

Taesung Park

List of Publications by Year in descending order

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Version: 2024-02-01

239
papers

8,699
citations

159358

30
h-index

49773

87
g-index

249
all docs

249
docs citations

249
times ranked

16554
citing authors

#	ARTICLE	IF	CITATIONS
1	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	13.7	3,249
2	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
3	A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. <i>Nature Genetics</i> , 2009, 41, 527-534.	9.4	937
4	Large-scale genome-wide association studies in east Asians identify new genetic loci influencing metabolic traits. <i>Nature Genetics</i> , 2011, 43, 990-995.	9.4	270
5	Statistical tests for identifying differentially expressed genes in time-course microarray experiments. <i>Bioinformatics</i> , 2003, 19, 694-703.	1.8	152
6	Odds ratio based multifactor-dimensionality reduction method for detecting gene-gene interactions. <i>Bioinformatics</i> , 2007, 23, 71-76.	1.8	144
7	Evaluation of normalization methods for microarray data. <i>BMC Bioinformatics</i> , 2003, 4, 33.	1.2	136
8	HNF4 β is a therapeutic target that links AMPK to WNT signalling in early-stage gastric cancer. <i>Gut</i> , 2016, 65, 19-32.	6.1	91
9	Joint Identification of Multiple Genetic Variants via Elastic Net Variable Selection in a Genome-wide Association Analysis. <i>Annals of Human Genetics</i> , 2010, 74, 416-428.	0.3	84
10	Log-linear model-based multifactor dimensionality reduction method to detect gene-gene interactions. <i>Bioinformatics</i> , 2007, 23, 2589-2595.	1.8	82
11	Personalized identification of altered pathways in cancer using accumulated normal tissue data. <i>Bioinformatics</i> , 2014, 30, i422-i429.	1.8	78
12	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015, 16, 130.	1.2	67
13	A novel method to identify high order gene-gene interactions in genome-wide association studies: Gene-based MDR. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	66
14	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.	1.4	65
15	Comprehensive Metabolomic Search for Biomarkers to Differentiate Early Stage Hepatocellular Carcinoma from Cirrhosis. <i>Cancers</i> , 2019, 11, 1497.	1.7	63
16	Associations of Variants in CHRNA5/A3/B4 Gene Cluster with Smoking Behaviors in a Korean Population. <i>PLoS ONE</i> , 2010, 5, e12183.	1.1	57
17	Enhancing inhibitory synaptic function reverses spatial memory deficits in Shank2 mutant mice. <i>Neuropharmacology</i> , 2017, 112, 104-112.	2.0	56
18	Large-scale genome-wide association study of Asian population reveals genetic factors in FRMD4A and other loci influencing smoking initiation and nicotine dependence. <i>Human Genetics</i> , 2012, 131, 1009-1021.	1.8	52

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19	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.	1.4	52
20	Circulating Microbiota-Based Metagenomic Signature for Detection of Hepatocellular Carcinoma. <i>Scientific Reports</i> , 2019, 9, 7536.	1.6	51
21	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.	2.0	50
22	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.	1.1	47
23	Î ² -Caryophyllene potently inhibits solid tumor growth and lymph node metastasis of B16F10 melanoma cells in high-fat diet-induced obese C57BL/6N mice. <i>Carcinogenesis</i> , 2015, 36, 1028-1039.	1.3	44
24	Combining multiple microarrays in the presence of controlling variables. <i>Bioinformatics</i> , 2006, 22, 1682-1689.	1.8	37
25	Serum fibronectin distinguishes the early stages of hepatocellular carcinoma. <i>Scientific Reports</i> , 2017, 7, 9449.	1.6	37
26	Gene-gene interaction analysis for the survival phenotype based on the Cox model. <i>Bioinformatics</i> , 2012, 28, i582-i588.	1.8	36
27	Nonsynonymous Variants in <i>PAX4</i> and <i>GLP1R</i> Are Associated With Type 2 Diabetes in an East Asian Population. <i>Diabetes</i> , 2018, 67, 1892-1902.	0.3	36
28	Powerful p-value combination methods to detect incomplete association. <i>Scientific Reports</i> , 2021, 11, 6980.	1.6	35
29	FARVAT: a family-based rare variant association test. <i>Bioinformatics</i> , 2014, 30, 3197-3205.	1.8	34
30	Definition of Smad3 Phosphorylation Events That Affect Malignant and Metastatic Behaviors in Breast Cancer Cells. <i>Cancer Research</i> , 2014, 74, 6139-6149.	0.4	33
31	Covariance models for nested repeated measures data: analysis of ovarian steroid secretion data. <i>Statistics in Medicine</i> , 2002, 21, 143-164.	0.8	32
32	Relationship between thyroid-stimulating hormone levels and risk of depression among the general population with normal free T4 levels. <i>Psychoneuroendocrinology</i> , 2015, 58, 114-119.	1.3	32
33	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.	1.7	32
34	Pathway-based approach using hierarchical components of collapsed rare variants. <i>Bioinformatics</i> , 2016, 32, i586-i594.	1.8	31
35	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
36	Development of Diagnostic Biomarkers for Detecting Diabetic Retinopathy at Early Stages Using Quantitative Proteomics. <i>Journal of Diabetes Research</i> , 2016, 2016, 1-22.	1.0	28

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37	Diagnostic performance enhancement of pancreatic cancer using proteomic multimarker panel. <i>Oncotarget</i> , 2017, 8, 93117-93130.	0.8	28
38	Pathway-Driven Approaches of Interaction between Oxidative Balance and Genetic Polymorphism on Metabolic Syndrome. <i>Oxidative Medicine and Cellular Longevity</i> , 2017, 2017, 1-9.	1.9	28
39	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.	3.3	28
40	Association of an IGHV3-66 gene variant with Kawasaki disease. <i>Journal of Human Genetics</i> , 2021, 66, 475-489.	1.1	27
41	An empirical fuzzy multifactor dimensionality reduction method for detecting gene-gene interactions. <i>BMC Genomics</i> , 2017, 18, 115.	1.2	26
42	Ceruloplasmin as a prognostic marker in patients with bile duct cancer. <i>Oncotarget</i> , 2017, 8, 29028-29037.	0.8	26
43	A Modified Entropy-Based Approach for Identifying Gene-Gene Interactions in Case-Control Study. <i>PLoS ONE</i> , 2013, 8, e69321.	1.1	25
44	A unified model based multifactor dimensionality reduction framework for detecting gene-gene interactions. <i>Bioinformatics</i> , 2016, 32, i605-i610.	1.8	24
45	Longitudinal analysis to better characterize Asthma-COPD overlap syndrome: Findings from an adult asthma cohort in Korea (COREA). <i>Clinical and Experimental Allergy</i> , 2019, 49, 603-614.	1.4	23
46	Association between ST8SIA2 and the Risk of Schizophrenia and Bipolar I Disorder across Diagnostic Boundaries. <i>PLoS ONE</i> , 2015, 10, e0139413.	1.1	23
47	Identification of gene-gene interactions in the presence of missing data using the multifactor dimensionality reduction method. <i>Genetic Epidemiology</i> , 2009, 33, 646-656.	0.6	22
48	Seasonality and its distinct clinical correlates in bipolar II disorder. <i>Psychiatry Research</i> , 2015, 225, 540-544.	1.7	22
49	Heavy metal accumulation in and food safety of shark meat from Jeju island, Republic of Korea. <i>PLoS ONE</i> , 2019, 14, e0212410.	1.1	22
50	Multivariate generalized multifactor dimensionality reduction to detect gene-gene interactions. <i>BMC Systems Biology</i> , 2013, 7, S15.	3.0	21
51	Multivariate Quantitative Multifactor Dimensionality Reduction for Detecting Gene-Gene Interactions. <i>Human Heredity</i> , 2015, 79, 168-181.	0.4	21
52	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	1.4	21
53	Rare variant association test with multiple phenotypes. <i>Genetic Epidemiology</i> , 2017, 41, 198-209.	0.6	21
54	Effects of government policies on the spread of COVID-19 worldwide. <i>Scientific Reports</i> , 2021, 11, 20495.	1.6	21

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55	Analysis of population-specific pharmacogenomic variants using next-generation sequencing data. <i>Scientific Reports</i> , 2017, 7, 8416.	1.6	20
56	New Common and Rare Variants Influencing Metabolic Syndrome and Its Individual Components in a Korean Population. <i>Scientific Reports</i> , 2018, 8, 5701.	1.6	20
57	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.	1.3	20
58	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.	0.4	20
59	Effects of covariance model assumptions on hypothesis tests for repeated measurements: analysis of ovarian hormone data and pituitary-pteryomaxillary distance data. <i>Statistics in Medicine</i> , 2001, 20, 2441-2453.	0.8	19
60	Cancer survival classification using integrated data sets and intermediate information. <i>Artificial Intelligence in Medicine</i> , 2014, 62, 23-31.	3.8	19
61	Long-term response to mood stabilizer treatment and its clinical correlates in patients with bipolar disorders: a retrospective observational study. <i>International Journal of Bipolar Disorders</i> , 2017, 5, 24.	0.8	19
62	Clinical validation of scoring systems of postoperative pancreatic fistula after pancreatoduodenectomy: applicability to Eastern cohorts?. <i>Hepatobiliary Surgery and Nutrition</i> , 2019, 8, 211-218.	0.7	19
63	Simple pattern-mixture models for longitudinal data with missing observations: analysis of urinary incontinence data. , 1999, 18, 2933-2941.		18
64	Improving Disease Prediction by Incorporating Family Disease History in Risk Prediction Models with Large-Scale Genetic Data. <i>Genetics</i> , 2017, 207, 1147-1155.	1.2	18
65	Integration of Traditional and Metabolomics Biomarkers Identifies Prognostic Metabolites for Predicting Responsiveness to Nutritional Intervention against Oxidative Stress and Inflammation. <i>Nutrients</i> , 2017, 9, 233.	1.7	18
66	Hierarchical structural component modeling of microRNA-mRNA integration analysis. <i>BMC Bioinformatics</i> , 2018, 19, 75.	1.2	17
67	Detecting differential DNA methylation from sequencing of bisulfite converted DNA of diverse species. <i>Briefings in Bioinformatics</i> , 2019, 20, 33-46.	3.2	17
68	Systematic approach identifies RHOA as a potential biomarker therapeutic target for Asian gastric cancer. <i>Oncotarget</i> , 2016, 7, 81435-81451.	0.8	17
69	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.	1.3	17
70	Statistical analysis of MMR vaccine adverse events on aseptic meningitis using the case cross-over design. <i>Statistics in Medicine</i> , 2004, 23, 1871-1883.	0.8	16
71	Joint Identification of Genetic Variants for Physical Activity in Korean Population. <i>International Journal of Molecular Sciences</i> , 2014, 15, 12407-12421.	1.8	16
72	A novel fuzzy set based multifactor dimensionality reduction method for detecting gene-gene interaction. <i>Computational Biology and Chemistry</i> , 2016, 65, 193-202.	1.1	16

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73	Development of Machine Learning Models to Predict Platinum Sensitivity of High-Grade Serous Ovarian Carcinoma. <i>Cancers</i> , 2021, 13, 1875.	1.7	16
74	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.	3.9	15
75	22q11-q13 as a hot spot for prediction of disease-free survival in bile duct cancer: integrative analysis of copy number variations. <i>Cancer Genetics</i> , 2014, 207, 57-69.	0.2	14
76	Practical issues in genome-wide association studies for physical activity. <i>Annals of the New York Academy of Sciences</i> , 2011, 1229, 38-44.	1.8	13
77	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.	1.2	13
78	Bis-class: a new classification tool of methylation status using bayes classifier and local methylation information. <i>BMC Genomics</i> , 2014, 15, 608.	1.2	12
79	Novel Trajectories for Identifying Asthma Phenotypes: A Longitudinal Study in Korean Asthma Cohort, COREA. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2019, 7, 1850-1857.e4.	2.0	12
80	Prevalence, behavioral manifestations and associated individual and climatic factors of seasonality in the Korean general population. <i>Comprehensive Psychiatry</i> , 2015, 57, 148-154.	1.5	11
81	Calibration of High-Density Lipoprotein Cholesterol Values From the Korea National Health and Nutrition Examination Survey Data, 2008 to 2015. <i>Annals of Laboratory Medicine</i> , 2017, 37, 1-8.	1.2	11
82	WISARD: workbench for integrated superfast association studies for related datasets. <i>BMC Medical Genomics</i> , 2018, 11, 39.	0.7	11
83	Risk prediction for malignant intraductal papillary mucinous neoplasm of the pancreas: logistic regression versus machine learning. <i>Scientific Reports</i> , 2020, 10, 20140.	1.6	11
84	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.	2.1	11
85	Diagnostic plots for detecting outlying slides in a cDNA microarray experiment. <i>BioTechniques</i> , 2005, 38, 463-471.	0.8	10
86	Patterns of Gene Expression Associated with Pten Deficiency in the Developing Inner Ear. <i>PLoS ONE</i> , 2014, 9, e97544.	1.1	10
87	HisCoM-GGI: Hierarchical structural component analysis of gene-gene interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840026.	0.3	10
88	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.	1.4	10
89	Risk Prediction Using Genome-Wide Association Studies on Type 2 Diabetes. <i>Genomics and Informatics</i> , 2016, 14, 138.	0.4	10
90	Joint Modelling of Repeated Measures and Survival Time Data. <i>Biometrical Journal</i> , 2003, 45, 647-658.	0.6	9

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91	Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. BMC Medical Genetics, 2015, 16, 62.	2.1	9
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.	0.9	9
93	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.	2.7	9
94	The influences of DNA methylation and epigenetic clocks, on metabolic disease, in middle-aged Koreans. Clinical Epigenetics, 2020, 12, 148.	1.8	9
95	Integrative Analysis of Multi-Omics Data Based on Blockwise Sparse Principal Components. International Journal of Molecular Sciences, 2020, 21, 8202.	1.8	9
96	Multi-omic biomarker panel prediction model for diagnosis of pancreatic cancer. Journal of Hepato-Biliary-Pancreatic Sciences, 2023, 30, 122-132.	1.4	9
97	The Homocysteine and Metabolic Syndrome: A Mendelian Randomization Study. Nutrients, 2021, 13, 2440.	1.7	9
98	Nonalcoholic fatty liver disease and early prediction of gestational diabetes mellitus using machine learning methods. Clinical and Molecular Hepatology, 2022, 28, 105-116.	4.5	9
99	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.	6.5	8
100	A Comparative Study on Multifactor Dimensionality Reduction Methods for Detecting Gene-Gene Interactions with the Survival Phenotype. BioMed Research International, 2015, 2015, 1-7.	0.9	8
101	Association between the zinc finger protein 804A (<i>ZNF804A</i>) gene and the risk of schizophrenia and bipolar I disorder across diagnostic boundaries. Bipolar Disorders, 2017, 19, 305-313.	1.1	8
102	Functional conservation of sequence determinants at rapidly evolving regulatory regions across mammals. PLoS Computational Biology, 2018, 14, e1006451.	1.5	8
103	Fuzzy set-based generalized multifactor dimensionality reduction analysis of gene-gene interactions. BMC Medical Genomics, 2018, 11, 32.	0.7	8
104	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, 2144.	1.2	8
105	Estimation of Undetected Asymptomatic COVID-19 Cases in South Korea Using a Probabilistic Model. International Journal of Environmental Research and Public Health, 2021, 18, 4946.	1.2	8
106	Bayesian methods for contingency tables using Gibbs sampling. Statistical Papers, 2004, 45, 33-50.	0.7	7
107	Phenotype prediction from genome-wide association studies: application to smoking behaviors. BMC Systems Biology, 2012, 6, S11.	3.0	7
108	Detecting Genetic Interactions for Quantitative Traits Using m-Spacing Entropy Measure. BioMed Research International, 2015, 2015, 1-10.	0.9	7

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109	Two simple algorithms on linear combination of multiple biomarkers to maximize partial area under the ROC curve. <i>Computational Statistics and Data Analysis</i> , 2015, 88, 15-27.	0.7	7
110	Gene-set association tests for next-generation sequencing data. <i>Bioinformatics</i> , 2016, 32, i611-i619.	1.8	7
111	Comparing family-based rare variant association tests for dichotomous phenotypes. <i>BMC Proceedings</i> , 2016, 10, 181-186.	1.8	7
112	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
113	Pathway-Based Integrative Analysis of Metabolome and Microbiome Data from Hepatocellular Carcinoma and Liver Cirrhosis Patients. <i>Cancers</i> , 2020, 12, 2705.	1.7	7
114	Diagnostic model for pancreatic cancer using a multi-biomarker panel. <i>Annals of Surgical Treatment and Research</i> , 2021, 100, 144.	0.4	7
115	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.	1.4	7
116	LPEseq: Local-Pooled-Error Test for RNA Sequencing Experiments with a Small Number of Replicates. <i>PLoS ONE</i> , 2016, 11, e0159182.	1.1	7
117	Nuclear receptor and VEGF pathways for gene-blood lead interactions, on bone mineral density, in Korean smokers. <i>PLoS ONE</i> , 2018, 13, e0193323.	1.1	7
118	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.	0.4	7
119	On the use of working correlation matrices in the gee approach for longitudinal data. <i>Communications in Statistics Part B: Simulation and Computation</i> , 1999, 28, 1011-1029.	0.6	6
120	Risk prediction of type 2 diabetes using common and rare variants. <i>International Journal of Data Mining and Bioinformatics</i> , 2018, 20, 77.	0.1	6
121	Gene-gene interaction analysis for quantitative trait using cluster-based multifactor dimensionality reduction method. <i>International Journal of Data Mining and Bioinformatics</i> , 2018, 20, 1.	0.1	6
122	Multivariate Cluster-Based Multifactor Dimensionality Reduction to Identify Genetic Interactions for Multiple Quantitative Phenotypes. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	6
123	Pathway analysis of rare variants for the clustered phenotypes by using hierarchical structured components analysis. <i>BMC Medical Genomics</i> , 2019, 12, 100.	0.7	6
124	HisCoM-PAGE: Hierarchical Structural Component Models for Pathway Analysis of Gene Expression Data. <i>Genes</i> , 2019, 10, 931.	1.0	6
125	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.	1.4	6
126	Robust Gene-Gene Interaction Analysis in Genome Wide Association Studies. <i>PLoS ONE</i> , 2015, 10, e0135016.	1.1	6

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127	Prediction of Quantitative Traits Using Common Genetic Variants: Application to Body Mass Index. <i>Genomics and Informatics</i> , 2016, 14, 149.	0.4	6
128	Clinicopathologic and protein markers distinguishing the "polymerase epsilon exonuclease" from the "copy number low" subtype of endometrial cancer. <i>Journal of Gynecologic Oncology</i> , 2022, 33, .	1.0	6
129	<i>FARVATX</i> : Family-Based Rare Variant Association Test for X-Linked Genes. <i>Genetic Epidemiology</i> , 2016, 40, 475-485.	0.6	5
130	Analysis of multiple related phenotypes in genome-wide association studies. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1644005.	0.3	5
131	Generalized estimating equations with stabilized working correlation structure. <i>Computational Statistics and Data Analysis</i> , 2017, 106, 1-11.	0.7	5
132	Structural equation modeling for hypertension and type 2 diabetes based on multiple SNPs and multiple phenotypes. <i>PLoS ONE</i> , 2019, 14, e0217189.	1.1	5
133	Gene-Gene Interaction Analysis for the Survival Phenotype Based on the Kaplan-Meier Median Estimate. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	5
134	PATHOME-Drug: a subpathway-based polypharmacology drug-repositioning method. <i>Bioinformatics</i> , 2022, 38, 444-452.	1.8	5
135	Prognostic significance of E-cadherin and ZEB1 expression in intraductal papillary mucinous neoplasm. <i>Oncotarget</i> , 2018, 9, 306-320.	0.8	5
136	CONCORD biomarker prediction for novel drug introduction to different cancer types. <i>Oncotarget</i> , 2018, 9, 1091-1106.	0.8	5
137	Confidence intervals for the COVID-19 neutralizing antibody retention rate in the Korean population. <i>Genomics and Informatics</i> , 2020, 18, e31.	0.4	5
138	Practical Issues in Screening and Variable Selection in Genome-Wide Association Analysis. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16350.	0.9	4
139	Unified Cox model based multifactor dimensionality reduction method for gene-gene interaction analysis of the survival phenotype. <i>BioData Mining</i> , 2018, 11, 27.	2.2	4
140	Changes in serum fibronectin levels predict tumor recurrence in patients with early hepatocellular carcinoma after curative treatment. <i>Scientific Reports</i> , 2020, 10, 21313.	1.6	4
141	Enhanced Permutation Tests via Multiple Pruning. <i>Frontiers in Genetics</i> , 2020, 11, 509.	1.1	4
142	Do we need to reconsider the CMAM admission and discharge criteria?; an analysis of CMAM data in South Sudan. <i>BMC Public Health</i> , 2020, 20, 511.	1.2	4
143	Forecasting of the COVID-19 pandemic situation of Korea. <i>Genomics and Informatics</i> , 2021, 19, e11.	0.4	4
144	Inclusive Quantification Assay of Serum Des ¹³ -Carboxyprothrombin Proteoforms for Hepatocellular Carcinoma Surveillance by Targeted Mass Spectrometry. <i>Hepatology Communications</i> , 2021, 5, 1767-1783.	2.0	4

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145	EFMDR-Fast: An Application of Empirical Fuzzy Multifactor Dimensionality Reduction for Fast Execution. <i>Genomics and Informatics</i> , 2018, 16, e37.	0.4	4
146	Comparison of survival prediction models for pancreatic cancer: Cox model versus machine learning models. <i>Genomics and Informatics</i> , 2022, 20, e23.	0.4	4
147	A chi-square test for detecting multiple joint genetic variants in genome-wide association studies. , 2011, , .		3
148	CARAT-GxG: CUDA-Accelerated Regression Analysis Toolkit for Large-Scale Gene-Gene Interaction with GPU Computing System. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16349.	0.9	3
149	Pathway-Driven Discovery of Rare Mutational Impact on Cancer. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	3
150	An Efficient Stepwise Statistical Test to Identify Multiple Linked Human Genetic Variants Associated with Specific Phenotypic Traits. <i>PLoS ONE</i> , 2015, 10, e0138700.	1.1	3
151	Using the Generalized Index of Dissimilarity to Detect Gene-Gene Interactions in Multi-Class Phenotypes. <i>PLoS ONE</i> , 2016, 11, e0158668.	1.1	3
152	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
153	Correlation estimation with singly truncated bivariate data. <i>Statistics in Medicine</i> , 2017, 36, 1977-1988.	0.8	3
154	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.	1.4	3
155	PreCimp: Pre-collapsing imputation approach increases imputation accuracy of rare variants in terms of collapsed variables. <i>Genetic Epidemiology</i> , 2017, 41, 41-50.	0.6	3
156	Statistical methods for metagenomics data analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 19, 366.	0.1	3
157	Fuzzy heaping mechanism for heaped count data with imprecision. <i>Soft Computing</i> , 2018, 22, 4585-4594.	2.1	3
158	Effect of Interaction between Early Menarche and Genetic Polymorphisms on Triglyceride. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-9.	1.9	3
159	Develop Nomogram to Predict Malignancy of Intraductal Papillary Mucinous Neoplasm. <i>Methods in Molecular Biology</i> , 2019, 1882, 23-32.	0.4	3
160	Hierarchical structural component model for pathway analysis of common variants. <i>BMC Medical Genomics</i> , 2020, 13, 26.	0.7	3
161	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.	1.2	3
162	Updated confidence intervals for the COVID-19 antibody retention rate in the Korean population. <i>Genomics and Informatics</i> , 2020, 18, e45.	0.4	3

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