Matthew P Conomos

List of Publications by Year
in descending order

48 papers	5,620 citations	236925 25 h-index	206112 48 g-index
58 all docs	58 docs citations	58 times ranked	10992 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	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
3	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
4	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. American Journal of Human Genetics, 2016, 98, 653-666.	6.2	347
5	Model-free Estimation of Recent Genetic Relatedness. American Journal of Human Genetics, 2016, 98, 127-148.	6.2	331
6	Robust Inference of Population Structure for Ancestry Prediction and Correction of Stratification in the Presence of Relatedness. Genetic Epidemiology, 2015, 39, 276-293.	1.3	330
7	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
8	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	4.1	260
9	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. Bioinformatics, 2012, 28, 3329-3331.	4.1	177
10	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
11	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
12	SeqArrayâ€"a storage-efficient high-performance data format for WGS variant calls. Bioinformatics, 2017, 33, 2251-2257.	4.1	127
13	A Multi-omic Association Study of Trimethylamine N-Oxide. Cell Reports, 2018, 24, 935-946.	6.4	115
14	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
15	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
16	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
17	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
18	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

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19	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	6.1	57
20	A meta-analysis of genome-wide association studies of asthma in PuertoÂRicans. European Respiratory Journal, 2017, 49, 1601505.	6.7	51
21	Genome-wide Association Study Identifies a Genetic Variant Associated with Risk for More Aggressive Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1196-1203.	2.5	48
22	Genetic Predisposition Impacts Clinical Changes in a Lifestyle Coaching Program. Scientific Reports, 2019, 9, 6805.	3.3	48
23	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	2.9	41
24	DUOX2 variants associate with preclinical disturbances in microbiota-immune homeostasis and increased inflammatory bowel disease risk. Journal of Clinical Investigation, 2021, 131, .	8.2	35
25	Genome-wide association study of iron traits and relation to diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL): potential genomic intersection of iron and glucose regulation?. Human Molecular Genetics, 2017, 26, 1966-1978.	2.9	31
26	Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 807-816.	2.9	29
27	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
28	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
29	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
30	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
31	Habitual sleep duration and sleep duration variation are independently associated with body mass index. International Journal of Obesity, 2018, 42, 794-800.	3.4	26
32	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	6.2	25
33	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	3.3	23
34	Heterogeneity in statin responses explained by variation in the human gut microbiome. Med, 2022, 3, 388-405.e6.	4.4	21
35	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
36	Estimating and adjusting for ancestry admixture in statistical methods for relatedness inference, heritability estimation, and association testing. BMC Proceedings, 2014, 8, S5.	1.6	16

#	Article	IF	Citations
37	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
38	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	2.5	13
39	Untargeted longitudinal analysis of a wellness cohort identifies markers of metastatic cancer years prior to diagnosis. Scientific Reports, 2020, 10, 16275.	3.3	12
40	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
41	Identity-by-descent graphs offer a flexible framework for imputation and both linkage and association analyses. BMC Proceedings, 2014, 8, S19.	1.6	7
42	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
43	Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program. Communications Biology, 2022, 5, 362.	4.4	5
44	Asymptotics of the spectral gap for the interchange process on large hypercubes. Journal of Statistical Mechanics: Theory and Experiment, 2011, 2011, P10018.	2.3	4
45	Estimating relationships between phenotypes and subjects drawn from admixed families. BMC Proceedings, 2016, 10, 357-362.	1.6	4
46	Genome-wide association study in the Taiwan Biobank identifies four novel genes for human height: NABP2, RASA2, RNF41 and SLC39A5. Human Molecular Genetics, 2021, 30, 2362-2369.	2.9	3
47	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.7	2
48	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506.	12.8	1