

Wonkuk Kim

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

118
citations

1684188

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1281871

11
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26
all docs

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docs citations

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times ranked

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| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | 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. Substance Abuse, 2022, 43, 442-450. | 2.3 | 1 |
| 2 | Correlates of Cannabis Use Disorders among urban women of color: childhood abuse, relationship with spouse/partner, and media exposure. Journal of Substance Use, 2021, 26, 132-137. | 0.7 | 0 |
| 3 | Adolescent Risk and Protective Factors Predicting Triple Trajectories of Substance Use from Adolescence into Adulthood. Journal of Child and Family Studies, 2020, 29, 403-412. | 1.3 | 6 |
| 4 | Robust Linear Trend Test for Low-Coverage Next-Generation Sequence Data Controlling for Covariates. Mathematics, 2020, 8, 217. | 2.2 | 0 |
| 5 | Introduction to Heterogeneity in Statistical Genetics. Statistics in the Health Sciences, 2020, , 1-51. | 0.2 | 0 |
| 6 | Threshold-Selected Quantitative Trait Loci and Pleiotropy. Statistics in the Health Sciences, 2020, , 323-341. | 0.2 | 0 |
| 7 | Bayesian information criterion accounting for the number of covariance parameters in mixed effects models. Communications for Statistical Applications and Methods, 2020, 27, 300-311. | 0.3 | 0 |
| 8 | Association Tests Allowing for Heterogeneity. Statistics in the Health Sciences, 2020, , 129-245. | 0.2 | 0 |
| 9 | Overview of Genomic Heterogeneity in Statistical Genetics. Statistics in the Health Sciences, 2020, , 53-97. | 0.2 | 0 |
| 10 | Designing Genetic Linkage and Association Studies that Maintain Desired Statistical Power in the Presence of Mixtures. Statistics in the Health Sciences, 2020, , 247-322. | 0.2 | 0 |
| 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. Substance Abuse, 2019, 40, 221-228. | 2.3 | 3 |
| 12 | Triple comorbid trajectories of alcohol, cigarette, and marijuana use from adolescence to adulthood predict insomnia in adulthood. Addictive Behaviors, 2019, 90, 437-443. | 3.0 | 5 |
| 13 | Genetic characteristics of non-familial epilepsy. PeerJ, 2019, 7, e8278. | 2.0 | 15 |
| 14 | Triple trajectories of alcohol use, tobacco use, and depressive symptoms as predictors of cannabis use disorders among urban adults.. Psychology of Addictive Behaviors, 2018, 32, 466-474. | 2.1 | 12 |
| 15 | Variance estimation by multivariate imputation methods in complex survey designs. Model Assisted Statistics and Applications, 2017, 12, 195-207. | 0.3 | 1 |
| 16 | Multifactor dimensionality reduction method based on area under receiver operating characteristic curve. Model Assisted Statistics and Applications, 2017, 12, 245-253. | 0.3 | 0 |
| 17 | Genetic association tests when a nuisance parameter is not identifiable under no association. Communications for Statistical Applications and Methods, 2017, 24, 663-671. | 0.3 | 1 |
| 18 | An Analytic Solution to the Computation of Power and Sample Size for Genetic Association Studies under a Pleiotropic Mode of Inheritance. Human Heredity, 2016, 81, 194-209. | 0.8 | 3 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | Mixture modeling of microarray gene expression data. <i>BMC Proceedings</i> , 2007, 1, S50. | 1.6 | 3 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |