Sungkyoung Choi

List of Publications by Year
in descending order

32	319	933447 10	888059 17
papers	citations	h-index	g-index

33	33	33	1037
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Unraveling the Genomic Architecture of the CYP3A Locus and ADME Genes for Personalized Tacrolimus Dosing. Transplantation, 2021, 105, 2213-2225.	1.0	6
2	Molecular Diagnosis of Craniosynostosis Using Targeted Next-Generation Sequencing. Neurosurgery, 2020, 87, 294-302.	1.1	20
3	A Case-Centered Approach to Nursing Ethics Education: A Qualitative Study. International Journal of Environmental Research and Public Health, 2020, 17, 7748.	2.6	11
4	HisCoM-GÃ—E: Hierarchical Structural Component Analysis of Gene-Based Geneâ€“Environment Interactions. International Journal of Molecular Sciences, 2020, 21, 6724.	4.1	2
5	Determinants of Legislation on Social Health Insurance in Transition Countries. International Journal of Health Services, 2020, 52, 002073142095201.	2.5	1
6	Medicolegal lessons learned from thyroidectomy-related lawsuits: an analysis of judicial precedents in South Korea from 1998 to 2019. Gland Surgery, 2020, 9, 1286-1297.	1.1	1
7	Characterization and Validation of an â€œAcute Aerobic Exercise Loadâ€•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
8	Longitudinal analysis to better characterize Asthmaâ€COPD overlap syndrome: Findings from an adult asthma cohort in Korea (COREA). Clinical and Experimental Allergy, 2019, 49, 603-614.	2.9	23
9	HisCoM-PAGE: Hierarchical Structural Component Models for Pathway Analysis of Gene Expression Data. Genes, 2019, 10, 931.	2.4	6
10	The Scope of Practice for Registered Nurses in 64 South Korean Laws. Journal of Korean Academy of Nursing, 2019, 49, 760.	1.2	4
11	Development and validation of a scoring system for advanced colorectal neoplasm in young Korean subjects less than age 50 years. Intestinal Research, 2019, 17, 253-264.	2.6	13
12	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.	7.1	28
13	HisCoM-GGI: Hierarchical structural component analysis of geneâ€“gene interactions. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840026.	0.8	10
14	Drug response prediction model using a hierarchical structural component modeling method. BMC Bioinformatics, 2018, 19, 288.	2.6	1
15	Nonsynonymous Variants in PAX4 and GLP1R Are Associated With Type 2 Diabetes in an East Asian Population. Diabetes, 2018, 67, 1892-1902.	0.6	36
16	WISARD: workbench for integrated superfast association studies for related datasets. BMC Medical Genomics, 2018, 11, 39.	1.5	11
17	Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes. BMC Bioinformatics, 2018, 19, 79.	2.6	6
18	Hierarchical structural component modeling of microRNA-mRNA integration analysis. BMC Bioinformatics, 2018, 19, 75.	2.6	17

#	Article	IF	Citations
19	Targeted next-generation sequencing to identify genetic polymorphism associated with levetiracetam-induced psychosis. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2018, WCP2018, OR11-2.	0.0	0
20	HisCoM-GGI: Software for Hierarchical Structural Component Analysis of Gene-Gene Interactions. Genomics and Informatics, 2018, 16, e38.	0.8	1
21	Derivation and validation of a risk scoring model to predict advanced colorectal neoplasm in adults of all ages. Journal of Gastroenterology and Hepatology (Australia), 2017, 32, 1328-1335.	2.8	22
22	FARVATX: Familyâ€Based Rare Variant Association Test for Xâ€Linked Genes. Genetic Epidemiology, 2016, 40, 475-485.	1.3	5
23	Pathway-based approach using hierarchical components of collapsed rare variants. Bioinformatics, 2016, 32, i586-i594.	4.1	31
24	Comparing family-based rare variant association tests for dichotomous phenotypes. BMC Proceedings, 2016, 10, 181-186.	1.6	7
25	A post-hoc genome-wide association study using matched samples. International Journal of Data Mining and Bioinformatics, 2016, 14, 197.	0.1	0
26	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
27	Competitive pathway analysis using Structural Equation Models (CPA-SEM) for gene expression data. , 2015, , .		0
28	Robust analysis with related samples under the presence of population substructure and its application to body mass index. Genes and Genomics, 2014, 36, 643-654.	1.4	0
29	FARVAT: a family-based rare variant association test. Bioinformatics, 2014, 30, 3197-3205.	4.1	34
30	Genome-wide association analysis with matched samples discloses additional novel risk loci. , 2014, , .		0
31	Fine-scale mapping of disease susceptibility locus with Bayesian partition model. Genes and Genomics, 2012, 34, 401-407.	1.4	0
32	Robust analysis of related samples under the presence of population substructure. , 2011, , .		0