Ginger A Metcalf

List of Publications by Year
in descending order

31 papers	3,220 citations	567144 15 h-index	477173 29 g-index
39 all docs	39 docs citations	39 times ranked	7635 citing authors

#	Article	IF	Citations
1	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.	2.6	24
2	Fully resolved assembly of Cryptosporidium parvum. GigaScience, 2022, 11, .	3.3	8
3	Whole-genome sequencing as an investigational device for return of hereditary disease risk and pharmacogenomic results as part of the All of Us Research Program. Genome Medicine, 2022, 14, 34.	3.6	27
4	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.	2.6	7
5	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	1.4	3
6	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
7	muCNV: genotyping structural variants for population-level sequencing. Bioinformatics, 2021, 37, 2055-2057.	1.8	7
8	The Implementation Science for Genomic Health Translation (INSIGHT) Study in Epilepsy: Protocol for a Learning Health Care System. JMIR Research Protocols, 2021, 10, e25576.	0.5	2
9	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
10	Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals. PLoS ONE, 2021, 16, e0244468.	1.1	20
11	Genetic testing in ambulatory cardiology clinics reveals high rate of findings with clinical management implications. Genetics in Medicine, 2021, 23, 2404-2414.	1.1	14
12	Transmission event of SARS-CoV-2 delta variant reveals multiple vaccine breakthrough infections. BMC Medicine, 2021, 19, 255.	2.3	137
13	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
14	HEARTCARE: ADVANCING PRECISION MEDICINE THROUGH COMPREHENSIVE CARDIOVASCULAR GENETIC TESTING. Journal of the American College of Cardiology, 2020, 75, 3643.	1.2	4
15	High-depth African genomes inform human migration and health. Nature, 2020, 586, 741-748.	13.7	197
16	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
17	Leveraging Human Microbiome Features to Diagnose and Stratify Children with Irritable Bowel Syndrome. Journal of Molecular Diagnostics, 2019, 21, 449-461.	1.2	59
18	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics, 2018, 209, 607-616.	1.2	8

#	Article	IF	Citations
19	Temporal development of the gut microbiome in early childhood from the TEDDY study. Nature, 2018, 562, 583-588.	13.7	1,220
20	Practical Approaches for Whole-Genome Sequence Analysis of Heart- and Blood-Related Traits. American Journal of Human Genetics, 2017, 100, 205-215.	2.6	50
21	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. Human Molecular Genetics, 2017, 26, 3442-3450.	1.4	25
22	The gut mycobiome of the Human Microbiome Project healthy cohort. Microbiome, 2017, 5, 153.	4.9	609
23	Whole genome sequence analysis of serum amino acid levels. Genome Biology, 2016, 17, 237.	3.8	17
24	Whole-exome sequencing reveals an inherited R566X mutation of the epithelial sodium channel Î²-subunit in a case of early-onset phenotype of Liddle syndrome. Journal of Physical Education and Sports Management, 2016, 2, a001255.	0.5	10
25	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	2.6	45
26	Loss-of-function variants influence the human serum metabolome. Science Advances, 2016, 2, e1600800.	4.7	46
27	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
28	Analysis of loss-of-function variants and 20 risk factor phenotypes in 8,554 individuals identifies loci influencing chronic disease. Nature Genetics, 2015, 47, 640-642.	9.4	49
29	Structure and function of the healthy pre-adolescent pediatric gut microbiome. Microbiome, 2015, 3, 36.	4.9	283
30	Abstract 148: Whole Exome Sequence Analysis of Cerebral White Matter Hyperintensities on MRI. Stroke, 2015, 46, .	1.0	0
31	Rare Genetic Variants Of The Protein-Coding Area Of The Genome and The Risk Of Inhibitor Development: An Exome-Sequencing Study Of 28 Patients With Severe Hemophilia A. Blood, 2013, 122, 571-571.	0.6	0