Catherine Schaefer

List of Publications by Year
in descending order

25 papers	2,481 citations	361413 20 h-index	552781 26 g-index
29 all docs	29 docs citations	29 times ranked	6625 citing authors

#	Article	IF	Citations
1	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	21.4	65
2	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	7.9	15
3	Pregnancy does not modify the risk of MS in genetically susceptible women. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, .	6.0	2
4	Identification of 31 loci for mammographic density phenotypes and their associations with breast cancer risk. Nature Communications, 2020, 11, 5116.	12.8	29
5	A multiethnic genome-wide analysis of 44,039 individuals identifies 41 new loci associated with central corneal thickness. Communications Biology, 2020, 3, 301.	4.4	28
6	Meta-Analysis of 26 638 Individuals Identifies Two Genetic Loci Associated With Left Ventricular Ejection Fraction. Circulation Genomic and Precision Medicine, 2020, 13, e002804.	3.6	10
7	The impact of adjusting for baseline in pharmacogenomic genome-wide association studies of quantitative change. Npj Genomic Medicine, 2020, 5, 1.	3.8	28
8	Genetic ancestry, skin pigmentation, and the risk of cutaneous squamous cell carcinoma in Hispanic/Latino and non-Hispanic white populations. Communications Biology, 2020, 3, 765.	4.4	6
9	A large electronic-health-record-based genome-wide study of serum lipids. Nature Genetics, 2018, 50, 401-413.	21.4	224
10	Characterization of Statin Low-Density Lipoprotein Cholesterol Dose-Response Using Electronic Health Records in a Large Population-Based Cohort. Circulation Genomic and Precision Medicine, 2018, 11, e002043.	3.6	25
11	A Large Multiethnic Genome-Wide Association Study of Adult Body Mass Index Identifies Novel Loci. Genetics, 2018, 210, 499-515.	2.9	131
12	A multiethnic genome-wide association study of primary open-angle glaucoma identifies novel risk loci. Nature Communications, 2018, 9, 2278.	12.8	124
13	Evidence for a causal relationship between low vitamin D, high BMI, and pediatric-onset MS. Neurology, 2017, 88, 1623-1629.	1.1	138
14	A large multi-ethnic genome-wide association study identifies novel genetic loci for intraocular pressure. Nature Communications, 2017, 8, 2108.	12.8	80
15	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. Nature Genetics, 2017, 49, 54-64.	21.4	281
16	A Large Genome-Wide Association Study of Age-Related Hearing Impairment Using Electronic Health Records. PLoS Genetics, 2016, 12, e1006371.	3.5	78
17	Mendelian randomization shows a causal effect of low vitamin D on multiple sclerosis risk. Neurology: Genetics, 2016, 2, e97.	1.9	166
18	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891.	9.4	111

#	Article	IF	Citations
19	Genotyping Informatics and Quality Control for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. Genetics, 2015, 200, 1051-1060.	2.9	177
20	Imputation of the Rare HOXB13 G84E Mutation and Cancer Risk in a Large Population-Based Cohort. PLoS Genetics, 2015, 11, e1004930.	3.5	36
21	Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. Genetics, 2015, 200, 1285-1295.	2.9	273
22	Interaction between passive smoking and two HLA genes with regard to multiple sclerosis risk. International Journal of Epidemiology, 2014, 43, 1791-1798.	1.9	57
23	Adverse socioeconomic position during the life course is associated with multiple sclerosis. Journal of Epidemiology and Community Health, 2014, 68, 622-629.	3.7	45
24	Next generation genome-wide association tool: Design and coverage of a high-throughput European-optimized SNP array. Genomics, 2011, 98, 79-89.	2.9	186
25	Design and coverage of high throughput genotyping arrays optimized for individuals of East Asian, African American, and Latino race/ethnicity using imputation and a novel hybrid SNP selection algorithm. Genomics, 2011, 98, 422-430.	2.9	156