Brian E Cade

List of Publications by Year
in descending order

83 papers	8,595 citations	109321 35 h-index	62596 80 g-index
109 all docs	109 docs citations	109 times ranked	11076 citing authors

#	Article	IF	Citations
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	Effect of Reducing Interns' Weekly Work Hours on Sleep and Attentional Failures. New England Journal of Medicine, 2004, 351, 1829-1837.	27.0	843
3	Extended Work Shifts and the Risk of Motor Vehicle Crashes among Interns. New England Journal of Medicine, 2005, 352, 125-134.	27.0	808
4	Impact of Extended-Duration Shifts on Medical Errors, Adverse Events, and Attentional Failures. PLoS Medicine, 2006, 3, e487.	8.4	379
5	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
6	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
7	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
8	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
9	Extended Work Duration and the Risk of Self-reported Percutaneous Injuries in Interns. JAMA - Journal of the American Medical Association, 2006, 296, 1055.	7.4	329
10	Sleep Disorders, Health, and Safety in Police Officers. JAMA - Journal of the American Medical Association, 2011, 306, 2567.	7.4	305
11	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	21.4	250
12	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
13	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
14	Interns' Compliance With Accreditation Council for Graduate Medical Education Work-Hour Limits. JAMA - Journal of the American Medical Association, 2006, 296, 1063.	7.4	130
15	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
16	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	12.8	117
17	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112
18	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

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19	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	5.6	107
20	Association of clonal hematopoiesis with chronic obstructive pulmonary disease. Blood, 2022, 139, 357-368.	1.4	106
21	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
22	Efficacy of bright light and sleep/darkness scheduling in alleviating circadian maladaptation to night work. American Journal of Physiology - Endocrinology and Metabolism, 2001, 281, E384-E391.	3.5	102
23	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
24	Searching Night and Day. Psychological Science, 2003, 14, 549-557.	3.3	94
25	Habitual sleep duration is associated with BMI and macronutrient intake and may be modified by CLOCK genetic variants. American Journal of Clinical Nutrition, 2015, 101, 135-143.	4.7	93
26	Sleep Apnea and COVID-19 Mortality and Hospitalization. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 1462-1464.	5.6	91
27	Impact of Common Diabetes Risk Variant in MTNR1B on Sleep, Circadian, and Melatonin Physiology. Diabetes, 2016, 65, 1741-1751.	0.6	75
28	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
29	Deterioration of Neurobehavioral Performance in Resident Physicians During Repeated Exposure to Extended Duration Work Shifts. Sleep, 2012, 35, 1137-46.	1.1	69
30	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
31	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
32	Association of Genetic Loci with Sleep Apnea in European Americans and African-Americans: The Candidate Gene Association Resource (CARe). PLoS ONE, 2012, 7, e48836.	2.5	64
33	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
34	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
35	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	2.9	41
36	Common variants inDRD2are associated with sleep duration: the CARe consortium. Human Molecular Genetics, 2016, 25, 167-179.	2.9	40

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37	Beyond type 2 diabetes, obesity and hypertension: an axis including sleep apnea, left ventricular hypertrophy, endothelial dysfunction, and aortic stiffness among Mexican Americans in Starr County, Texas. Cardiovascular Diabetology, 2016, 15, 86.	6.8	32
38	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. Genetic Epidemiology, 2016, 40, 222-232.	1.3	32
39	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
40	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
41	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
42	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	3.4	29
43	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
44	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	2.9	28
45	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
46	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
47	Increasing Generality and Power of Rare-Variant Tests by Utilizing Extended Pedigrees. American Journal of Human Genetics, 2016, 99, 846-859.	6.2	26
48	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
49	Transferability and fine-mapping of glucose and insulin quantitative trait loci across populations: CARe, the Candidate Gene Association Resource. Diabetologia, 2012, 55, 2970-2984.	6.3	23
50	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23
51	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	2.9	21
52	Effect of Reducing Interns??? Weekly Work Hours on Sleep and Attentional Failures. Obstetrical and Gynecological Survey, 2005, 60, 226-228.	0.4	20
53	Sleep health, diseases, and pain syndromes: findings from an electronic health record biobank. Sleep, 2021, 44, .	1.1	18
54	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18

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55	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	3.5	18
56	Brief (<4 hr) sleep episodes are insufficient for restoring performance in first-year resident physicians working overnight extended-duration work shifts. Sleep, 2019, 42, .	1.1	17
57	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
58	Interaction of obesity polygenic score with lifestyle risk factors in an electronic health record biobank. BMC Medicine, 2022, 20, 5.	5.5	17
59	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
60	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
61	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
62	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
63	Sleep duration does not mediate or modify association of common genetic variants with type 2 diabetes. Diabetologia, 2014, 57, 339-346.	6.3	10
64	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
65	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	6.2	9
66	Genome-wide association study of neck circumference identifies sex-specific loci independent of generalized adiposity. International Journal of Obesity, 2021, 45, 1532-1541.	3.4	8
67	Sleep apnea phenotyping and relationship to disease in a large clinical biobank. JAMIA Open, 2022, 5, ooab117.	2.0	8
68	Evaluation of an automated pipeline for large-scale EEG spectral analysis: the National Sleep Research Resource. Sleep Medicine, 2018, 47, 126-136.	1.6	7
69	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. EBioMedicine, 2020, 56, 102803.	6.1	7
70	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	3.6	7
71	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	6.2	7
72	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6

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73	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. Mitochondrion, 2021, 60, 33-42.	3.4	6
74	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
75	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
76	The genetic etiology of periodic limb movement in sleep. Sleep, 2023, 46, .	1.1	4
77	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	3.3	2
78	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
79	Assessing the contribution of rare genetic variants to phenotypes of chronic obstructive pulmonary disease using whole-genome sequence data. Human Molecular Genetics, 2022, 31, 3873-3885.	2.9	2
80	Reply to Mulla and Pathak: Sleep Apnea and Poor COVID-19 Outcomes: Beware of Causal Intermediates and Colliders. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1326-1327.	5.6	1
81	0026 Targeted genome sequencing identifies multiple rare variants in Caveolin-1 associated with obstructive sleep apnea. Sleep, 2022, 45, A12-A12.	1.1	1
82	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
83	0033 Dysregulated sleep and NREM sleep electroencephalogram delta power induced by intermittent hypoxia exposure are attenuated in NLRP3 knockout mice. Sleep, 2022, 45, A15-A16.	1.1	0