Heming Wang

List of Publications by Year
in descending order

47 papers	2,465 citations	331670 21 h-index	265206 42 g-index
61 all docs	61 docs citations	61 times ranked	4680 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. Nature Communications, 2019, 10, 1100.	12.8	369
2	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
3	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	21.4	250
4	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
5	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	12.8	136
6	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
7	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	12.8	117
8	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
9	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
10	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2560-2569.	7.1	71
11	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	2.9	65
12	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
13	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
14	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	2.9	41
15	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. Genetic Epidemiology, 2016, 40, 222-232.	1.3	32
16	Non-REM Apnea and Hypopnea Duration Varies across Population Groups and Physiologic Traits. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1173-1182.	5.6	32
17	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
18	Is disrupted sleep a risk factor for Alzheimerâ€™s disease? Evidence from a two-sample Mendelian randomization analysis. International Journal of Epidemiology, 2021, 50, 817-828.	1.9	31

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19	Evolutionarily conserved regulation of sleep by epidermal growth factor receptor signaling. Science Advances, 2019, 5, eaax4249.	10.3	29
20	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	3.5	28
21	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. Sleep, 2019, 42, .	1.1	27
22	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22
23	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	2.9	21
24	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	3.5	18
25	The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. PLoS Genetics, 2014, 10, e1004641.	3.5	16
26	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
27	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
28	Associations Between Sleep Health and Amygdala Reactivity to Negative Facial Expressions in the UK Biobank Cohort. Biological Psychiatry, 2022, 92, 693-700.	1.3	12
29	De novo mutations discovered in 8 Mexican American families through whole genome sequencing. BMC Proceedings, 2014, 8, S24.	1.6	11
30	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
31	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.	6.2	10
32	Genomeâ€wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. Genetic Epidemiology, 2017, 41, 122-135.	1.3	9
33	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. EBioMedicine, 2020, 56, 102803.	6.1	7
34	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. Mitochondrion, 2021, 60, 33-42.	3.4	6
35	Genomeâ€wide pleiotropy analysis identifies novel blood pressure variants and improves its polygenic risk scores. Genetic Epidemiology, 2022, 46, 105-121.	1.3	6
36	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	2.8	5

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37	Associations of sleep duration and sleepâ€“wake rhythm with lung parenchymal abnormalities on computed tomography: TheÂMESA study. Journal of Sleep Research, 2022, 31, e13475.	3.2	5
38	Targeted Genome Sequencing Identifies Multiple Rare Variants in Caveolin-1 Associated with Obstructive Sleep Apnea. American Journal of Respiratory and Critical Care Medicine, 0, , .	5.6	5
39	Local Ancestry Inference in Large Pedigrees. Scientific Reports, 2020, 10, 189.	3.3	3
40	Cutting the fat: advances and challenges in sleep apnoea genetics. European Respiratory Journal, 2021, 57, 2004644.	6.7	2
41	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	3.3	2
42	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
43	0698 Genetic susceptibility to elevated C-reactive protein and risk of obstructive sleep apnea in US men and women. Sleep, 2022, 45, A306-A306.	1.1	1
44	0026 Targeted genome sequencing identifies multiple rare variants in Caveolin-1 associated with obstructive sleep apnea. Sleep, 2022, 45, A12-A12.	1.1	1
45	Genetics of obstructive sleep apnea. , 2023, , 55-64.		0
46	0034 Genetic Determinants of Cardiometabolic and Pulmonary Traits and Obstructive Sleep Apnea in the Hispanic Community Health Study/Study of Latinos. Sleep, 2022, 45, A16-A16.	1.1	0
47	0285 Excessive daytime sleepiness with long sleep duration increases myocardial infarction risk. Sleep, 2022, 45, A129-A129.	1.1	0