

Wonkuk Kim

List of Publications by Year in descending order

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26
papers

118
citations

1684188

5
h-index

1281871

11
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26
all docs

26
docs citations

26
times ranked

180
citing authors

#	ARTICLE	IF	CITATIONS
1	The Effects of SNP Genotyping Errors on the Power of The Cochran-Armitage Linear Trend Test for Case/Control Association Studies. <i>Annals of Human Genetics</i> , 2007, 71, 249-261.	0.8	36
2	Computing Power and Sample Size for Case-Control Association Studies with Copy Number Polymorphism: Application of Mixture-Based Likelihood Ratio Test. <i>PLoS ONE</i> , 2008, 3, e3475.	2.5	15
3	Genetic characteristics of non-familial epilepsy. <i>PeerJ</i> , 2019, 7, e8278.	2.0	15
4	Triple trajectories of alcohol use, tobacco use, and depressive symptoms as predictors of cannabis use disorders among urban adults.. <i>Psychology of Addictive Behaviors</i> , 2018, 32, 466-474.	2.1	12
5	Single-Variant and Multi-Variant Trend Tests for Genetic Association with Next-Generation Sequencing That Are Robust to Sequencing Error. <i>Human Heredity</i> , 2012, 74, 172-183.	0.8	10
6	Adolescent Risk and Protective Factors Predicting Triple Trajectories of Substance Use from Adolescence into Adulthood. <i>Journal of Child and Family Studies</i> , 2020, 29, 403-412.	1.3	6
7	Triple comorbid trajectories of alcohol, cigarette, and marijuana use from adolescence to adulthood predict insomnia in adulthood. <i>Addictive Behaviors</i> , 2019, 90, 437-443.	3.0	5
8	Transmission Disequilibrium Tests Based on Read Counts for Low-Coverage Next-Generation Sequence Data. <i>Human Heredity</i> , 2015, 80, 36-49.	0.8	4
9	Mixture modeling of microarray gene expression data. <i>BMC Proceedings</i> , 2007, 1, S50.	1.6	3
10	An Analytic Solution to the Computation of Power and Sample Size for Genetic Association Studies under a Pleiotropic Mode of Inheritance. <i>Human Heredity</i> , 2016, 81, 194-209.	0.8	3
11	Single and dual diagnoses of major depressive disorder and posttraumatic stress disorder predicted by triple comorbid trajectories of tobacco, alcohol, and marijuana use among urban adults. <i>Substance Abuse</i> , 2019, 40, 221-228.	2.3	3
12	Data mining of RNA expression and DNA genotype data: Presentation Group 5 contributions to Genetic Analysis Workshop 15. <i>Genetic Epidemiology</i> , 2007, 31, S43-S50.	1.3	1
13	A dose-response test via closed-form solutions for constrained MLEs in survival/sacrifice experiments. <i>Statistics in Medicine</i> , 2007, 26, 694-708.	1.6	1
14	Use of p-value plots to diagnose and remedy problems with statistical analysis of microarray data. <i>Genes and Genomics</i> , 2016, 38, 45-52.	1.4	1
15	Variance estimation by multivariate imputation methods in complex survey designs. <i>Model Assisted Statistics and Applications</i> , 2017, 12, 195-207.	0.3	1
16	Genetic association tests when a nuisance parameter is not identifiable under no association. <i>Communications for Statistical Applications and Methods</i> , 2017, 24, 663-671.	0.3	1
17	Latent Triple Trajectories of Substance use as Predictors for the Onset of Antisocial Personality Disorder among Urban African American and Puerto Rican Adults: A 22-Year Longitudinal Study. <i>Substance Abuse</i> , 2022, 43, 442-450.	2.3	1
18	Multifactor dimensionality reduction method based on area under receiver operating characteristic curve. <i>Model Assisted Statistics and Applications</i> , 2017, 12, 245-253.	0.3	0

#	ARTICLE	IF	CITATIONS
19	Robust Linear Trend Test for Low-Coverage Next-Generation Sequence Data Controlling for Covariates. <i>Mathematics</i> , 2020, 8, 217.	2.2	0
20	Correlates of Cannabis Use Disorders among urban women of color: childhood abuse, relationship with spouse/partner, and media exposure. <i>Journal of Substance Use</i> , 2021, 26, 132-137.	0.7	0
21	Introduction to Heterogeneity in Statistical Genetics. <i>Statistics in the Health Sciences</i> , 2020, , 1-51.	0.2	0
22	Threshold-Selected Quantitative Trait Loci and Pleiotropy. <i>Statistics in the Health Sciences</i> , 2020, , 323-341.	0.2	0
23	Bayesian information criterion accounting for the number of covariance parameters in mixed effects models. <i>Communications for Statistical Applications and Methods</i> , 2020, 27, 300-311.	0.3	0
24	Association Tests Allowing for Heterogeneity. <i>Statistics in the Health Sciences</i> , 2020, , 129-245.	0.2	0
25	Overview of Genomic Heterogeneity in Statistical Genetics. <i>Statistics in the Health Sciences</i> , 2020, , 53-97.	0.2	0
26	Designing Genetic Linkage and Association Studies that Maintain Desired Statistical Power in the Presence of Mixtures. <i>Statistics in the Health Sciences</i> , 2020, , 247-322.	0.2	0