

Taesung Park

List of Publications by Year in descending order

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Version: 2024-02-01

239
papers

8,699
citations

159585

30
h-index

49909

87
g-index

249
all docs

249
docs citations

249
times ranked

16554
citing authors

#	ARTICLE	IF	CITATIONS
1	Development, validation, and comparison of a nomogram based on radiologic findings for predicting malignancy in intraductal papillary mucinous neoplasms of the pancreas: An international multicenter study. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2023, 30, 133-143.	2.6	7
2	Multi-omics biomarker panel prediction model for diagnosis of pancreatic cancer. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2023, 30, 122-132.	2.6	9
3	PATHOME-Drug: a subpathway-based polypharmacology drug-repositioning method. <i>Bioinformatics</i> , 2022, 38, 444-452.	4.1	5
4	Nonalcoholic fatty liver disease and early prediction of gestational diabetes mellitus using machine learning methods. <i>Clinical and Molecular Hepatology</i> , 2022, 28, 105-116.	8.9	9
5	Hierarchical Structured Component Analysis for Microbiome Data Using Taxonomy Assignments. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1302-1312.	3.0	0
6	Clinicopathologic and protein markers distinguishing the microsatellite instability-high subtype from the microsatellite stability subtype of endometrial cancer. <i>Journal of Gynecologic Oncology</i> , 2022, 33, .	2.2	6
7	Editorial introduction to this issue (Genomics and Informatics; 20:1, 2022). <i>Genomics and Informatics</i> , 2022, 20, e1.	0.8	0
8	Meta-Analysis of Randomized Clinical Trials Evaluating Effectiveness of a Multivitamin Supplementation against Oxidative Stress in Healthy Subjects. <i>Nutrients</i> , 2022, 14, 1170.	4.1	0
9	Transethnic meta-analysis of exome-wide variants identifies new loci associated with male-specific metabolic syndrome. <i>Genes and Genomics</i> , 2022, , 1.	1.4	0
10	Kernel-based hierarchical structural component models for pathway analysis. <i>Bioinformatics</i> , 2022, 38, 3078-3086.	4.1	2
11	Editorial: Current Status and Future Challenges of Biobank Data Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 882611.	2.3	0
12	Gene-environment interaction in type 2 diabetes in Korean cohorts: Interaction of a type 2 diabetes polygenic risk score with triglyceride and cholesterol on fasting glucose levels. <i>Genetic Epidemiology</i> , 2022, 46, 285-302.	1.3	0
13	Microbiome markers of pancreatic cancer based on bacteria-derived extracellular vesicles acquired from blood samples: A retrospective propensity score matching analysis. <i>Annals of Hepato-biliary-pancreatic Surgery</i> , 2022, 26, S55-S55.	0.1	0
14	Identification of the associations between genes and quantitative traits using entropy-based kernel density estimation. <i>Genomics and Informatics</i> , 2022, 20, e17.	0.8	1
15	Editorial introduction to this issue (Genomics and Informatics; 20:2, 2022). <i>Genomics and Informatics</i> , 2022, 20, e15.	0.8	0
16	Comparison of survival prediction models for pancreatic cancer: Cox model versus machine learning models. <i>Genomics and Informatics</i> , 2022, 20, e23.	0.8	4
17	Bayesian analysis of longitudinal traits in the Korea Association Resource (KARE) cohort. <i>Genomics and Informatics</i> , 2022, 20, e16.	0.8	0
18	Mathematical modeling of the impact of Omicron variant on the COVID-19 situation in South Korea. <i>Genomics and Informatics</i> , 2022, 20, e22.	0.8	2

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19	Association of an IGHV3-66 gene variant with Kawasaki disease. <i>Journal of Human Genetics</i> , 2021, 66, 475-489.	2.3	27
20	Diagnostic model for pancreatic cancer using a multi-biomarker panel. <i>Annals of Surgical Treatment and Research</i> , 2021, 100, 144.	1.0	7
21	Clinical Characteristics and Outcomes of COVID-19 Cohort Patients in Daegu Metropolitan City Outbreak in 2020. <i>Journal of Korean Medical Science</i> , 2021, 36, e12.	2.5	47
22	Statistical Estimation of Effects of Implemented Government Policies on COVID-19 Situation in South Korea. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 2144.	2.6	8
23	Identification of genetic loci affecting body mass index through interaction with multiple environmental factors using structured linear mixed model. <i>Scientific Reports</i> , 2021, 11, 5001.	3.3	1
24	Editor's introduction to this issue (G&I 19:1, 2021). <i>Genomics and Informatics</i> , 2021, 19, e1.	0.8	2
25	Forecasting of the COVID-19 pandemic situation of Korea. <i>Genomics and Informatics</i> , 2021, 19, e11.	0.8	4
26	Powerful p-value combination methods to detect incomplete association. <i>Scientific Reports</i> , 2021, 11, 6980.	3.3	35
27	Microbiome Markers of Pancreatic Cancer Based on Bacteria-Derived Extracellular Vesicles Acquired from Blood Samples: A Retrospective Propensity Score Matching Analysis. <i>Biology</i> , 2021, 10, 219.	2.8	20
28	Development of Machine Learning Models to Predict Platinum Sensitivity of High-Grade Serous Ovarian Carcinoma. <i>Cancers</i> , 2021, 13, 1875.	3.7	16
29	Prediction Models for the Clinical Severity of Patients With COVID-19 in Korea: Retrospective Multicenter Cohort Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e25852.	4.3	11
30	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). <i>Gut and Liver</i> , 2021, 15, 912-921.	2.9	6
31	Association between the Arylalkylamine N-Acetyltransferase (AANAT) Gene and Seasonality in Patients with Bipolar Disorder. <i>Psychiatry Investigation</i> , 2021, 18, 453-462.	1.6	2
32	Estimation of Undetected Asymptomatic COVID-19 Cases in South Korea Using a Probabilistic Model. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 4946.	2.6	8
33	The relationships of present vegetation, bacteria, and soil properties with soil organic matter characteristics in moist acidic tundra in Alaska. <i>Science of the Total Environment</i> , 2021, 772, 145386.	8.0	15
34	Identifying miRNA-mRNA Integration Set Associated With Survival Time. <i>Frontiers in Genetics</i> , 2021, 12, 634922.	2.3	1
35	Editor's introduction to this issue (G&I 19:2, 2021). <i>Genomics and Informatics</i> , 2021, 19, e12.	0.8	0
36	Inclusive Quantification Assay of Serum Des β -Carboxyprothrombin Proteoforms for Hepatocellular Carcinoma Surveillance by Targeted Mass Spectrometry. <i>Hepatology Communications</i> , 2021, 5, 1767-1783.	4.3	4

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37	Which National Factors Are Most Influential in the Spread of COVID-19?. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 7592.	2.6	3
38	The Homocysteine and Metabolic Syndrome: A Mendelian Randomization Study. <i>Nutrients</i> , 2021, 13, 2440.	4.1	9
39	Penalized generalized estimating equations approach to longitudinal data with multinomial responses. <i>Journal of the Korean Statistical Society</i> , 2021, 50, 844-859.	0.4	0
40	Effects of government policies on the spread of COVID-19 worldwide. <i>Scientific Reports</i> , 2021, 11, 20495.	3.3	21
41	Spatial rank-based multifactor dimensionality reduction to detect gene-gene interactions for multivariate phenotypes. <i>BMC Bioinformatics</i> , 2021, 22, 480.	2.6	3
42	Genome-wide association study identified a novel genetic variation in HLA DRB1 associated with drug hypersensitivity. <i>Annals of Allergy, Asthma and Immunology</i> , 2021, , .	1.0	2
43	Editor's introduction to this issue (G&I 19:4, 2021). <i>Genomics and Informatics</i> , 2021, 19, e35.	0.8	0
44	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). <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2020, 27, 75-83.	2.6	10
45	The influences of DNA methylation and epigenetic clocks, on metabolic disease, in middle-aged Koreans. <i>Clinical Epigenetics</i> , 2020, 12, 148.	4.1	9
46	Pathway-Based Integrative Analysis of Metabolome and Microbiome Data from Hepatocellular Carcinoma and Liver Cirrhosis Patients. <i>Cancers</i> , 2020, 12, 2705.	3.7	7
47	Risk prediction for malignant intraductal papillary mucinous neoplasm of the pancreas: logistic regression versus machine learning. <i>Scientific Reports</i> , 2020, 10, 20140.	3.3	11
48	Changes in serum fibronectin levels predict tumor recurrence in patients with early hepatocellular carcinoma after curative treatment. <i>Scientific Reports</i> , 2020, 10, 21313.	3.3	4
49	HisCoM-G&E: Hierarchical Structural Component Analysis of Gene-Based Gene-Environment Interactions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6724.	4.1	2
50	Integrative Analysis of Multi-Omics Data Based on Blockwise Sparse Principal Components. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8202.	4.1	9
51	Metagenomic Analysis of Serum Microbe-Derived Extracellular Vesicles and Diagnostic Models to Differentiate Ovarian Cancer and Benign Ovarian Tumor. <i>Cancers</i> , 2020, 12, 1309.	3.7	32
52	Gene-Gene Interaction Analysis for the Survival Phenotype Based on the Kaplan-Meier Median Estimate. <i>BioMed Research International</i> , 2020, 2020, 1-10.	1.9	5
53	Enhanced Permutation Tests via Multiple Pruning. <i>Frontiers in Genetics</i> , 2020, 11, 509.	2.3	4
54	Hierarchical structural component model for pathway analysis of common variants. <i>BMC Medical Genomics</i> , 2020, 13, 26.	1.5	3

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55	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.	2.9	4
56	Confidence intervals for the COVID-19 neutralizing antibody retention rate in the Korean population. Genomics and Informatics, 2020, 18, e31.	0.8	5
57	Updated confidence intervals for the COVID-19 antibody retention rate in the Korean population. Genomics and Informatics, 2020, 18, e45.	0.8	3
58	Editor's introduction to this issue (G&I 18:4, 2020). Genomics and Informatics, 2020, 18, e34.	0.8	0
59	HisCoM-PCA: software for hierarchical structural component analysis for pathway analysis based using principal component analysis. Genomics and Informatics, 2020, 18, e11.	0.8	0
60	Editor's introduction to this issue (G&I 18:1, 2020). Genomics and Informatics, 2020, 18, e1.	0.8	0
61	Editor's introduction to this issue (G&I 18:3, 2020). Genomics and Informatics, 2020, 18, e25.	0.8	0
62	Editor's introduction to this issue (G&I 18:3, 2020). Genomics and Informatics, 2020, 18, e25.	0.8	0
63	Multivariate Cluster-Based Multifactor Dimensionality Reduction to Identify Genetic Interactions for Multiple Quantitative Phenotypes. BioMed Research International, 2019, 2019, 1-10.	1.9	6
64	Pathway analysis of rare variants for the clustered phenotypes by using hierarchical structured components analysis. BMC Medical Genomics, 2019, 12, 100.	1.5	6
65	Meta-Qtest: meta-analysis of quadratic test for rare variants. BMC Medical Genomics, 2019, 12, 102.	1.5	2
66	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.	3.8	12
67	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, 1-14.	4.0	2
68	Structural equation modeling for hypertension and type 2 diabetes based on multiple SNPs and multiple phenotypes. PLoS ONE, 2019, 14, e0217189.	2.5	5
69	Comprehensive Metabolomic Search for Biomarkers to Differentiate Early Stage Hepatocellular Carcinoma from Cirrhosis. Cancers, 2019, 11, 1497.	3.7	63
70	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.	2.9	23
71	Clinical validation of scoring systems of postoperative pancreatic fistula after pancreatoduodenectomy: applicability to Eastern cohorts?. Hepatobiliary Surgery and Nutrition, 2019, 8, 211-218.	1.5	19
72	Circulating Microbiota-Based Metagenomic Signature for Detection of Hepatocellular Carcinoma. Scientific Reports, 2019, 9, 7536.	3.3	51

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73	Glycoprotein 96 polymorphisms are associated with the risk of systemic lupus erythematosus: A case-control study. <i>International Journal of Rheumatic Diseases</i> , 2019, 22, 905-912.	1.9	0
74	Heavy metal accumulation in and food safety of shark meat from Jeju island, Republic of Korea. <i>PLoS ONE</i> , 2019, 14, e0212410.	2.5	22
75	Effect of Interaction between Early Menarche and Genetic Polymorphisms on Triglyceride. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-9.	4.0	3
76	HisCoM-PAGE: Hierarchical Structural Component Models for Pathway Analysis of Gene Expression Data. <i>Genes</i> , 2019, 10, 931.	2.4	6
77	Psychopathologic structure of bipolar disorders: exploring dimensional phenotypes, their relationships, and their associations with bipolar I and II disorders. <i>Psychological Medicine</i> , 2019, 49, 2177-2185.	4.5	9
78	Develop Nomogram to Predict Malignancy of Intraductal Papillary Mucinous Neoplasm. <i>Methods in Molecular Biology</i> , 2019, 1882, 23-32.	0.9	3
79	Detecting differential DNA methylation from sequencing of bisulfite converted DNA of diverse species. <i>Briefings in Bioinformatics</i> , 2019, 20, 33-46.	6.5	17
80	Development of Web-Based Nomograms to Predict Treatment Response and Prognosis of Epithelial Ovarian Cancer. <i>Cancer Research and Treatment</i> , 2019, 51, 1144-1155.	3.0	17
81	Clinical validation of the 2017 international consensus guidelines on intraductal papillary mucinous neoplasm of the pancreas. <i>Annals of Surgical Treatment and Research</i> , 2019, 97, 58.	1.0	20
82	Pure additive contribution of genetic variants to a risk prediction model using propensity score matching: application to type 2 diabetes. <i>Genomics and Informatics</i> , 2019, 17, e47.	0.8	1
83	HisCoM-mimi: Software for Hierarchical Structural Component Analysis for miRNA-mRNA Integration Model for Binary Phenotypes. <i>Genomics and Informatics</i> , 2019, 17, e10.	0.8	1
84	In this issue, there are 10 articles: two review articles, six original articles, one clinical genomics, and one application note. <i>Genomics and Informatics</i> , 2019, 17, e1.	0.8	0
85	Editor's introduction to this issue (G&I 17:3, 2019). <i>Genomics and Informatics</i> , 2019, 17, e22.	0.8	0
86	Editor's introduction to this issue (G&I 17:4, 2019). <i>Genomics and Informatics</i> , 2019, 17, e35.	0.8	0
87	HisCoM-PAGE: software for hierarchical structural component models for pathway analysis of gene expression data. <i>Genomics and Informatics</i> , 2019, 17, e45.	0.8	0
88	New Common and Rare Variants Influencing Metabolic Syndrome and Its Individual Components in a Korean Population. <i>Scientific Reports</i> , 2018, 8, 5701.	3.3	20
89	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 379-384.	7.1	28
90	GxGrare: gene-gene interaction analysis method for rare variants from high-throughput sequencing data. <i>BMC Systems Biology</i> , 2018, 12, 19.	3.0	7

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91	Exact association test for small size sequencing data. BMC Medical Genomics, 2018, 11, 30.	1.5	1
92	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.	2.0	9
93	Fuzzy heaping mechanism for heaped count data with imprecision. Soft Computing, 2018, 22, 4585-4594.	3.6	3
94	Risk prediction of type 2 diabetes using common and rare variants. International Journal of Data Mining and Bioinformatics, 2018, 20, 77.	0.1	6
95	Detecting population structures by independent component analysis. , 2018, , .		1
96	Topological data analysis can extract subgroups with high incidence rates of Type 2 diabetes. , 2018, , .		0
97	HisCoM-GGI: Hierarchical structural component analysis of gene-gene interactions. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840026.	0.8	10
98	Analysis of significant protein abundance from multiple reaction-monitoring data. BMC Systems Biology, 2018, 12, 123.	3.0	0
99	Unified Cox model based multifactor dimensionality reduction method for gene-gene interaction analysis of the survival phenotype. BioData Mining, 2018, 11, 27.	4.0	4
100	Functional conservation of sequence determinants at rapidly evolving regulatory regions across mammals. PLoS Computational Biology, 2018, 14, e1006451.	3.2	8
101	Gene-gene interaction analysis for quantitative trait using cluster-based multifactor dimensionality reduction method. International Journal of Data Mining and Bioinformatics, 2018, 20, 1.	0.1	6
102	Nonsynonymous Variants in <i>PAX4</i> and <i>GLP1R</i> Are Associated With Type 2 Diabetes in an East Asian Population. Diabetes, 2018, 67, 1892-1902.	0.6	36
103	Fuzzy set-based generalized multifactor dimensionality reduction analysis of gene-gene interactions. BMC Medical Genomics, 2018, 11, 32.	1.5	8
104	WISARD: workbench for integrated superfast association studies for related datasets. BMC Medical Genomics, 2018, 11, 39.	1.5	11
105	Hierarchical structural component modeling of microRNA-mRNA integration analysis. BMC Bioinformatics, 2018, 19, 75.	2.6	17
106	Nuclear receptor and VEGF pathways for gene-blood lead interactions, on bone mineral density, in Korean smokers. PLoS ONE, 2018, 13, e0193323.	2.5	7
107	Prognostic significance of E-cadherin and ZEB1 expression in intraductal papillary mucinous neoplasm. Oncotarget, 2018, 9, 306-320.	1.8	5
108	CONCORD biomarker prediction for novel drug introduction to different cancer types. Oncotarget, 2018, 9, 1091-1106.	1.8	5

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109	EFMDR-Fast: An Application of Empirical Fuzzy Multifactor Dimensionality Reduction for Fast Execution. <i>Genomics and Informatics</i> , 2018, 16, e37.	0.8	4
110	Editor's Introduction to This Issue (G&I 16:4, 2018). <i>Genomics and Informatics</i> , 2018, 16, e16.	0.8	1
111	Ovarian Cancer Prognostic Prediction Model Using RNA Sequencing Data. <i>Genomics and Informatics</i> , 2018, 16, e32.	0.8	0
112	HisCoM-GGI: Software for Hierarchical Structural Component Analysis of Gene-Gene Interactions. <i>Genomics and Informatics</i> , 2018, 16, e38.	0.8	1
113	Integration of a Large-Scale Genetic Analysis Workbench Increases the Accessibility of a High-Performance Pathway-Based Analysis Method. <i>Genomics and Informatics</i> , 2018, 16, e39.	0.8	0
114	Rare variant association test with multiple phenotypes. <i>Genetic Epidemiology</i> , 2017, 41, 198-209.	1.3	21
115	Association between mutations of critical pathway genes and survival outcomes according to the tumor location in colorectal cancer. <i>Cancer</i> , 2017, 123, 3513-3523.	4.1	50
116	Association between the zinc finger protein 804A (<i>ZNF804A</i>) gene and the risk of schizophrenia and bipolar I disorder across diagnostic boundaries. <i>Bipolar Disorders</i> , 2017, 19, 305-313.	1.9	8
117	Correlation estimation with singly truncated bivariate data. <i>Statistics in Medicine</i> , 2017, 36, 1977-1988.	1.6	3
118	Serum fibronectin distinguishes the early stages of hepatocellular carcinoma. <i>Scientific Reports</i> , 2017, 7, 9449.	3.3	37
119	Improving Disease Prediction by Incorporating Family Disease History in Risk Prediction Models with Large-Scale Genetic Data. <i>Genetics</i> , 2017, 207, 1147-1155.	2.9	18
120	Analysis of population-specific pharmacogenomic variants using next-generation sequencing data. <i>Scientific Reports</i> , 2017, 7, 8416.	3.3	20
121	Proposed new staging system for ampulla of Vater cancer with greater discriminatory ability: multinational study from eastern and western centers. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2017, 24, 475-484.	2.6	3
122	An empirical fuzzy multifactor dimensionality reduction method for detecting gene-gene interactions. <i>BMC Genomics</i> , 2017, 18, 115.	2.8	26
123	PreCimp: Pre-collapsing imputation approach increases imputation accuracy of rare variants in terms of collapsed variables. <i>Genetic Epidemiology</i> , 2017, 41, 41-50.	1.3	3
124	Enhancing inhibitory synaptic function reverses spatial memory deficits in Shank2 mutant mice. <i>Neuropharmacology</i> , 2017, 112, 104-112.	4.1	56
125	Generalized estimating equations with stabilized working correlation structure. <i>Computational Statistics and Data Analysis</i> , 2017, 106, 1-11.	1.2	5
126	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31

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127	Risk prediction using common and rare genetic variants: Application to Type 2 diabetes. , 2017, , .		1
128	Sample size calculation for comparing multiple groups in cross-over designs. , 2017, , .		0
129	Cluster-based multifactor dimensionality reduction method to identify gene-gene interactions for quantitative traits in genome-wide studies. , 2017, , .		1
130	Diagnostic performance enhancement of pancreatic cancer using proteomic multimarker panel. Oncotarget, 2017, 8, 93117-93130.	1.8	28
131	Statistical methods for metagenomics data analysis. International Journal of Data Mining and Bioinformatics, 2017, 19, 366.	0.1	3
132	Integration of Traditional and Metabolomics Biomarkers Identifies Prognostic Metabolites for Predicting Responsiveness to Nutritional Intervention against Oxidative Stress and Inflammation. Nutrients, 2017, 9, 233.	4.1	18
133	Pathway-Driven Approaches of Interaction between Oxidative Balance and Genetic Polymorphism on Metabolic Syndrome. Oxidative Medicine and Cellular Longevity, 2017, 2017, 1-9.	4.0	28
134	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.	2.2	19
135	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.	2.5	11
136	Ceruloplasmin as a prognostic marker in patients with bile duct cancer. Oncotarget, 2017, 8, 29028-29037.	1.8	26
137	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.	0.1	1
138	Statistical analysis for aggregated count data in genetic association studies. International Journal of Data Mining and Bioinformatics, 2016, 16, 77.	0.1	0
139	Development of Diagnostic Biomarkers for Detecting Diabetic Retinopathy at Early Stages Using Quantitative Proteomics. Journal of Diabetes Research, 2016, 2016, 1-22.	2.3	28
140	Using the Generalized Index of Dissimilarity to Detect Gene-Gene Interactions in Multi-Class Phenotypes. PLoS ONE, 2016, 11, e0158668.	2.5	3
141	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
142	<i>FARVATX</i> : Family-Based Rare Variant Association Test for X-Linked Genes. Genetic Epidemiology, 2016, 40, 475-485.	1.3	5
143	Conditional estimation of local pooled dispersion parameter in small-sample RNA-Seq data improves differential expression test. Journal of Bioinformatics and Computational Biology, 2016, 14, 1644006.	0.8	0
144	Multivariate approach to the analysis of correlated RNA-seq data. , 2016, , .		1

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145	Analysis of multiple related phenotypes in genome-wide association studies. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1644005.	0.8	5
146	A novel fuzzy set based multifactor dimensionality reduction method for detecting gene-gene interaction. <i>Computational Biology and Chemistry</i> , 2016, 65, 193-202.	2.3	16
147	A unified model based multifactor dimensionality reduction framework for detecting gene-gene interactions. <i>Bioinformatics</i> , 2016, 32, i605-i610.	4.1	24
148	Gene-set association tests for next-generation sequencing data. <i>Bioinformatics</i> , 2016, 32, i611-i619.	4.1	7
149	Pathway-based approach using hierarchical components of collapsed rare variants. <i>Bioinformatics</i> , 2016, 32, i586-i594.	4.1	31
150	Multifactor dimensionality reduction analysis of multiple binary traits for gene-gene interaction. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 14, 293.	0.1	3
151	Comparing family-based rare variant association tests for dichotomous phenotypes. <i>BMC Proceedings</i> , 2016, 10, 181-186.	1.6	7
152	Molecular subtypes of pancreatic cancer based on miRNA expression profiles have independent prognostic value. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2016, 31, 1160-1167.	2.8	52
153	HNF4 α is a therapeutic target that links AMPK to WNT signalling in early-stage gastric cancer. <i>Gut</i> , 2016, 65, 19-32.	12.1	91
154	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	2.9	21
155	LPseq: Local-Pooled-Error Test for RNA Sequencing Experiments with a Small Number of Replicates. <i>PLoS ONE</i> , 2016, 11, e0159182.	2.5	7
156	Systematic approach identifies RHOA as a potential biomarker therapeutic target for Asian gastric cancer. <i>Oncotarget</i> , 2016, 7, 81435-81451.	1.8	17
157	Risk Prediction Using Genome-Wide Association Studies on Type 2 Diabetes. <i>Genomics and Informatics</i> , 2016, 14, 138.	0.8	10
158	Prediction of Quantitative Traits Using Common Genetic Variants: Application to Body Mass Index. <i>Genomics and Informatics</i> , 2016, 14, 149.	0.8	6
159	Gene-Gene Interaction Analysis for the Accelerated Failure Time Model Using a Unified Model-Based Multifactor Dimensionality Reduction Method. <i>Genomics and Informatics</i> , 2016, 14, 166.	0.8	7
160	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. <i>Genomics and Informatics</i> , 2016, 14, 181.	0.8	1
161	Editor's Introduction to This Issue. <i>Genomics and Informatics</i> , 2016, 14, 137.	0.8	0
162	Genetic association tests for cigarettes per day. , 2015, , .		0

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163	Clinical implication of serum carcinoembryonic antigen and carbohydrate antigen 19-9 for the prediction of malignancy in intraductal papillary mucinous neoplasm of pancreas. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2015, 22, 699-707.	2.6	65
164	A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. <i>BMC Genomics</i> , 2015, 16, 1109.	2.8	13
165	An Efficient Stepwise Statistical Test to Identify Multiple Linked Human Genetic Variants Associated with Specific Phenotypic Traits. <i>PLoS ONE</i> , 2015, 10, e0138700.	2.5	3
166	Statistical Analysis of High-Dimensional Genetic Data in Complex Traits. <i>BioMed Research International</i> , 2015, 2015, 1-2.	1.9	0
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