics*, **2016**, 32, i586-i594	7.2	23
165	Nonsynonymous Variants in and Are Associated With Type 2 Diabetes in an East Asian Population. *Diabetes*, **2018**, 67, 1892-1902	0.9	23
164	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
163	Development of Diagnostic Biomarkers for Detecting Diabetic Retinopathy at Early Stages Using Quantitative Proteomics. *Journal of Diabetes Research*, **2016**, 2016, 6571976	3.9	22
162	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 379-384	11.5	21
161	An empirical fuzzy multifactor dimensionality reduction method for detecting gene-gene interactions. *BMC Genomics*, **2017**, 18, 115	4.5	21

160	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics*, **2016**, 25, 2070-2081	5.6	20
159	FARVAT: a family-based rare variant association test. *Bioinformatics*, **2014**, 30, 3197-205	7.2	20
158	Diagnostic performance enhancement of pancreatic cancer using proteomic multimarker panel. *Oncotarget*, **2017**, 8, 93117-93130	3.3	20
157	A modified entropy-based approach for identifying gene-gene interactions in case-control study. *PLoS ONE*, **2013**, 8, e69321	3.7	20
156	Identification of gene-gene interactions in the presence of missing data using the multifactor dimensionality reduction method. *Genetic Epidemiology*, **2009**, 33, 646-56	2.6	20
155	Association between ST8SIA2 and the Risk of Schizophrenia and Bipolar I Disorder across Diagnostic Boundaries. *PLoS ONE*, **2015**, 10, e0139413	3.7	19
154	Seasonality and its distinct clinical correlates in bipolar II disorder. *Psychiatry Research*, **2015**, 225, 540-4	9.9	18
153	A unified model based multifactor dimensionality reduction framework for detecting gene-gene interactions. *Bioinformatics*, **2016**, 32, i605-i610	7.2	18
152	Effects of covariance model assumptions on hypothesis tests for repeated measurements: analysis of ovarian hormone data and pituitary-pteryomaxillary distance data. *Statistics in Medicine*, **2001**, 20, 2441-53	2.3	17
151	Analysis of population-specific pharmacogenomic variants using next-generation sequencing data. *Scientific Reports*, **2017**, 7, 8416	4.9	16
150	Simple pattern-mixture models for longitudinal data with missing observations: analysis of urinary incontinence data. *Statistics in Medicine*, **1999**, 18, 2933-41	2.3	16
149	Longitudinal analysis to better characterize Asthma-COPD overlap syndrome: Findings from an adult asthma cohort in Korea (COREA). *Clinical and Experimental Allergy*, **2019**, 49, 603-614	4.1	15
148	Pathway-Driven Approaches of Interaction between Oxidative Balance and Genetic Polymorphism on Metabolic Syndrome. *Oxidative Medicine and Cellular Longevity*, **2017**, 2017, 6873197	6.7	15
147	New Common and Rare Variants Influencing Metabolic Syndrome and Its Individual Components in a Korean Population. *Scientific Reports*, **2018**, 8, 5701	4.9	15
146	Rare variant association test with multiple phenotypes. *Genetic Epidemiology*, **2017**, 41, 198-209	2.6	14
145	Cancer survival classification using integrated data sets and intermediate information. *Artificial Intelligence in Medicine*, **2014**, 62, 23-31	7.4	14
144	Multivariate generalized multifactor dimensionality reduction to detect gene-gene interactions. *BMC Systems Biology*, **2013**, 7 Suppl 6, S15	3.5	14
143	Ceruloplasmin as a prognostic marker in patients with bile duct cancer. *Oncotarget*, **2017**, 8, 29028-29037	3.3	14

142	Clinical validation of the 2017 international consensus guidelines on intraductal papillary mucinous neoplasm of the pancreas. *Annals of Surgical Treatment and Research*, **2019**, 97, 58-64	2	14
141	Multivariate Quantitative Multifactor Dimensionality Reduction for Detecting Gene-Gene Interactions. *Human Heredity*, **2015**, 79, 168-81	1.1	13
140	Long-term response to mood stabilizer treatment and its clinical correlates in patients with bipolar disorders: a retrospective observational study. *International Journal of Bipolar Disorders*, **2017**, 5, 24	5.4	13
139	Practical issues in genome-wide association studies for physical activity. *Annals of the New York Academy of Sciences*, **2011**, 1229, 38-44	6.5	13
138	Integration of Traditional and Metabolomics Biomarkers Identifies Prognostic Metabolites for Predicting Responsiveness to Nutritional Intervention against Oxidative Stress and Inflammation. *Nutrients*, **2017**, 9,	6.7	12
137	Statistical analysis of MMR vaccine adverse events on aseptic meningitis using the case cross-over design. *Statistics in Medicine*, **2004**, 23, 1871-83	2.3	12
136	A novel fuzzy set based multifactor dimensionality reduction method for detecting gene-gene interaction. *Computational Biology and Chemistry*, **2016**, 65, 193-202	3.6	12
135	Heavy metal accumulation in and food safety of shark meat from Jeju island, Republic of Korea. *PLoS ONE*, **2019**, 14, e0212410	3.7	11
134	Hierarchical structural component modeling of microRNA-mRNA integration analysis. *BMC Bioinformatics*, **2018**, 19, 75	3.6	11
133	Joint identification of genetic variants for physical activity in Korean population. *International Journal of Molecular Sciences*, **2014**, 15, 12407-21	6.3	11
132	Systematic approach identifies RHOA as a potential biomarker therapeutic target for Asian gastric cancer. *Oncotarget*, **2016**, 7, 81435-81451	3.3	11
131	22q11-q13 as a hot spot for prediction of disease-free survival in bile duct cancer: integrative analysis of copy number variations. *Cancer Genetics*, **2014**, 207, 57-69	2.3	10
130	Prevalence, behavioral manifestations and associated individual and climatic factors of seasonality in the Korean general population. *Comprehensive Psychiatry*, **2015**, 57, 148-54	7.3	10
129	Clinical validation of scoring systems of postoperative pancreatic fistula after pancreatoduodenectomy: applicability to Eastern cohorts?. *Hepatobiliary Surgery and Nutrition*, **2019**, 8, 211-218	2.1	9
128	Metagenomic Analysis of Serum Microbe-Derived Extracellular Vesicles and Diagnostic Models to Differentiate Ovarian Cancer and Benign Ovarian Tumor. *Cancers*, **2020**, 12,	6.6	9
127	Calibration of High-Density Lipoprotein Cholesterol Values From the Korea National Health and Nutrition Examination Survey Data, 2008 to 2015. *Annals of Laboratory Medicine*, **2017**, 37, 1-8	3.1	9
126	Diagnostic plots for detecting outlying slides in a cDNA microarray experiment. *BioTechniques*, **2005**, 38, 463-71	2.5	9
125	Development of Web-Based Nomograms to Predict Treatment Response and Prognosis of Epithelial Ovarian Cancer. *Cancer Research and Treatment*, **2019**, 51, 1144-1155	5.2	9

124	Risk Prediction Using Genome-Wide Association Studies on Type 2 Diabetes. *Genomics and Informatics*, **2016**, 14, 138-148	1.9	9
123	Detecting differential DNA methylation from sequencing of bisulfite converted DNA of diverse species. *Briefings in Bioinformatics*, **2019**, 20, 33-46	13.4	9
122	Association of an IGHV3-66 gene variant with Kawasaki disease. *Journal of Human Genetics*, **2021**, 66, 475-489	4.3	9
121	Association between the zinc finger protein 804A (ZNF804A) gene and the risk of schizophrenia and bipolar I disorder across diagnostic boundaries. *Bipolar Disorders*, **2017**, 19, 305-313	3.8	8
120	Novel Trajectories for Identifying Asthma Phenotypes: A Longitudinal Study in Korean Asthma Cohort, COREA. *Journal of Allergy and Clinical Immunology: in Practice*, **2019**, 7, 1850-1857.e4	5.4	8
119	Bis-class: a new classification tool of methylation status using bayes classifier and local methylation information. *BMC Genomics*, **2014**, 15, 608	4.5	8
118	Error-pooling-based statistical methods for identifying novel temporal replication profiles of human chromosomes observed by DNA tiling arrays. *Nucleic Acids Research*, **2007**, 35, e69	20.1	8
117	Joint Modelling of Repeated Measures and Survival Time Data. *Biometrical Journal*, **2003**, 45, 647-658	1.5	8
116	HisCoM-GGI: Hierarchical structural component analysis of gene-gene interactions. *Journal of Bioinformatics and Computational Biology*, **2018**, 16, 1840026	1	8
115	Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. *BMC Medical Genetics*, **2015**, 16, 62	2.1	7
114	Fuzzy set-based generalized multifactor dimensionality reduction analysis of gene-gene interactions. *BMC Medical Genomics*, **2018**, 11, 32	3.7	7
113	WISARD: workbench for integrated superfast association studies for related datasets. *BMC Medical Genomics*, **2018**, 11, 39	3.7	7
112	Improving Disease Prediction by Incorporating Family Disease History in Risk Prediction Models with Large-Scale Genetic Data. *Genetics*, **2017**, 207, 1147-1155	4	7
111	A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. *BMC Genomics*, **2015**, 16, 1109	4.5	7
110	Two simple algorithms on linear combination of multiple biomarkers to maximize partial area under the ROC curve. *Computational Statistics and Data Analysis*, **2015**, 88, 15-27	1.6	7
109	Bayesian methods for contingency tables using Gibbs sampling. *Statistical Papers*, **2004**, 45, 33-50	1	7
108	Effects of genetic variants of ST8SIA2 and NCAM1 genes on seasonal mood changes and circadian preference in the general population. *Chronobiology International*, **2018**, 35, 405-415	3.6	7
107	A Comparative Study on Multifactor Dimensionality Reduction Methods for Detecting Gene-Gene Interactions with the Survival Phenotype. *BioMed Research International*, **2015**, 2015, 671859	3	6

106	Robust Gene-Gene Interaction Analysis in Genome Wide Association Studies. *PLoS ONE*, **2015**, 10, e0135816	3.7	6
105	Prediction of Quantitative Traits Using Common Genetic Variants: Application to Body Mass Index. *Genomics and Informatics*, **2016**, 14, 149-159	1.9	6
104	Gene-Gene Interaction Analysis for the Accelerated Failure Time Model Using a Unified Model-Based Multifactor Dimensionality Reduction Method. *Genomics and Informatics*, **2016**, 14, 166-172	1.9	6
103	Microbiome Markers of Pancreatic Cancer Based on Bacteria-Derived Extracellular Vesicles Acquired from Blood Samples: A Retrospective Propensity Score Matching Analysis. *Biology*, **2021**, 10,	4.9	6
102	Psychopathologic structure of bipolar disorders: exploring dimensional phenotypes, their relationships, and their associations with bipolar I and II disorders. *Psychological Medicine*, **2019**, 49, 2177-2185	6.9	6
101	Pathway analysis of rare variants for the clustered phenotypes by using hierarchical structured components analysis. *BMC Medical Genomics*, **2019**, 12, 100	3.7	5
100	Detecting Genetic Interactions for Quantitative Traits Using m-Spacing Entropy Measure. *BioMed Research International*, **2015**, 2015, 523641	3	5
99	Phenotype prediction from genome-wide association studies: application to smoking behaviors. *BMC Systems Biology*, **2012**, 6 Suppl 2, S11	3.5	5
98	Nuclear receptor and VEGF pathways for gene-blood lead interactions, on bone mineral density, in Korean smokers. *PLoS ONE*, **2018**, 13, e0193323	3.7	5
97	Prognostic significance of E-cadherin and ZEB1 expression in intraductal papillary mucinous neoplasm. *Oncotarget*, **2018**, 9, 306-320	3.3	5
96	Risk prediction for malignant intraductal papillary mucinous neoplasm of the pancreas: logistic regression versus machine learning. *Scientific Reports*, **2020**, 10, 20140	4.9	5
95	Analysis of multiple related phenotypes in genome-wide association studies. *Journal of Bioinformatics and Computational Biology*, **2016**, 14, 1644005	1	5
94	Functional conservation of sequence determinants at rapidly evolving regulatory regions across mammals. *PLoS Computational Biology*, **2018**, 14, e1006451	5	5
93	Gene-gene interaction analysis for quantitative trait using cluster-based multifactor dimensionality reduction method. *International Journal of Data Mining and Bioinformatics*, **2018**, 20, 1	0.5	5
92	GxGrare: gene-gene interaction analysis method for rare variants from high-throughput sequencing data. *BMC Systems Biology*, **2018**, 12, 19	3.5	4
91	Gene-set association tests for next-generation sequencing data. *Bioinformatics*, **2016**, 32, i611-i619	7.2	4
90	Comparing family-based rare variant association tests for dichotomous phenotypes. *BMC Proceedings*, **2016**, 10, 181-186	2.3	4
89	Practical issues in screening and variable selection in genome-wide association analysis. *Cancer Informatics*, **2014**, 13, 55-65	2.4	4

88	Generalized estimating equations with stabilized working correlation structure. *Computational Statistics and Data Analysis*, **2017**, 106, 1-11	1.6	4
87	On the use of working correlation matrices in the gee approach for longitudinal data. *Communications in Statistics Part B: Simulation and Computation*, **1999**, 28, 1011-1029	0.6	4
86	LPEseq: Local-Pooled-Error Test for RNA Sequencing Experiments with a Small Number of Replicates. *PLoS ONE*, **2016**, 11, e0159182	3.7	4
85	EFMDR-Fast: An Application of Empirical Fuzzy Multifactor Dimensionality Reduction for Fast Execution. *Genomics and Informatics*, **2018**, 16, e37	1.9	4
84	Confidence intervals for the COVID-19 neutralizing antibody retention rate in the Korean population. *Genomics and Informatics*, **2020**, 18, e31	1.9	4
83	Development of Machine Learning Models to Predict Platinum Sensitivity of High-Grade Serous Ovarian Carcinoma. *Cancers*, **2021**, 13,	6.6	4
82	Estimation of Undetected Asymptomatic COVID-19 Cases in South Korea Using a Probabilistic Model. *International Journal of Environmental Research and Public Health*, **2021**, 18,	4.6	4
81	The relationships of present vegetation, bacteria, and soil properties with soil organic matter characteristics in moist acidic tundra in Alaska. *Science of the Total Environment*, **2021**, 772, 145386	10.2	4
80	HisCoM-PAGE: Hierarchical Structural Component Models for Pathway Analysis of Gene Expression Data. *Genes*, **2019**, 10,	4.2	4
79	Diagnostic model for pancreatic cancer using a multi-biomarker panel. *Annals of Surgical Treatment and Research*, **2021**, 100, 144-153	2	4
78	Correlation estimation with singly truncated bivariate data. *Statistics in Medicine*, **2017**, 36, 1977-1988	2.3	3
77	Gene-Gene Interaction Analysis for the Survival Phenotype Based on the Kaplan-Meier Median Estimate. *BioMed Research International*, **2020**, 2020, 5282345	3	3
76	Multifactor dimensionality reduction analysis of multiple binary traits for gene-gene interaction. *International Journal of Data Mining and Bioinformatics*, **2016**, 14, 293	0.5	3
75	Multivariate Cluster-Based Multifactor Dimensionality Reduction to Identify Genetic Interactions for Multiple Quantitative Phenotypes. *BioMed Research International*, **2019**, 2019, 4578983	3	3
74	Proposal of the minimal number of retrieved regional lymph nodes for accurate staging of distal bile duct cancer and clinical validation of the three-tier lymph node staging system (AJCC 8th edition). *Journal of Hepato-Biliary-Pancreatic Sciences*, **2020**, 27, 75-83	2.8	3
73	PreCimp: Pre-collapsing imputation approach increases imputation accuracy of rare variants in terms of collapsed variables. *Genetic Epidemiology*, **2017**, 41, 41-50	2.6	3
72	An Efficient Stepwise Statistical Test to Identify Multiple Linked Human Genetic Variants Associated with Specific Phenotypic Traits. *PLoS ONE*, **2015**, 10, e0138700	3.7	3
71	Patterns of gene expression associated with Pten deficiency in the developing inner ear. *PLoS ONE*, **2014**, 9, e97544	3.7	3

70	CARAT-GxG: CUDA-Accelerated Regression Analysis Toolkit for Large-Scale Gene-Gene Interaction with GPU Computing System. *Cancer Informatics*, **2014**, 13, 27-33	2.4	3
69	Pathway-driven discovery of rare mutational impact on cancer. *BioMed Research International*, **2014**, 2014, 171892	3	3
68	Updated confidence intervals for the COVID-19 antibody retention rate in the Korean population. *Genomics and Informatics*, **2020**, 18, e45	1.9	3
67	Forecasting of the COVID-19 pandemic situation of Korea. *Genomics and Informatics*, **2021**, 19, e11	1.9	3
66	Prediction Models for the Clinical Severity of Patients With COVID-19 in Korea: Retrospective Multicenter Cohort Study. *Journal of Medical Internet Research*, **2021**, 23, e25852	7.6	3
65	Multi-biomarker panel prediction model for diagnosis of pancreatic cancer. *Journal of Hepato-Biliary-Pancreatic Sciences*, **2021**,	2.8	3
64	Using the Generalized Index of Dissimilarity to Detect Gene-Gene Interactions in Multi-Class Phenotypes. *PLoS ONE*, **2016**, 11, e0158668	3.7	3
63	FARVATX: Family-Based Rare Variant Association Test for X-Linked Genes. *Genetic Epidemiology*, **2016**, 40, 475-85	2.6	3
62	Fuzzy heaping mechanism for heaped count data with imprecision. *Soft Computing*, **2018**, 22, 4585-4594	3.5	3
61	Risk prediction of type 2 diabetes using common and rare variants. *International Journal of Data Mining and Bioinformatics*, **2018**, 20, 77	0.5	3
60	Unified Cox model based multifactor dimensionality reduction method for gene-gene interaction analysis of the survival phenotype. *BioData Mining*, **2018**, 11, 27	4.3	3
59	Structural equation modeling for hypertension and type 2 diabetes based on multiple SNPs and multiple phenotypes. *PLoS ONE*, **2019**, 14, e0217189	3.7	2
58	Integrative Analysis of Multi-Omics Data Based on Blockwise Sparse Principal Components. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	2
57	Hierarchical structural component model for pathway analysis of common variants. *BMC Medical Genomics*, **2020**, 13, 26	3.7	2
56	Statistical methods for metagenomics data analysis. *International Journal of Data Mining and Bioinformatics*, **2017**, 19, 366	0.5	2
55	VizEpis : A visualization and mapping tool for interpreting epistasis **2015**,		2
54	A chi-square test for detecting multiple joint genetic variants in genome-wide association studies **2011**,		2
53	Searching susceptibility genes for antipsychotic-induced weight gain: is the 5-HT2C receptor gene a promising candidate?. *Personalized Medicine*, **2007**, 4, 357-361	2.2	2

52	CONCORD biomarker prediction for novel drug introduction to different cancer types. *Oncotarget*, **2018**, 9, 1091-1106	3.3	2
51	Spatial rank-based multifactor dimensionality reduction to detect gene-gene interactions for multivariate phenotypes. *BMC Bioinformatics*, **2021**, 22, 480	3.6	2
50	The influences of DNA methylation and epigenetic clocks, on metabolic disease, in middle-aged Koreans. *Clinical Epigenetics*, **2020**, 12, 148	7.7	2
49	Pathway-Based Integrative Analysis of Metabolome and Microbiome Data from Hepatocellular Carcinoma and Liver Cirrhosis Patients. *Cancers*, **2020**, 12,	6.6	2
48	Changes in serum fibronectin levels predict tumor recurrence in patients with early hepatocellular carcinoma after curative treatment. *Scientific Reports*, **2020**, 10, 21313	4.9	2
47	Powerful p-value combination methods to detect incomplete association. *Scientific Reports*, **2021**, 11, 6980	4.9	2
46	Development and External Validation of Survival Prediction Model for Pancreatic Cancer Using Two Nationwide Databases: Surveillance, Epidemiology and End Results (SEER) and Korea Tumor Registry System-Biliary Pancreas (KOTUS-BP). *Gut and Liver*, **2021**, 15, 912-921	4.8	2
45	The Homocysteine and Metabolic Syndrome: A Mendelian Randomization Study. *Nutrients*, **2021**, 13,	6.7	2
44	Statistical Estimation of Effects of Implemented Government Policies on COVID-19 Situation in South Korea. *International Journal of Environmental Research and Public Health*, **2021**, 18,	4.6	2
43	Effect of Interaction between Early Menarche and Genetic Polymorphisms on Triglyceride. *Oxidative Medicine and Cellular Longevity*, **2019**, 2019, 9148920	6.7	1
42	Comparative studies for developing protein based cancer prediction model to maximise the ROC-AUC with various variable selection methods. *International Journal of Data Mining and Bioinformatics*, **2016**, 16, 64	0.5	1
41	Enhanced Permutation Tests via Multiple Pruning. *Frontiers in Genetics*, **2020**, 11, 509	4.5	1
40	Exact association test for small size sequencing data. *BMC Medical Genomics*, **2018**, 11, 30	3.7	1
39	Proposed new staging system for ampulla of Vater cancer with greater discriminatory ability: multinational study from eastern and western centers. *Journal of Hepato-Biliary-Pancreatic Sciences* , **2017**, 24, 475-484	2.8	1
38	Biomarker development for pancreatic ductal adenocarcinoma using integrated analysis of mRNA and miRNA expression **2014**,		1
37	Clinicopathologic and protein markers distinguishing the "polymerase epsilon exonuclease" from the "copy number low" subtype of endometrial cancer.. *Journal of Gynecologic Oncology*, **2022**,	4	1
36	Pure additive contribution of genetic variants to a risk prediction model using propensity score matching: application to type 2 diabetes. *Genomics and Informatics*, **2019**, 17, e47	1.9	1
35	Effects of government policies on the spread of COVID-19 worldwide. *Scientific Reports*, **2021**, 11, 20495	4.9	1

34	Editor’s Introduction to This Issue (G&I 16:4, 2018). *Genomics and Informatics*, **2018**, 16, e16	1.9	1
33	HisCoM-GGI: Software for Hierarchical Structural Component Analysis of Gene-Gene Interactions. *Genomics and Informatics*, **2018**, 16, e38	1.9	1
32	HisCoM-mimi: Software for Hierarchical Structural Component Analysis for miRNA-mRNA Integration Model for Binary Phenotypes. *Genomics and Informatics*, **2019**, 17, e10	1.9	1
31	Selection of differentially expressed gene in the colon of the mice fed high-fat diet associated with blood adipokine concentrations as early biomarkers of pathological changes. *FASEB Journal*, **2013**, 27, 865.3	0.9	1
30	Identification of genetic loci affecting body mass index through interaction with multiple environmental factors using structured linear mixed model. *Scientific Reports*, **2021**, 11, 5001	4.9	1
29	Inclusive Quantification Assay of Serum Des-γ-Carboxyprothrombin Proteoforms for Hepatocellular Carcinoma Surveillance by Targeted Mass Spectrometry. *Hepatology Communications*, **2021**, 5, 1767-1783	6	1
28	Which National Factors Are Most Influential in the Spread of COVID-19?. *International Journal of Environmental Research and Public Health*, **2021**, 18,	4.6	1
27	Develop Nomogram to Predict Malignancy of Intraductal Papillary Mucinous Neoplasm. *Methods in Molecular Biology*, **2019**, 1882, 23-32	1.4	1
26	Do we need to reconsider the CMAM admission and discharge criteria?; an analysis of CMAM data in South Sudan. *BMC Public Health*, **2020**, 20, 511	4.1	1
25	Meta-Qtest: meta-analysis of quadratic test for rare variants. *BMC Medical Genomics*, **2019**, 12, 102	3.7	0
24	Characterization and Validation of an "Acute Aerobic Exercise Load" as a Tool to Assess Antioxidative and Anti-inflammatory Nutrition in Healthy Subjects Using a Statistically Integrated Approach in a Comprehensive Clinical Trial. *Oxidative Medicine and Cellular Longevity*, **2019**, 2019, 9526725	6.7	0
23	Analysis of pharmacogenomic variants associated with population differentiation. *PLoS ONE*, **2015**, 10, e0119994	3.7	0
22	Genetic Association Analysis of Fasting and 1- and 2-Hour Glucose Tolerance Test Data Using a Generalized Index of Dissimilarity Measure for the Korean Population. *Genomics and Informatics*, **2016**, 14, 181-186	1.9	0
21	Identifying miRNA-mRNA Integration Set Associated With Survival Time. *Frontiers in Genetics*, **2021**, 12, 634922	4.5	0
20	Glycoprotein 96 polymorphisms are associated with the risk of systemic lupus erythematosus: A case-control study. *International Journal of Rheumatic Diseases*, **2019**, 22, 905-912	2.3	
19	Statistical analysis for aggregated count data in genetic association studies. *International Journal of Data Mining and Bioinformatics*, **2016**, 16, 77	0.5	
18	Correlation of Lifetime Symptom Dimensions with Cognitive Function and Other Clinical Characteristics in Schizophrenia Patients. *Korean Journal of Schizophrenia Research*, **2014**, 17, 72	0.7	
17	Multivariate Analysis of Microarray Data: Application of MANOVA **2010**, 151-166		

16	Statistical Models, Inference, and Algorithms for Large Biological Data Analysis **2010**, 185-199	
15	Spot intensity ratio statistics in two-channel microarray experiments. *Journal of Bioinformatics and Computational Biology*, **2007**, 5, 865-73	1
14	Mixed Models: Covariance Models for Nested Repeated Measures Data: Analysis of Ovarian Steroid Secretion Data **2005**, 187-208	
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