

Heming Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3107233/publications.pdf>

Version: 2024-02-01

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	Genetics of obstructive sleep apnea. , 2023, , 55-64.		0
2	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22
3	Associations of sleep duration and sleepâ€“wake rhythm with lung parenchymal abnormalities on computed tomography: TheÂˆMESA study. Journal of Sleep Research, 2022, 31, e13475.	3.2	5
4	Genomeâ€“wide pleiotropy analysis identifies novel blood pressure variants and improves its polygenic risk scores. Genetic Epidemiology, 2022, 46, 105-121.	1.3	6
5	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	3.3	2
6	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
7	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
8	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
9	0026 Targeted genome sequencing identifies multiple rare variants in Caveolin-1 associated with obstructive sleep apnea. Sleep, 2022, 45, A12-A12.	1.1	1
10	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
11	0285 Excessive daytime sleepiness with long sleep duration increases myocardial infarction risk. Sleep, 2022, 45, A129-A129.	1.1	0
12	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
13	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
14	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	12.8	136
15	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
16	Cutting the fat: advances and challenges in sleep apnoea genetics. European Respiratory Journal, 2021, 57, 2004644.	6.7	2
17	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
18	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16

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19	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. <i>Mitochondrion</i> , 2021, 60, 33-42.	3.4	6
20	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020, 56, 102803.	6.1	7
21	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.	3.6	11
22	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2560-2569.	7.1	71
23	Local Ancestry Inference in Large Pedigrees. <i>Scientific Reports</i> , 2020, 10, 189.	3.3	3
24	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. <i>Nature Communications</i> , 2019, 10, 3503.	12.8	117
25	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.	12.8	62
26	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.	6.2	10
27	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
28	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. <i>Sleep</i> , 2019, 42, .	1.1	27
29	Associations of variants in the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. <i>PLoS Genetics</i> , 2019, 15, e1007739.	3.5	28
30	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. <i>Nature Communications</i> , 2019, 10, 1100.	12.8	369
31	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	2.9	31
32	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
33	Biological and clinical insights from genetics of insomnia symptoms. <i>Nature Genetics</i> , 2019, 51, 387-393.	21.4	250
34	Evolutionarily conserved regulation of sleep by epidermal growth factor receptor signaling. <i>Science Advances</i> , 2019, 5, eaax4249.	10.3	29
35	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. <i>Human Molecular Genetics</i> , 2019, 28, 675-687.	2.9	41
36	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. <i>European Journal of Human Genetics</i> , 2019, 27, 269-277.	2.8	5

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37	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
38	Multiethnic Meta-Analysis Identifies <i>RAI1</i> as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 58, 391-401.	2.9	65
39	Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. <i>Genetic Epidemiology</i> , 2017, 41, 122-135.	1.3	9
40	Rare variants in fox-1 homolog A (RBFox1) are associated with lower blood pressure. <i>PLoS Genetics</i> , 2017, 13, e1006678.	3.5	18
41	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , 2017, 13, e1006728.	3.5	88
42	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. <i>Genetic Epidemiology</i> , 2016, 40, 222-232.	1.3	32
43	Variants in angiotensin-converting enzyme 2 (<i>ANGPT2</i>) contribute to variation in nocturnal oxyhaemoglobin saturation level. <i>Human Molecular Genetics</i> , 2016, 25, ddw324.	2.9	21
44	The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. <i>PLoS Genetics</i> , 2014, 10, e1004641.	3.5	16
45	De novo mutations discovered in 8 Mexican American families through whole genome sequencing. <i>BMC Proceedings</i> , 2014, 8, S24.	1.6	11
46	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. <i>American Journal of Human Genetics</i> , 2013, 93, 545-554.	6.2	189
47	Targeted Genome Sequencing Identifies Multiple Rare Variants in Caveolin-1 Associated with Obstructive Sleep Apnea. <i>American Journal of Respiratory and Critical Care Medicine</i> , 0, , .	5.6	5