Jacqueline M Lane

List of Publications by Year
in descending order

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Version: 2024-02-01

30 papers	5,331 citations	304743 22 h-index	454955 30 g-index
42 all docs	42 docs citations	42 times ranked	10237 citing authors

#	Article	IF	Citations
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
2	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	12.8	417
3	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
4	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. Nature Genetics, 2017, 49, 274-281.	21.4	280
5	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	21.4	250
6	Genome-wide association analysis identifies novel loci for chronotype in 100,420 individuals from the UK Biobank. Nature Communications, 2016, 7, 10889.	12.8	237
7	Night Shift Work, Genetic Risk, and Type 2 Diabetes in the UK Biobank. Diabetes Care, 2018, 41, 762-769.	8.6	196
8	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. Nature Communications, 2019, 10, 1585.	12.8	189
9	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	12.8	136
10	Operating characteristics of the rankâ€based inverse normal transformation for quantitative trait analysis in genomeâ€wide association studies. Biometrics, 2020, 76, 1262-1272.	1.4	120
11	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	12.8	117
12	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
13	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
14	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. BMJ: British Medical Journal, 2019, 365, l2327.	2.3	79
15	Impact of Common Diabetes Risk Variant in MTNR1B on Sleep, Circadian, and Melatonin Physiology. Diabetes, 2016, 65, 1741-1751.	0.6	75
16	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
17	Time spent in outdoor light is associated with mood, sleep, and circadian rhythm-related outcomes: A cross-sectional and longitudinal study in over 400,000 UK Biobank participants. Journal of Affective Disorders, 2021, 295, 347-352.	4.1	57
18	CSF1Rmosaicism in a family with hereditary diffuse leukoencephalopathy with spheroids. Brain, 2016, 139, 1666-1672.	7.6	53

#	Article	IF	Citations
19	Genome-wide association study of breakfast skipping links clock regulation with food timing. American Journal of Clinical Nutrition, 2019, 110, 473-484.	4.7	34
20	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
21	Evolutionarily conserved regulation of sleep by epidermal growth factor receptor signaling. Science Advances, 2019, 5, eaax4249.	10.3	29
22	Development of an OP9 Derived Cell Line as a Robust Model to Rapidly Study Adipocyte Differentiation. PLoS ONE, 2014, 9, e112123.	2.5	25
23	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. Diabetes Care, 2022, 45, 772-781.	8.6	25
24	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22
25	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
26	Common Variants in CLOCK Are Not Associated with Measures of Sleep Duration in People of European Ancestry from the Sleep Heart Health Study. Biological Psychiatry, 2013, 74, e33-e35.	1.3	13
27	Objective assessment of sleep regularity in 60 000 UK Biobank participants using an open-source package. Sleep, 2021, 44, .	1.1	13
28	Association ofDAT1genetic variants with habitual sleep duration in the UK Biobank. Sleep, 2019, 42, .	1.1	10
29	Selection into shift work is influenced by educational attainment and body mass index: a Mendelian randomization study in the UK Biobank. International Journal of Epidemiology, 2021, 50, 1229-1240.	1.9	9
30	Sleep and circadian phenotypes: risk factors for COVID-19 severity?. Sleep, 2022, 45, .	1.1	1