Charles C Gu

List of Publications by Year
in descending order

95 papers	4,192 citations	147566 31 h-index	128067 60 g-index
99 all docs	99 docs citations	99 times ranked	8500 citing authors

#	Article	IF	Citations
1	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
2	Resveratrol Supplementation Does Not Improve Metabolic Function in Nonobese Women with Normal Glucose Tolerance. Cell Metabolism, 2012, 16, 658-664.	7.2	336
3	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. Nature Genetics, 2012, 44, 890-894.	9.4	295
4	Admixture mapping for hypertension loci with genome-scan markers. Nature Genetics, 2005, 37, 177-181.	9.4	246
5	Inflammatory Bowel Diseases Phenotype, C. difficile and NOD2 Genotype Are Associated with Shifts in Human Ileum Associated Microbial Composition. PLoS ONE, 2012, 7, e26284.	1.1	207
6	Multi-Center Genetic Study of Hypertension. Hypertension, 2002, 39, 3-9.	1.3	171
7	Genome-wide association study in Chinese identifies novel loci for blood pressure and hypertension. Human Molecular Genetics, 2015, 24, 865-874.	1.4	157
8	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.	9.4	146
9	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.	2.6	123
10	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.	9.4	112
11	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
12	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
13	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	2.6	77
14	Risk Factors for Surgical Recurrence after Ileocolic Resection of Crohn's Disease. Diseases of the Colon and Rectum, 2008, 51, 1211-1216.	0.7	74
15	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. BMC Genomics, 2017, 18, 724.	1.2	71
16	Genome-Wide Association Study Identifies 8 Novel Loci Associated With Blood Pressure Responses to Interventions in Han Chinese. Circulation: Cardiovascular Genetics, 2013, 6, 598-607.	5.1	64
17	A Systematic Mapping Approach of 16q12.2/FTO and BMI in More Than 20,000 African Americans Narrows in on the Underlying Functional Variation: Results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2013, 9, e1003171.	1.5	63
18	Three geneticâ€“environmental networks for human personality. Molecular Psychiatry, 2021, 26, 3858-3875.	4.1	58

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19	Genetic Effect on Blood Pressure Is Modulated by Age. Hypertension, 2009, 53, 35-41.	1.3	56
20	Meta-analysis methodology for combining non-parametric sibpair linkage results: Genetic homogeneity and identical markers. Genetic Epidemiology, 1998, 15, 609-626.	0.6	52
21	Genetic Variation in NCAM1 Contributes to Left Ventricular Wall Thickness in Hypertensive Families. Circulation Research, 2011, 108, 279-283.	2.0	47
22	Mining gold dust under the genome wide significance level: a twoâ€stage approach to analysis of GWAS. Genetic Epidemiology, 2011, 35, 111-118.	0.6	46
23	Genetic Susceptibility to Lipid Levels and Lipid Change Over Time and Risk of Incident Hyperlipidemia in Chinese Populations. Circulation: Cardiovascular Genetics, 2016, 9, 37-44.	5.1	46
24	Genome-Wide Detection of Allele Specific Copy Number Variation Associated with Insulin Resistance in African Americans from the HyperGEN Study. PLoS ONE, 2011, 6, e24052.	1.1	45
25	Genome-Wide Geneâ€“Sodium Interaction Analyses on Blood Pressure. Hypertension, 2016, 68, 348-355.	1.3	44
26	A Custom Correlation Coefficient (CCC) Approach for Fast Identification of Multiâ€SNP Association Patterns in Genomeâ€Wide SNPs Data. Genetic Epidemiology, 2014, 38, 610-621.	0.6	38
27	Association of Genetic Variants in the Apelin-APJ System and ACE2 With Blood Pressure Responses to Potassium Supplementation: The GenSalt Study. American Journal of Hypertension, 2010, 23, 606-613.	1.0	37
28	Familial resemblance for glucose and insulin metabolism indices derived from an intravenous glucose tolerance test in Blacks and Whites of the HERITAGE Family Study. Clinical Genetics, 2001, 60, 22-30.	1.0	36
29	Combining least absolute shrinkage and selection operator (LASSO) and principal-components analysis for detection of gene-gene interactions in genome-wide association studies. BMC Proceedings, 2009, 3, S62.	1.8	36
30	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
31	Admixture Mapping of Quantitative Trait Loci for BMI in African Americans: Evidence for Loci on Chromosomes 3q, 5q, and 15q. Obesity, 2009, 17, 1226-1231.	1.5	35
32	Genetic association mapping under founder heterogeneity via weighted haplotype similarity analysis in candidate genes. Genetic Epidemiology, 2004, 27, 182-191.	0.6	32
33	Role of gene expression microarray analysis in finding complex disease genes. Genetic Epidemiology, 2002, 23, 37-56.	0.6	31
34	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	1.8	31
35	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.	1.4	31
36	NOD2 status and human ileal gene expressionâ€â€¡. Inflammatory Bowel Diseases, 2010, 16, 1649-1657.	0.9	28

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37	Genome-wide distribution of ancestry in Mexican Americans. Human Genetics, 2008, 124, 207-214.	1.8	27
38	An investigation of genome-wide associations of hypertension with microsatellite markers in the family blood pressure program (FBPP). Human Genetics, 2007, 121, 577-590.	1.8	26
39	Association Between Blood Pressure Responses to the Cold Pressor Test and Dietary Sodium Intervention in a Chinese Population. Archives of Internal Medicine, 2008, 168, 1740.	4.3	26
40	Pathway-based genome-wide association analysis of coronary heart disease identifies biologically important gene sets. European Journal of Human Genetics, 2012, 20, 1168-1173.	1.4	26
41	Osteopontin Promoter Polymorphism Is Associated With Increased Carotid Intima-Media Thickness. Journal of the American Society of Echocardiography, 2008, 21, 954-960.	1.2	25
42	Common Genetic Variants in the Endothelial System Predict Blood Pressure Response to Sodium Intake: The GenSalt Study. American Journal of Hypertension, 2013, 26, 643-656.	1.0	24
43	Blood Pressure Genetic Risk Score Predicts Blood Pressure Responses to Dietary Sodium and Potassium. Hypertension, 2017, 70, 1106-1112.	1.3	24
44	Novel Genetic Variants in the Î±-Adducin and Guanine Nucleotide Binding Protein Î²-Polypeptide 3 Genes and Salt Sensitivity of Blood Pressure. American Journal of Hypertension, 2009, 22, 985-992.	1.0	23
45	Testing causal hypotheses in multivariate linkage analysis of quantitative traits: General formulation and application to sibpair data. , 1998, 15, 263-278.		22
46	Haplotype Association Analysis of AGT Variants with Hypertension-Related Traits: The HyperGEN Study. Human Heredity, 2005, 60, 164-176.	0.4	22
47	A Gene-Based Analysis of Variants in the Serum/Glucocorticoid Regulated Kinase (SGK) Genes with Blood Pressure Responses to Sodium Intake: The GenSalt Study. PLoS ONE, 2014, 9, e98432.	1.1	21
48	Interactions of Genetic Variants With Physical Activity Are Associated With Blood Pressure in Chinese: The GenSalt Study. American Journal of Hypertension, 2011, 24, 1035-1040.	1.0	20
49	Genotype-by-Sex Interaction on Fasting Insulin Concentration: The HyperGEN Study. Diabetes, 2007, 56, 137-142.	0.3	19
50	Gene Expression and Functional Studies of the Optic Nerve Head Astrocyte Transcriptome from Normal African Americans and Caucasian Americans Donors. PLoS ONE, 2008, 3, e2847.	1.1	19
51	Relation of Albuminuria to Left Ventricular Mass (from the HyperGEN Study). American Journal of Cardiology, 2008, 101, 212-216.	0.7	17
52	Genome-wide joint SNP and CNV analysis of aortic root diameter in African Americans: the HyperGEN study. BMC Medical Genomics, 2011, 4, 4.	0.7	17
53	Five Blood Pressure Loci Identified by an Updated Genome-Wide Linkage Scan: Meta-Analysis of the Family Blood Pressure Program. American Journal of Hypertension, 2011, 24, 347-354.	1.0	17
54	Uncovering the complex genetics of human personality: response from authors on the PGMRA Model. Molecular Psychiatry, 2020, 25, 2210-2213.	4.1	17

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55	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
56	On transferability of genomeâ€wide tagSNPs. Genetic Epidemiology, 2008, 32, 89-97.	0.6	16
57	Generalization and fine mapping of European ancestry-based central adiposity variants in African ancestry populations. International Journal of Obesity, 2017, 41, 324-331.	1.6	16
58	Power Loss for Linkage Analysis due to the Dichotomization of Trichotomous Phenotypes. Human Heredity, 2004, 57, 21-27.	0.4	15
59	Rare coding variants associated with blood pressure variation in 15â€Š914 individuals of African ancestry. Journal of Hypertension, 2017, 35, 1381-1389.	0.3	15
60	ATRAID regulates the action of nitrogen-containing bisphosphonates on bone. Science Translational Medicine, 2020, 12, .	5.8	15
61	Variable set enrichment analysis in genome-wide association studies. European Journal of Human Genetics, 2011, 19, 893-900.	1.4	14
62	Associations Between Genetic Variants of NADPH Oxidase-Related Genes and Blood Pressure Responses to Dietary Sodium Intervention: The GenSalt Study. American Journal of Hypertension, 2017, 30, 427-434.	1.0	14
63	Selection of important variables by statistical learning in genome-wide association analysis. BMC Proceedings, 2009, 3, S70.	1.8	13
64	Genotype Imputation for <scp>A</scp>frican <scp>A</scp>mericans Using Data From <scp>H</scp>ap<scp>M</scp>ap Phase <scp>II</scp> Versus 1000 <scp>G</scp>enomes <scp>P</scp>rojects. Genetic Epidemiology, 2012, 36, 508-516.	0.6	13
65	Genome-Wide Linkage and Positional Association Analyses Identify Associations of Novel AFF3 and NTM Genes with Triglycerides: The GenSalt Study. Journal of Genetics and Genomics, 2015, 42, 107-117.	1.7	13
66	Trans-ethnic analysis of metabochip data identifies two new loci associated with BMI. International Journal of Obesity, 2018, 42, 384-390.	1.6	13
67	Heritability of Blood Pressure Responses to Cold Pressor Test in a Chinese Population. American Journal of Hypertension, 2009, 22, 1096-1100.	1.0	12
68	Gene-lifestyle interactions in the genomics of human complex traits. European Journal of Human Genetics, 2022, 30, 730-739.	1.4	11
69	Characterization of LD Structures and the Utility of HapMap in Genetic Association Studies. Advances in Genetics, 2008, 60, 407-435.	0.8	10
70	Associations of epithelial sodium channel genes with blood pressure: the GenSalt study. Journal of Human Hypertension, 2015, 29, 224-228.	1.0	10
71	A Wholeâ€Genome Simulator Capable of Modeling Highâ€Order Epistasis for Complex Disease. Genetic Epidemiology, 2013, 37, 686-694.	0.6	9
72	Donor-specific phenotypic variation in hiPSC cardiomyocyte-derived exosomes impacts endothelial cell function. American Journal of Physiology - Heart and Circulatory Physiology, 2021, 320, H954-H968.	1.5	8

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73	Global transmission/disequilibrium tests based on haplotype sharing in multiple candidate genes. Genetic Epidemiology, 2005, 29, 323-335.	0.6	7
74	Enhanced detection of genetic association of hypertensive heart disease by analysis of latent phenotypes. Genetic Epidemiology, 2008, 32, 528-538.	0.6	7
75	Comparison between single-marker analysis using Merlin and multi-marker analysis using LASSO for Framingham simulated data. BMC Proceedings, 2009, 3, S27.	1.8	7
76	Characterization of autosomal copy-number variation in African Americans: the HyperGEN Study. European Journal of Human Genetics, 2011, 19, 1271-1275.	1.4	7
77	Comprehensive linkage and linkage heterogeneity analysis of 4344 sibling pairs affected with hypertension from the Family Blood Pressure Program. Genetic Epidemiology, 2007, 31, 195-210.	0.6	6
78	Random forest fishing: a novel approach to identifying organic group of risk factors in genome-wide association studies. European Journal of Human Genetics, 2014, 22, 254-259.	1.4	6
79	Genetic association of left ventricular mass assessed by M-mode and two-dimensional echocardiography. Journal of Hypertension, 2016, 34, 88-96.	0.3	6
80	Designing an optimum genetic association study using dense SNP markers and family-based sample. Frontiers in Bioscience - Landmark, 2003, 8, s68-80.	3.0	5
81	Measuring Marker Information Content by the Ambiguity of Block Boundaries Observed in Dense SNP Data. Annals of Human Genetics, 2007, 71, 127-140.	0.3	5
82	Genetic association analysis of coronary heart disease by profiling gene-environment interaction based on latent components in longitudinal endophenotypes. BMC Proceedings, 2009, 3, S86.	1.8	5
83	Association and interaction of PPAR-complex gene variants with latent traits of left ventricular diastolic function. BMC Medical Genetics, 2010, 11, 65.	2.1	5
84	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.4	5
85	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	1.4	5
86	A Novel Method Combining Linkage Disequilibrium Information and Imputed Functional Knowledge for tagSNP Selection. Human Heredity, 2007, 64, 243-249.	0.4	4
87	Enrichment analysis of genetic association in genes and pathways by aggregating signals from both rare and common variants. BMC Proceedings, 2011, 5, S52.	1.8	3
88	Whole-Exome Sequencing and hiPSC Cardiomyocyte Models Identify MYRIP, TRAPPC11, and SLC27A6 of Potential Importance to Left Ventricular Hypertrophy in an African Ancestry Population. Frontiers in Genetics, 2021, 12, 588452.	1.1	3
89	Associations Between Genetic Variants of the Natriuretic Peptide System and Blood Pressure Response to Dietary Sodium Intervention: The GenSalt Study. American Journal of Hypertension, 2016, 29, 397-404.	1.0	2
90	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2

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91	Probabilities of identity-by-descent patterns in sibships when the parents are not genotyped. Genetic Epidemiology, 1997, 14, 909-913.	0.6	1
92	The Association of Cell Cycle Checkpoint 2 Variants and Kidney Function: Findings of the Family Blood Pressure Program and the Atherosclerosis Risk in Communities Study. American Journal of Hypertension, 2009, 22, 552-558.	1.0	1
93	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506.	5.8	1
94	Aggregate blood pressure responses to serial dietary sodium and potassium intervention: defining responses using independent component analysis. BMC Genetics, 2015, 16, 64.	2.7	0
95	Whole Exome Analyses to Examine the Impact of Rare Variants on Left Ventricular Traits in African American Participants from the HyperGEN and GENOA Studies. Journal of Hypertension and Management, 2017, 3, .	0.1	0