

# Jacqueline M Lane

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/526967/publications.pdf>

Version: 2024-02-01

30  
papers

5,331  
citations

346980

22  
h-index

511568

30  
g-index

42  
all docs

42  
docs citations

42  
times ranked

11289  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
2	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. <i>Nature Communications</i> , 2019, 10, 343.	5.8	417
3	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.	5.8	369
4	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. <i>Nature Genetics</i> , 2017, 49, 274-281.	9.4	280
5	Biological and clinical insights from genetics of insomnia symptoms. <i>Nature Genetics</i> , 2019, 51, 387-393.	9.4	250
6	Genome-wide association analysis identifies novel loci for chronotype in 100,420 individuals from the UK Biobank. <i>Nature Communications</i> , 2016, 7, 10889.	5.8	237
7	Night Shift Work, Genetic Risk, and Type 2 Diabetes in the UK Biobank. <i>Diabetes Care</i> , 2018, 41, 762-769.	4.3	196
8	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. <i>Nature Communications</i> , 2019, 10, 1585.	5.8	189
9	Genetic determinants of daytime napping and effects on cardiometabolic health. <i>Nature Communications</i> , 2021, 12, 900.	5.8	136
10	Operating characteristics of the rank-based inverse normal transformation for quantitative trait analysis in genome-wide association studies. <i>Biometrics</i> , 2020, 76, 1262-1272.	0.8	120
11	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. <i>Nature Communications</i> , 2019, 10, 3503.	5.8	117
12	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
13	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.	1.5	88
14	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. <i>BMJ: British Medical Journal</i> , 2019, 365, l2327.	2.4	79
15	Impact of Common Diabetes Risk Variant in <i>MTNR1B</i> on Sleep, Circadian, and Melatonin Physiology. <i>Diabetes</i> , 2016, 65, 1741-1751.	0.3	75
16	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.	1.4	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. <i>Journal of Affective Disorders</i> , 2021, 295, 347-352.	2.0	57
18	<i>CSF1R</i> mosaicism in a family with hereditary diffuse leukoencephalopathy with spheroids. <i>Brain</i> , 2016, 139, 1666-1672.	3.7	53

#	ARTICLE	IF	CITATIONS
19	Genome-wide association study of breakfast skipping links clock regulation with food timing. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 473-484.	2.2	34
20	Is disrupted sleep a risk factor for Alzheimer's disease? Evidence from a two-sample Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2021, 50, 817-828.	0.9	31
21	Evolutionarily conserved regulation of sleep by epidermal growth factor receptor signaling. <i>Science Advances</i> , 2019, 5, eaax4249.	4.7	29
22	Development of an OP9 Derived Cell Line as a Robust Model to Rapidly Study Adipocyte Differentiation. <i>PLoS ONE</i> , 2014, 9, e112123.	1.1	25
23	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. <i>Diabetes Care</i> , 2022, 45, 772-781.	4.3	25
24	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. <i>Nature Human Behaviour</i> , 2022, 6, 155-163.	6.2	22
25	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.	3.6	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. <i>Biological Psychiatry</i> , 2013, 74, e33-e35.	0.7	13
27	Objective assessment of sleep regularity in 60 000 UK Biobank participants using an open-source package. <i>Sleep</i> , 2021, 44, .	0.6	13
28	Association of <i>DAT1</i> genetic variants with habitual sleep duration in the UK Biobank. <i>Sleep</i> , 2019, 42, .	0.6	10
29	Selection into shift work is influenced by educational attainment and body mass index: a Mendelian randomization study in the UK Biobank. <i>International Journal of Epidemiology</i> , 2021, 50, 1229-1240.	0.9	9
30	Sleep and circadian phenotypes: risk factors for COVID-19 severity?. <i>Sleep</i> , 2022, 45, .	0.6	1