

Samuel E Jones

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

3,583

citations

31

h-index

59

g-index

82

ext. papers

5,560

ext. citations

11.1

avg, IF

4.78

L-index

#	Paper	IF	Citations
62	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study.. <i>Diabetes Care</i> , 2022 , 45, 772-781	14.6	1
61	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	7.8	5
60	Estimating disease prevalence in large datasets using genetic risk scores. <i>Nature Communications</i> , 2021 , 12, 6441	17.4	1
59	Objective assessment of sleep regularity in 60 000 UK Biobank participants using an open-source package. <i>Sleep</i> , 2021 , 44,	1.1	1
58	Association of accelerometer-derived sleep measures with lifetime psychiatric diagnoses: A cross-sectional study of 89,205 participants from the UK Biobank. <i>PLoS Medicine</i> , 2021 , 18, e1003782	11.6	3
57	Sleep characteristics across the lifespan in 1.1 million people from the Netherlands, United Kingdom and United States: a systematic review and meta-analysis. <i>Nature Human Behaviour</i> , 2021 , 5, 113-122	12.8	46
56	Genetic determinants of daytime napping and effects on cardiometabolic health. <i>Nature Communications</i> , 2021 , 12, 900	17.4	18
55	Genetic evidence that higher central adiposity causes gastro-oesophageal reflux disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2020 , 49, 1270-1281	7.8	7
54	Comparison of Genetic Liability for Sleep Traits Among Individuals With Bipolar Disorder I or II and Control Participants. <i>JAMA Psychiatry</i> , 2020 , 77, 303-310	14.5	19
53	Effects of body mass index on relationship status, social contact and socio-economic position: Mendelian randomization and within-sibling study in UK Biobank. <i>International Journal of Epidemiology</i> , 2020 , 49, 1173-1184	7.8	19
52	A single nucleotide polymorphism genetic risk score to aid diagnosis of coeliac disease: a pilot study in clinical care. <i>Alimentary Pharmacology and Therapeutics</i> , 2020 , 52, 1165-1173	6.1	8
51	A Mendelian Randomization Study Provides Evidence That Adiposity and Dyslipidemia Lead to Lower Urinary Albumin-to-Creatinine Ratio, a Marker of Microvascular Function. <i>Diabetes</i> , 2020 , 69, 1072-1082	9.9	7
50	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. <i>Nature Communications</i> , 2019 , 10, 343	17.4	205
49	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. <i>PLoS Medicine</i> , 2019 , 16, e1002739	11.6	77
48	Assessing the Pathogenicity, Penetrance, and Expressivity of Putative Disease-Causing Variants in a Population Setting. <i>American Journal of Human Genetics</i> , 2019 , 104, 275-286	11	80
47	Genome-Wide Association Study of Microscopic Colitis in the UK Biobank Confirms Immune-Related Pathogenesis. <i>Journal of Crohns and Colitis</i> , 2019 , 13, 1578-1582	1.5	16
46	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019 , 51, 804-814	36.3	181

45	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	17.4	147
44	Chronotype Genetic Variant in PER2 is Associated with Intrinsic Circadian Period in Humans. <i>Scientific Reports</i> , 2019 , 9, 5350	4.9	12
43	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. <i>Nature Communications</i> , 2019 , 10, 1585	17.4	92
42	Association of Genetic Variants in NUDT15 With Thiopurine-Induced Myelosuppression in Patients With Inflammatory Bowel Disease. <i>JAMA - Journal of the American Medical Association</i> , 2019 , 321, 773-783	27.4	75
41	Biological and clinical insights from genetics of insomnia symptoms. <i>Nature Genetics</i> , 2019 , 51, 387-393	36.3	101
40	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. <i>Nature Communications</i> , 2019 , 10, 3503	17.4	47
39	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. <i>BMJ, The</i> , 2019 , 365, l2327	5.9	36
38	A genome-wide association study implicates multiple mechanisms influencing raised urinary albumin-creatinine ratio. <i>Human Molecular Genetics</i> , 2019 , 28, 4197-4207	5.6	8
37	Mosaic Turner syndrome shows reduced penetrance in an adult population study. <i>Genetics in Medicine</i> , 2019 , 21, 877-886	8.1	40
36	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. <i>American Journal of Human Genetics</i> , 2019 , 104, 157-163	11	12
35	Using genetics to understand the causal influence of higher BMI on depression. <i>International Journal of Epidemiology</i> , 2019 , 48, 834-848	7.8	81
34	Development and Standardization of an Improved Type 1 Diabetes Genetic Risk Score for Use in Newborn Screening and Incident Diagnosis. <i>Diabetes Care</i> , 2019 , 42, 200-207	14.6	92
33	Response to Prakash et al. <i>Genetics in Medicine</i> , 2019 , 21, 1884-1885	8.1	4
32	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. <i>Diabetes</i> , 2019 , 68, 207-219	0.9	46
31	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2019 , 28, 166-174	5.6	258
30	Genetic risk scores in adult-onset type 1 diabetes - AuthorsReply. <i>Lancet Diabetes and Endocrinology</i> , 2018 , 6, 169	18.1	3
29	Genome-wide association study of offspring birth weight in 86 577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. <i>Human Molecular Genetics</i> , 2018 , 27, 742-756	5.6	98
28	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. <i>Cell Reports</i> , 2018 , 23, 327-336	10.6	48

27	Frequency and phenotype of type 1 diabetes in the first six decades of life: a cross-sectional, genetically stratified survival analysis from UK Biobank. <i>Lancet Diabetes and Endocrinology</i> , 2018 , 6, 122-129	18.1	191
26	0055 Genome-Wide Association Analysis of Accelerometer-Derived Traits Reveals Novel Genetic Loci Associated with Rest-Activity Patterns in the UK Biobank. <i>Sleep</i> , 2018 , 41, A22-A22	1.1	
25	Estimating sleep parameters using an accelerometer without sleep diary. <i>Scientific Reports</i> , 2018 , 8, 12975	12.9	123
24	Gene-obesogenic environment interactions in the UK Biobank study. <i>International Journal of Epidemiology</i> , 2017 , 46, 559-575	7.8	105
23	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017 , 8, 744	17.4	37
22	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. <i>PLoS ONE</i> , 2017 , 12, e0185083	3.7	28
21	Quantifying the extent to which index event biases influence large genetic association studies. <i>Human Molecular Genetics</i> , 2017 , 26, 1018-1030	5.6	30
20	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. <i>BMJ</i> , 2016 , 352, i582	5.9	153
19	Variants in the FTO and CDKAL1 loci have recessive effects on risk of obesity and type 2 diabetes, respectively. <i>Diabetologia</i> , 2016 , 59, 1214-21	10.3	38
18	Genetic evidence that lower circulating FSH levels lengthen menstrual cycle, increase age at menopause and impact female reproductive health. <i>Human Reproduction</i> , 2016 , 31, 473-81	5.7	37
17	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. <i>PLoS Genetics</i> , 2016 , 12, e1006125	6	222
16	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. <i>Aging</i> , 2016 , 8, 547-60	5.6	84
15	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. <i>Diabetes</i> , 2016 , 65, 2448-60	0.9	86
14	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016 , 538, 248-252	2.4	266
13	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
12	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015 , 70, 758-762	2.4	
11	Dynamo action in the ABC flows using symmetries. <i>Geophysical and Astrophysical Fluid Dynamics</i> , 2014 , 108, 83-116	1.4	31
10	Projectile impact a major cause for fracture of flat glass. <i>Journal of Failure Analysis and Prevention</i> , 2003 , 3, 5-11		0

9	Stress distributions in the vicinity of a neck. <i>Journal of Applied Physics</i> , 1979 , 50, 3168-3173	2.5	3
8	An Analytical Solution for the Tapered Arbor Spring Slip Clutch. <i>Journal of Engineering for Industry</i> , 1974 , 96, 931-935		
7	HUMAN LONGEVITY IS INFLUENCED BY MANY GENETIC VARIANTS: EVIDENCE FROM 75,000 UK BIOBANK PARTICIPANTS		4
6	Estimating population level disease prevalence using genetic risk scores		3
5	Biological and clinical insights from genetics of insomnia symptoms		2
4	GWAS in 446,118 European adults identifies 78 genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates		5
3	Genetic studies of accelerometer-based sleep measures in 85,670 individuals yield new insights into human sleep behaviour		5
2	Genome-wide association analyses of chronotype in 697,828 individuals provides new insights into circadian rhythms in humans and links to disease		5
1	Assessing the pathogenicity, penetrance and expressivity of putative disease-causing variants in a population setting		4