Seunggeun Lee

List of Publications by Year
in descending order

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50 papers	7,042 citations	279798 23 h-index	189892 50 g-index
72 all docs	72 docs citations	72 times ranked	12509 citing authors

#	Article	IF	Citations
1	NETMAGE: A human disease phenotype map generator for the network-based visualization of phenome-wide association study results. GigaScience, 2022, 11, .	6.4	5
2	Integrating external controls in caseâ€“control studies improves power for rareâ€variant tests. Genetic Epidemiology, 2022, 46, 145-158.	1.3	2
3	Trans-ethnic meta-analysis of rare variants in sequencing association studies. Biostatistics, 2021, 22, 706-722.	1.5	1
4	Novel score test to increase power in association test by integrating external controls. Genetic Epidemiology, 2021, 45, 293-304.	1.3	10
5	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. American Journal of Human Genetics, 2021, 108, 669-681.	6.2	8
6	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. American Journal of Human Genetics, 2021, 108, 825-839.	6.2	25
7	Scalable and Robust Regression Methods for Phenome-Wide Association Analysis on Large-Scale Biobank Data. Frontiers in Genetics, 2021, 12, 682638.	2.3	2
8	Understanding the Patterns of Serological Testing for COVID-19 Pre- and Post-Vaccination Rollout in Michigan. Journal of Clinical Medicine, 2021, 10, 4341.	2.4	3
9	On cross-ancestry cancer polygenic risk scores. PLoS Genetics, 2021, 17, e1009670.	3.5	32
10	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. American Journal of Human Genetics, 2020, 106, 3-12.	6.2	56
11	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. Nature Communications, 2020, 11, 4093.	12.8	24
12	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
13	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639.	21.4	124
14	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	21.4	129
15	Fast and robust ancestry prediction using principal component analysis. Bioinformatics, 2020, 36, 3439-3446.	4.1	21
16	A Fast and Accurate Method for Genome-Wide Time-to-Event Data Analysis and Its Application to UK Biobank. American Journal of Human Genetics, 2020, 107, 222-233.	6.2	57
17	Metaâ€MultiSKAT: Multiple phenotype metaâ€analysis for regionâ€based association test. Genetic Epidemiology, 2019, 43, 800-814.	1.3	9
18	A Fast and Accurate Method for Genome-wide Scale Phenome-wide G Ã— E Analysis and Its Application to UK Biobank. American Journal of Human Genetics, 2019, 105, 1182-1192.	6.2	20

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19	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. Nature Communications, 2019, 10, 1847.	12.8	55
20	Robust metaâ€analysis of biobankâ€based genomeâ€wide association studies with unbalanced binary phenotypes. Genetic Epidemiology, 2019, 43, 462-476.	1.3	7
21	Asymptotic properties of principal component analysis and shrinkage-bias adjustment under the generalized spiked population model. Journal of Multivariate Analysis, 2019, 173, 145-164.	1.0	6
22	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
23	Multiâ€SKAT: General framework to test for rareâ€variant association with multiple phenotypes. Genetic Epidemiology, 2019, 43, 4-23.	1.3	40
24	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. American Journal of Epidemiology, 2018, 187, 366-377.	3.4	8
25	Subset-Based Analysis Using Gene-Environment Interactions for Discovery of Genetic Associations across Multiple Studies or Phenotypes. Human Heredity, 2018, 83, 283-314.	0.8	5
26	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
27	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
28	Set-Based Tests for the Geneâ€“Environment Interaction in Longitudinal Studies. Journal of the American Statistical Association, 2017, 112, 966-978.	3.1	14
29	A Fast and Accurate Algorithm to Test for Binary Phenotypes and Its Application to PheWAS. American Journal of Human Genetics, 2017, 101, 37-49.	6.2	116
30	Rareâ€variant association tests in longitudinal studies, with an application to the Multiâ€Ethnic Study of Atherosclerosis (MESA). Genetic Epidemiology, 2017, 41, 801-810.	1.3	3
31	Unified Sequence-Based Association Tests Allowing for Multiple Functional Annotations and Meta-analysis of Noncoding Variation in Metabochip Data. American Journal of Human Genetics, 2017, 101, 340-352.	6.2	45
32	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 762-770.	3.4	79
33	Improving power for rareâ€variant tests by integrating external controls. Genetic Epidemiology, 2017, 41, 610-619.	1.3	18
34	Association analysis of rare variants near the APOE region with CSF and neuroimaging biomarkers of Alzheimerâ€™s disease. BMC Medical Genomics, 2017, 10, 29.	1.5	28
35	Knowledge-driven binning approach for rare variant association analysis: application to neuroimaging biomarkers in Alzheimerâ€™s disease. BMC Medical Informatics and Decision Making, 2017, 17, 61.	3.0	16
36	A Novel Random Effect Model for GWAS Meta-Analysis and Its Application to Trans-Ethnic Meta-Analysis. Biometrics, 2016, 72, 945-954.	1.4	17

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37	An efficient resampling method for calibrating single and gene-based rare variant association analysis in caseâ€“control studies. Biostatistics, 2016, 17, 1-15.	1.5	46
38	Applying Novel Methods for Assessing Individual- and Neighborhood-Level Social and Psychosocial Environment Interactions with Genetic Factors in the Prediction of Depressive Symptoms in the Multi-Ethnic Study of Atherosclerosis. Behavior Genetics, 2016, 46, 89-99.	2.1	8
39	Setâ€based tests for genetic association in longitudinal studies. Biometrics, 2015, 71, 606-615.	1.4	13
40	Evaluating the Calibration and Power of Three Gene-Based Association Tests of Rare Variants for the X Chromosome. Genetic Epidemiology, 2015, 39, 499-508.	1.3	12
41	Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT). Statistics and Its Interface, 2015, 8, 495-505.	0.3	11
42	Convergence of sample eigenvalues, eigenvectors, and principal component scores for ultra-high dimensional data. Biometrika, 2014, 101, 484-490.	2.4	18
43	General Framework for Meta-analysis of Rare Variants in Sequencing Association Studies. American Journal of Human Genetics, 2013, 93, 42-53.	6.2	211
44	Sequence Kernel Association Tests for the Combined Effect of Rare and Common Variants. American Journal of Human Genetics, 2013, 92, 841-853.	6.2	393
45	GEEâ€Based SNP Set Association Test for Continuous and Discrete Traits in Familyâ€Based Association Studies. Genetic Epidemiology, 2013, 37, 778-786.	1.3	55
46	Kernel Machine SNPâ€Set Testing Under Multiple Candidate Kernels. Genetic Epidemiology, 2013, 37, 267-275.	1.3	60
47	Optimal tests for rare variant effects in sequencing association studies. Biostatistics, 2012, 13, 762-775.	1.5	581
48	Optimal Unified Approach for Rare-Variant Association Testing with Application to Small-Sample Case-Control Whole-Exome Sequencing Studies. American Journal of Human Genetics, 2012, 91, 224-237.	6.2	880
49	Rare-Variant Association Testing for Sequencing Data with the Sequence Kernel Association Test. American Journal of Human Genetics, 2011, 89, 82-93.	6.2	2,060
50	Convergence and prediction of principal component scores in high-dimensional settings. Annals of Statistics, 2010, 38, 3605-3629.	2.6	60