

# Yongkang Kim

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

1,856  
citations

516561

16  
h-index

289141

40  
g-index

68  
all docs

68  
docs citations

68  
times ranked

5358  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
2	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	9.4	142
3	Proposed Nomogram Predicting the Individual Risk of Malignancy in the Patients With Branch Duct Type Intraductal Papillary Mucinous Neoplasms of the Pancreas. <i>Annals of Surgery</i> , 2017, 266, 1062-1068.	2.1	110
4	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95
5	Î²-Caryophyllene potently inhibits solid tumor growth and lymph node metastasis of B16F10 melanoma cells in high-fat dietâ€‘induced obese C57BL/6N mice. <i>Carcinogenesis</i> , 2015, 36, 1028-1039.	1.3	44
6	Serum fibronectin distinguishes the early stages of hepatocellular carcinoma. <i>Scientific Reports</i> , 2017, 7, 9449.	1.6	37
7	Integrative analysis of multi-omics data for identifying multi-markers for diagnosing pancreatic cancer. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	35
8	Estimation of Parental Effects Using Polygenic Scores. <i>Behavior Genetics</i> , 2021, 51, 264-278.	1.4	34
9	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
10	Diagnostic performance enhancement of pancreatic cancer using proteomic multimarker panel. <i>Oncotarget</i> , 2017, 8, 93117-93130.	0.8	28
11	Ceruloplasmin as a prognostic marker in patients with bile duct cancer. <i>Oncotarget</i> , 2017, 8, 29028-29037.	0.8	26
12	Benzyl isothiocyanate suppresses highâ€‘fat dietâ€‘stimulated mammary tumor progression via the alteration of tumor microenvironments in obesityâ€‘resistant BALB/c mice. <i>Molecular Carcinogenesis</i> , 2015, 54, 72-82.	1.3	22
13	Rare variant association test with multiple phenotypes. <i>Genetic Epidemiology</i> , 2017, 41, 198-209.	0.6	21
14	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
15	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
16	Hierarchical structural component modeling of microRNA-mRNA integration analysis. <i>BMC Bioinformatics</i> , 2018, 19, 75.	1.2	17
17	Biomarker Development for Intraductal Papillary Mucinous Neoplasms Using Multiple Reaction Monitoring Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 100-113.	1.8	16
18	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

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19	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
20	HisCoM-GGI: Hierarchical structural component analysis of gene-gene interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840026.	0.3	10
21	Effects of genetic variants of ST8SIA2 and NCAM1 genes on seasonal mood changes and circadian preference in the general population. <i>Chronobiology International</i> , 2018, 35, 405-415.	0.9	9
22	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.	2.7	9
23	Bias and Precision of Parameter Estimates from Models Using Polygenic Scores to Estimate Environmental and Genetic Parental Influences. <i>Behavior Genetics</i> , 2021, 51, 279-288.	1.4	9
24	A Comparative Study on Multifactor Dimensionality Reduction Methods for Detecting Gene-Gene Interactions with the Survival Phenotype. <i>BioMed Research International</i> , 2015, 2015, 1-7.	0.9	8
25	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.	1.1	8
26	Diagnostic model for pancreatic cancer using a multi-biomarker panel. <i>Annals of Surgical Treatment and Research</i> , 2021, 100, 144.	0.4	7
27	Manikin Families Representing Obese Airline Passengers in the US. <i>Journal of Healthcare Engineering</i> , 2014, 5, 479-504.	1.1	6
28	Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes. <i>BMC Bioinformatics</i> , 2018, 19, 79.	1.2	6
29	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
30	HisCoM-PAGE: Hierarchical Structural Component Models for Pathway Analysis of Gene Expression Data. <i>Genes</i> , 2019, 10, 931.	1.0	6
31	Robust Gene-Gene Interaction Analysis in Genome Wide Association Studies. <i>PLoS ONE</i> , 2015, 10, e0135016.	1.1	6
32	Prognostic significance of E-cadherin and ZEB1 expression in intraductal papillary mucinous neoplasm. <i>Oncotarget</i> , 2018, 9, 306-320.	0.8	5
33	Practical Issues in Screening and Variable Selection in Genome-Wide Association Analysis. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16350.	0.9	4
34	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
35	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
36	Develop Nomogram to Predict Malignancy of Intraductal Papillary Mucinous Neoplasm. <i>Methods in Molecular Biology</i> , 2019, 1882, 23-32.	0.4	3

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37	Biomarker development for pancreatic ductal adenocarcinoma using integrated analysis of mRNA and miRNA expression. , 2014, , .		2
38	VizEpis : A visualization and mapping tool for interpreting epistasis. , 2015, , .		2
39	A Model-Based Joint Identification of Differentially Expressed Genes and Phenotype-Associated Genes. PLoS ONE, 2016, 11, e0149086.	1.1	2
40	Meta-Qtest: meta-analysis of quadratic test for rare variants. BMC Medical Genomics, 2019, 12, 102.	0.7	2
41	Association between the Arylalkylamine N-Acetyltransferase (AANAT) Gene and Seasonality in Patients with Bipolar Disorder. Psychiatry Investigation, 2021, 18, 453-462.	0.7	2
42	An Application of Regularized Extended Redundancy Analysis via Generalized Estimating Equations to the Study of Co-occurring Substance Use Among US Adults. Springer Proceedings in Mathematics and Statistics, 2020, , 365-376.	0.1	2
43	Developing cancer prediction model based on stepwise selection by AUC measure for proteomics data. , 2015, , .		1
44	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
45	Detecting population structures by independent component analysis. , 2018, , .		1
46	Identifying miRNA-mRNA Integration Set Associated With Survival Time. Frontiers in Genetics, 2021, 12, 634922.	1.1	1
47	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.	0.4	1
48	Topological data analysis can extract sub-groups with high incidence rates of Type 2 diabetes. International Journal of Data Mining and Bioinformatics, 2019, 22, 44.	0.1	1
49	HisCoM-mimi: Software for Hierarchical Structural Component Analysis for miRNA-mRNA Integration Model for Binary Phenotypes. Genomics and Informatics, 2019, 17, e10.	0.4	1
50	Identifying differentially expressed genes for ordinal phenotypes. , 2014, , .		0
51	Quality control plot for high dimensional omics data. , 2016, , .		0
52	Statistical quality control analysis of high-dimensional omics data. International Journal of Data Mining and Bioinformatics, 2017, 18, 210.	0.1	0
53	Topological data analysis can extract subgroups with high incidence rates of Type 2 diabetes. , 2018, , .		0
54	Analysis of significant protein abundance from multiple reaction-monitoring data. BMC Systems Biology, 2018, 12, 123.	3.0	0

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55	F133. Genetic Variations Within Acyl-CoA Synthetase Bubblegum Family Member 1 (ACSBG1) Gene Showed a Genome-Widely Significant Association With a Phenotype Dimension Characterized by Bulimic and Anxiety Comorbidities in Subjects With Bipolar Disorders. <i>Biological Psychiatry</i> , 2018, 83, S289.	0.7	0
56	F130. Association Study of Melatonin Pathway Genes With Seasonality and Circadian Preference in Bipolar Disorder. <i>Biological Psychiatry</i> , 2018, 83, S288.	0.7	0
57	Topological data analysis can extract sub-groups with high incidence rates of Type 2 diabetes. <i>International Journal of Data Mining and Bioinformatics</i> , 2019, 22, 44.	0.1	0
58	Development of a Nomogram Based on Radiologic Findings for Predicting Malignancy and Invasiveness in Intraductal Papillary Mucinous Neoplasms of the Pancreas: an International, Multicenter Study. <i>Hpb</i> , 2019, 21, S199-S200.	0.1	0
59	Comparative studies for developing protein based cancer prediction model to maximise the ROC-AUC with various variable selection methods. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 16, 64.	0.1	0
60	Statistical quality control analysis of high-dimensional omics data. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 18, 210.	0.1	0
61	Exploratory analysis for detecting population structures by iterative pruning based on independent component analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2019, 22, 61.	0.1	0