

# Charleston Wen-Kai Chiang

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

4,226  
citations

279798

23  
h-index

223800

46  
g-index

70  
all docs

70  
docs citations

70  
times ranked

9989  
citing authors

#	ARTICLE	IF	CITATIONS
1	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
2	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. <i>PLoS ONE</i> , 2008, 3, e3583.	2.5	339
3	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
4	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	27.8	328
5	Evidence of widespread selection on standing variation in Europe at height-associated SNPs. <i>Nature Genetics</i> , 2012, 44, 1015-1019.	21.4	315
6	Direct Regulation of Adult Brain Function by the Male-Specific Factor SRY. <i>Current Biology</i> , 2006, 16, 415-420.	3.9	298
7	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	6.0	276
8	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013, 45, 690-696.	21.4	232
9	Population structure of Han Chinese in the modern Taiwanese population based on 10,000 participants in the Taiwan Biobank project. <i>Human Molecular Genetics</i> , 2016, 25, ddw346.	2.9	196
10	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. <i>Nature Genetics</i> , 2015, 47, 1272-1281.	21.4	193
11	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	27.8	161
12	Height-reducing variants and selection for short stature in Sardinia. <i>Nature Genetics</i> , 2015, 47, 1352-1356.	21.4	96
13	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020, 11, 939.	12.8	96
14	Genome-wide association of anthropometric traits in African- and African-derived populations. <i>Human Molecular Genetics</i> , 2010, 19, 2725-2738.	2.9	90
15	A Comprehensive Map of Genetic Variation in the World's Largest Ethnic Group—Han Chinese. <i>Molecular Biology and Evolution</i> , 2018, 35, 2736-2750.	8.9	86
16	Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARE consortium. <i>Human Molecular Genetics</i> , 2011, 20, 2285-2295.	2.9	77
17	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
18	Genomic history of the Sardinian population. <i>Nature Genetics</i> , 2018, 50, 1426-1434.	21.4	71

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19	Genome-wide Association of Copy-Number Variation Reveals an Association between Short Stature and the Presence of Low-Frequency Genomic Deletions. <i>American Journal of Human Genetics</i> , 2011, 89, 751-759.	6.2	63
20	Rapid Assessment of Genetic Ancestry in Populations of Unknown Origin by Genome-Wide Genotyping of Pooled Samples. <i>PLoS Genetics</i> , 2010, 6, e1000866.	3.5	47
21	Conflation of Short Identity-by-Descent Segments Bias Their Inferred Length Distribution. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1287-1296.	1.8	38
22	Ultraconserved Elements: Analyses of Dosage Sensitivity, Motifs and Boundaries. <i>Genetics</i> , 2008, 180, 2277-2293.	2.9	37
23	Genetic determinants of blood-cell traits influence susceptibility to childhood acute lymphoblastic leukemia. <i>American Journal of Human Genetics</i> , 2021, 108, 1823-1835.	6.2	37
24	Population-specific reference panels are crucial for genetic analyses: an example of the CREBRF locus in Native Hawaiians. <i>Human Molecular Genetics</i> , 2020, 29, 2275-2284.	2.9	27
25	Variant to function mapping at single-cell resolution through network propagation. <i>Nature Biotechnology</i> , 2022, 40, 1644-1653.	17.5	25
26	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. <i>American Journal of Human Genetics</i> , 2014, 94, 710-720.	6.2	24
27	Keck OSIRIS AO LIRG Analysis (KOALA): Feedback in the Nuclei of Luminous Infrared Galaxies. <i>Astrophysical Journal</i> , 2019, 871, 166.	4.5	23
28	Association of structural variation with cardiometabolic traits in Finns. <i>American Journal of Human Genetics</i> , 2021, 108, 583-596.	6.2	22
29	The impact of global and local Polynesian genetic ancestry on complex traits in Native Hawaiians. <i>PLoS Genetics</i> , 2021, 17, e1009273.	3.5	20
30	Spatial Localization of Recent Ancestors for Admixed Individuals. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2505-2518.	1.8	19
31	Heritable variation at the chromosome 21 gene ERG is associated with acute lymphoblastic leukemia risk in children with and without Down syndrome. <i>Leukemia</i> , 2019, 33, 2746-2751.	7.2	18
32	Genetic Studies of Hypertrophic Cardiomyopathy in Singaporeans Identify Variants in <i>TNNI3</i> and <i>TNNT2</i> That Are Common in Chinese Patients. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 424-434.	3.6	18
33	Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan. <i>American Journal of Human Genetics</i> , 2020, 107, 60-71.	6.2	18
34	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021, 108, 564-582.	6.2	18
35	Ultraconserved Elements in the Human Genome: Association and Transmission Analyses of Highly Constrained Single-Nucleotide Polymorphisms. <i>Genetics</i> , 2012, 192, 253-266.	2.9	17
36	Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France. <i>Scientific Reports</i> , 2015, 4, 4666.	3.3	16

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37	A genealogical estimate of genetic relationships. American Journal of Human Genetics, 2022, 109, 812-824.	6.2	13
38	Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia. Leukemia, 2022, 36, 865-868.	7.2	9
39	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.	2.9	7
40	The Opportunities and Challenges of Integrating Population Histories Into Genetic Studies for Diverse Populations: A Motivating Example From Native Hawaiians. Frontiers in Genetics, 2021, 12, 643883.	2.3	5
41	The efficacy of detecting variants with small effects on the Affymetrix 6.0 platform using pooled DNA. Human Genetics, 2011, 130, 607-621.	3.8	3
42	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits. The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.7	3
43	Allele frequency differentiation at height-associated SNPs among continental human populations. European Journal of Human Genetics, 2021, 29, 1542-1548.	2.8	2
44	KLFDAPC: a supervised machine learning approach for spatial genetic structure analysis. Briefings in Bioinformatics, 2022, 23, .	6.5	2
45	Abstract IA38: What causes the increased risk of acute lymphoblastic leukemia in Latinos?. , 2020, , .		0
46	Genetic Determinants of Blood Cell Traits Play a Role in Susceptibility to Acute Lymphoblastic Leukemia. Blood, 2020, 136, 10-11.	1.4	0