

Jiwon Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4349181/publications.pdf>

Version: 2024-02-01

24
papers

1,109
citations

840119

11
h-index

580395

25
g-index

27
all docs

27
docs citations

27
times ranked

2060
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	3.0	29
2	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
3	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. <i>Sleep</i> , 2021, 44, .	0.6	5
4	Genome-wide association study of neck circumference identifies sex-specific loci independent of generalized adiposity. <i>International Journal of Obesity</i> , 2021, 45, 1532-1541.	1.6	8
5	Multi-ancestry genome-wide gene–sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	4.1	13
6	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	5.8	17
7	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. <i>American Journal of Epidemiology</i> , 2021, 190, 1977-1992.	1.6	29
8	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100040.	1.0	2
9	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003300.	1.6	7
10	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.	3.6	16
11	Evolutionary Characterization of the Short Protein SPAAR. <i>Genes</i> , 2021, 12, 1864.	1.0	3
12	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
13	The Role of Focal Epilepsy Features in Defining <i>SCN1A</i> Mutation-positive Dravet Syndrome as Generalized and Focal Epilepsy. <i>Journal of Epilepsy Research</i> , 2021, 11, 127-135.	0.1	3
14	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.	5.8	32
15	Clinical outcomes of pediatric Anti-NMDA receptor encephalitis. <i>European Journal of Paediatric Neurology</i> , 2020, 29, 87-91.	0.7	11
16	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
17	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020, 56, 102803.	2.7	7
18	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002772.	1.6	11

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19	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. <i>American Journal of Human Genetics</i> , 2020, 106, 112-120.	2.6	9
20	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	5.8	62
21	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. <i>American Journal of Human Genetics</i> , 2019, 105, 1057-1068.	2.6	10
22	Variants Associated with the Ankle Brachial Index Differ by Hispanic/Latino Ethnic Group: a genome-wide association study in the Hispanic Community Health Study/Study of Latinos. <i>Scientific Reports</i> , 2019, 9, 11410.	1.6	10
23	Associations of variants in the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. <i>PLoS Genetics</i> , 2019, 15, e1007739.	1.5	28
24	The ketogenic diet for super-refractory status epilepticus patients in intensive care units. <i>Brain and Development</i> , 2019, 41, 420-427.	0.6	39