

Matthew P Conomos

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

5,620
citations

236612

25
h-index

205818

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. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
2	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	13.7	679
3	Detectable clonal mosaicism from birth to old age and its relationship to cancer. <i>Nature Genetics</i> , 2012, 44, 642-650.	9.4	511
4	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. <i>American Journal of Human Genetics</i> , 2016, 98, 653-666.	2.6	347
5	Model-free Estimation of Recent Genetic Relatedness. <i>American Journal of Human Genetics</i> , 2016, 98, 127-148.	2.6	331
6	Robust Inference of Population Structure for Ancestry Prediction and Correction of Stratification in the Presence of Relatedness. <i>Genetic Epidemiology</i> , 2015, 39, 276-293.	0.6	330
7	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Human Genetics</i> , 2016, 98, 165-184.	2.6	266
8	Genetic association testing using the GENESIS R/Bioconductor package. <i>Bioinformatics</i> , 2019, 35, 5346-5348.	1.8	260
9	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 3329-3331.	1.8	177
10	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	9.4	156
11	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	9.4	146
12	SeqArray—a storage-efficient high-performance data format for WGS variant calls. <i>Bioinformatics</i> , 2017, 33, 2251-2257.	1.8	127
13	A Multi-omic Association Study of Trimethylamine N-Oxide. <i>Cell Reports</i> , 2018, 24, 935-946.	2.9	115
14	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 886-897.	2.5	107
15	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , 2017, 49, 1560-1563.	9.4	93
16	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. <i>American Journal of Human Genetics</i> , 2016, 98, 229-242.	2.6	71
17	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
18	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

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19	African Ancestry-Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 915-922.	3.0	57
20	A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. <i>European Respiratory Journal</i> , 2017, 49, 1601505.	3.1	51
21	Genome-wide Association Study Identifies a Genetic Variant Associated with Risk for More Aggressive Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1196-1203.	1.1	48
22	Genetic Predisposition Impacts Clinical Changes in a Lifestyle Coaching Program. <i>Scientific Reports</i> , 2019, 9, 6805.	1.6	48
23	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. <i>Human Molecular Genetics</i> , 2019, 28, 675-687.	1.4	41
24	DUOX2 variants associate with preclinical disturbances in microbiota-immune homeostasis and increased inflammatory bowel disease risk. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	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?. <i>Human Molecular Genetics</i> , 2017, 26, 1966-1978.	1.4	31
26	Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). <i>Human Molecular Genetics</i> , 2016, 25, 807-816.	1.4	29
27	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	5.8	29
28	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	3.0	29
29	Associations of variants in the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. <i>PLoS Genetics</i> , 2019, 15, e1007739.	1.5	28
30	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893.	2.6	28
31	Habitual sleep duration and sleep duration variation are independently associated with body mass index. <i>International Journal of Obesity</i> , 2018, 42, 794-800.	1.6	26
32	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. <i>American Journal of Human Genetics</i> , 2022, 109, 1175-1181.	2.6	25
33	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. <i>Scientific Reports</i> , 2017, 7, 17075.	1.6	23
34	Heterogeneity in statin responses explained by variation in the human gut microbiome. <i>Med</i> , 2022, 3, 388-405.e6.	2.2	21
35	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. <i>Heart Rhythm</i> , 2017, 14, 1675-1684.	0.3	18
36	Estimating and adjusting for ancestry admixture in statistical methods for relatedness inference, heritability estimation, and association testing. <i>BMC Proceedings</i> , 2014, 8, S5.	1.8	16

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37	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851.	2.6	14
38	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	1.1	13
39	Untargeted longitudinal analysis of a wellness cohort identifies markers of metastatic cancer years prior to diagnosis. <i>Scientific Reports</i> , 2020, 10, 16275.	1.6	12
40	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. <i>Human Molecular Genetics</i> , 2022, 31, 347-361.	1.4	9
41	Identity-by-descent graphs offer a flexible framework for imputation and both linkage and association analyses. <i>BMC Proceedings</i> , 2014, 8, S19.	1.8	7
42	Robust, flexible, and scalable tests for Hardy-Weinberg equilibrium across diverse ancestries. <i>Genetics</i> , 2021, 218, .	1.2	6
43	Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program. <i>Communications Biology</i> , 2022, 5, 362.	2.0	5
44	Asymptotics of the spectral gap for the interchange process on large hypercubes. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2011, 2011, P10018.	0.9	4
45	Estimating relationships between phenotypes and subjects drawn from admixed families. <i>BMC Proceedings</i> , 2016, 10, 357-362.	1.8	4
46	Genome-wide association study in the Taiwan Biobank identifies four novel genes for human height: <i>NABP2</i> , <i>SA2</i> , <i>RNF41</i> and <i>SLC39A5</i> . <i>Human Molecular Genetics</i> , 2021, 30, 2362-2369.	1.4	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. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100040.	1.0	2
48	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. <i>Nature Communications</i> , 2021, 12, 3506.	5.8	1