Jiwon Lee

List of Publications by Year in descending order

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

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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	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
2	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
3	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	5.8	62
4	The ketogenic diet for super-refractory status epilepticus patients in intensive care units. Brain and Development, 2019, 41, 420-427.	0.6	39
5	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
6	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	1.6	29
7	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
8	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
9	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
10	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
11	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
12	Multi-ancestry genome-wide geneâ€"sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
13	Clinical outcomes of pediatric Anti-NMDA receptor encephalitis. European Journal of Paediatric Neurology, 2020, 29, 87-91.	0.7	11
14	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	1.6	11
15	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	2.6	10
16	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. Scientific Reports, 2019, 9, 11410.	1.6	10
17	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
18	Genome-wide association study of neck circumference identifies sex-specific loci independent of generalized adiposity. International Journal of Obesity, 2021, 45, 1532-1541.	1.6	8

#	Article	IF	Citations
19	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. EBioMedicine, 2020, 56, 102803.	2.7	7
20	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	1.6	7
21	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. Sleep, 2021, 44, .	0.6	5
22	Evolutionary Characterization of the Short Protein SPAAR. Genes, 2021, 12, 1864.	1.0	3
23	The Role of Focal Epilepsy Features in Defining <i>SCN1A</i> Mutation-positive Dravet Syndrome as Generalized and Focal Epilepsy. Journal of Epilepsy Research, 2021, 11, 127-135.	0.1	3
24	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.0	2