Chaolong Wang

List of Publications by Year
in descending order

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54 papers	6,041 citations	185998 28 h-index	168136 53 g-index
61 all docs	61 docs citations	61 times ranked	12369 citing authors

#	Article	IF	Citations
1	Association of Public Health Interventions With the Epidemiology of the COVID-19 Outbreak in Wuhan, China. JAMA - Journal of the American Medical Association, 2020, 323, 1915.	3.8	1,333
2	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
3	Prevalence, risk factors, and management of asthma in China: a national cross-sectional study. Lancet, The, 2019, 394, 407-418.	6.3	377
4	Reconstruction of the full transmission dynamics of COVID-19 in Wuhan. Nature, 2020, 584, 420-424.	13.7	371
5	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
6	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.	2.6	347
7	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
8	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	9.4	158
9	Improved Ancestry Estimation for both Genotyping and Sequencing Data using Projection Procrustes Analysis and Genotype Imputation. American Journal of Human Genetics, 2015, 96, 926-937.	2.6	137
10	Ancestry estimation and control of population stratification for sequence-based association studies. Nature Genetics, 2014, 46, 409-415.	9.4	136
11	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
12	Prevalence and risk factors of small airway dysfunction, and association with smoking, in China: findings from a national cross-sectional study. Lancet Respiratory Medicine,the, 2020, 8, 1081-1093.	5.2	129
13	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	13.5	126
14	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	2.5	107
15	A Quantitative Comparison of the Similarity between Genes and Geography in Worldwide Human Populations. PLoS Genetics, 2012, 8, e1002886.	1.5	106
16	Inference of Unexpected Genetic Relatedness among Individuals in HapMap Phase III. American Journal of Human Genetics, 2010, 87, 457-464.	2.6	104
17	Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 13.	0.2	103
18	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	2.6	103

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19	Cooking fuels and risk of all-cause and cardiopulmonary mortality in urban China: a prospective cohort study. The Lancet Global Health, 2020, 8, e430-e439.	2.9	85
20	The Relationship between Imputation Error and Statistical Power in Genetic Association Studies in Diverse Populations. American Journal of Human Genetics, 2009, 85, 692-698.	2.6	68
21	Test for Rare Variants by Environment Interactions in Sequencing Association Studies. Biometrics, 2016, 72, 156-164.	0.8	68
22	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.	1.4	65
23	A Maximum-Likelihood Method to Correct for Allelic Dropout in Microsatellite Data with No Replicate Genotypes. Genetics, 2012, 192, 651-669.	1.2	54
24	Lack of Population Diversity in Commonly Used Human Embryonic Stem-Cell Lines. New England Journal of Medicine, 2010, 362, 183-185.	13.9	49
25	Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. BMC Genetics, 2009, 10, 80.	2.7	46
26	Dynamics and Correlation Among Viral Positivity, Seroconversion, and Disease Severity in COVID-19. Annals of Internal Medicine, 2021, 174, 453-461.	2.0	46
27	Dynamics of the SARS-CoV-2 antibody response up to 10 months after infection. Cellular and Molecular Immunology, 2021, 18, 1832-1834.	4.8	45
28	Genome-Wide Analysis of Protein-Coding Variants in Leprosy. Journal of Investigative Dermatology, 2017, 137, 2544-2551.	0.3	37
29	LASER server: ancestry tracing with genotypes or sequence reads. Bioinformatics, 2017, 33, 2056-2058.	1.8	30
30	Trans-ethnic genome-wide association study of severe COVID-19. Communications Biology, 2021, 4, 1034.	2.0	29
31	Mendelian randomization analysis of 37 clinical factors and coronary artery disease in East Asian and European populations. Genome Medicine, 2022, 14, .	3.6	29
32	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. PLoS Genetics, 2017, 13, e1007021.	1.5	27
33	A Corrected Goodness-of-Fit Index (CGFI) for Model Evaluation in Structural Equation Modeling. Structural Equation Modeling, 2020, 27, 735-749.	2.4	21
34	Genome-wide gene by lead exposure interaction analysis identifies UNC5D as a candidate gene for neurodevelopment. Environmental Health, 2017, 16, 81.	1.7	20
35	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
36	Longitudinal relationships of polycyclic aromatic hydrocarbons exposure and genetic susceptibility with blood lipid profiles. Environment International, 2022, 164, 107259.	4.8	13

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37	Association of G6PD variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. BMJ Open Diabetes Research and Care, 2020, 8, e001091.	1.2	12
38	Risk factors for mortality of critically ill patients with COVID-19 receiving invasive ventilation. International Journal of Medical Sciences, 2021, 18, 1198-1206.	1.1	12
39	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	2.0	10
40	Prospective Study on Plasma MicroRNAâ€4286 and Incident Acute Coronary Syndrome. Journal of the American Heart Association, 2021, 10, e018999.	1.6	10
41	Exploring the Relationship Between Psychiatric Traits and the Risk of Mouth Ulcers Using Bi-Directional Mendelian Randomization. Frontiers in Genetics, 2020, 11, 608630.	1.1	10
42	Causal Graph Among Serum Lipids and Glycemic Traits: A Mendelian Randomization Study. Diabetes, 2022, 71, 1818-1826.	0.3	10
43	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 3854-3864.	1.8	9
44	Liver and Kidney Function Biomarkers, Blood Cell Traits and Risk of Severe COVID-19: A Mendelian Randomization Study. Frontiers in Genetics, 2021, 12, 647303.	1.1	9
45	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	8
46	Genetic Admixture in the Culturally Unique Peranakan Chinese Population in Southeast Asia. Molecular Biology and Evolution, 2021, 38, 4463-4474.	3.5	8
47	Rare variant association test in family-based sequencing studies. Briefings in Bioinformatics, 2016, 18, bbw083.	3.2	6
48	LLR: a latent low-rank approach to colocalizing genetic risk variants in multiple GWAS. Bioinformatics, 2017, 33, 3878-3886.	1.8	6
49	Deconvolution of Bulk Gene Expression Profiles with Single-Cell Transcriptomics to Develop a Cell Type Composition-Based Prognostic Model for Acute Myeloid Leukemia. Frontiers in Cell and Developmental Biology, 2021, 9, 762260.	1.8	5
50	Alternations in the gut microbiota and metabolome with newly diagnosed unstable angina. Journal of Genetics and Genomics, 2022, 49, 240-248.	1.7	3
51	Integrative analysis of scRNA-seq and GWAS data pinpoints periportal hepatocytes as the relevant liver cell types for blood lipids. Human Molecular Genetics, 2020, 29, 3145-3153.	1.4	2
52	Rare variant association tests for ancestry-matched case-control data based on conditional logistic regression. Briefings in Bioinformatics, 2022, , .	3.2	2
53	Sequence Robust Association Test for Familial Data. Biometrics, 2017, 73, 876-884.	0.8	1
54	Factors Associated with Early Invasive Ventilation in Critically Ill Patients with COVID-19: A Single-Centered, Retrospective, Observational Study. SSRN Electronic Journal, 0, , .	0.4	1