Hongsheng Gui

List of Publications by Year
in descending order

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48	2,763	394421	223800
papers	citations	19 h-index	46 g-index

55	55	55	8279
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
2	GATES: A Rapid and Powerful Gene-Based Association Test Using Extended Simes Procedure. American Journal of Human Genetics, 2011, 88, 283-293.	6.2	350
3	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. Nature Communications, 2018, 9, 5269.	12.8	331
4	Evaluating the heritability explained by known susceptibility variants: a survey of ten complex diseases. Genetic Epidemiology, 2011, 35, 310-317.	1.3	265
5	Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2014, 13, 893-903.	10.2	264
6	A comprehensive framework for prioritizing variants in exome sequencing studies of Mendelian diseases. Nucleic Acids Research, 2012, 40, e53-e53.	14.5	229
7	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	21.4	106
8	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
9	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. Genome Biology, 2017, 18, 48.	8.8	72
10	Correction of Hirschsprung-Associated Mutations in Human Induced Pluripotent Stem Cells Via Clustered Regularly Interspaced Short Palindromic Repeats/Cas9, Restores NeuralÂCrest Cell Function. Gastroenterology, 2017, 153, 139-153.e8.	1.3	72
11	Comparisons of seven algorithms for pathway analysis using the WTCCC Crohn's Disease dataset. BMC Research Notes, 2011, 4, 386.	1.4	49
12	Genetic variation in CFH predicts phenytoin-induced maculopapular exanthema in European-descent patients. Neurology, 2018, 90, e332-e341.	1.1	43
13	RET and NRG1 interplay in Hirschsprung disease. Human Genetics, 2013, 132, 591-600.	3.8	42
14	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. Human Molecular Genetics, 2016, 25, ddw333.	2.9	38
15	Prenatal immune activation alters the adult neural epigenome but can be partly stabilised by a n-3 polyunsaturated fatty acid diet. Translational Psychiatry, 2018, 8, 125.	4.8	35
16	Integrative approach identifies corticosteroid response variant in diverse populations with asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 1791-1802.	2.9	33
17	Integrative omics of schizophrenia: from genetic determinants to clinical classification and risk prediction. Molecular Psychiatry, 2022, 27, 113-126.	7.9	33
18	Exome sequencing reveals a high genetic heterogeneity on familial Hirschsprung disease. Scientific Reports, 2015, 5, 16473.	3.3	29

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19	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
20	A Genome-Wide Linkage and Association Scan Reveals Novel Loci for Hypertension and Blood Pressure Traits. PLoS ONE, 2012, 7, e31489.	2.5	26
21	Rare variants and de novo variants in mesial temporal lobe epilepsy with hippocampal sclerosis. Neurology: Genetics, 2018, 4, e245.	1.9	18
22	Polygenic Score for Î²-Blocker Survival Benefit in European Ancestry Patients With Reduced Ejection Fraction Heart Failure. Circulation: Heart Failure, 2020, 13, e007012.	3.9	18
23	Mapping the 17q12â€“21.1 Locus for Variants Associated with Early-Onset Asthma in African Americans. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 424-436.	5.6	16
24	Asthma and its relationship to mitochondrial copy number: Results from the Asthma Translational Genomics Collaborative (ATGC) of the Trans-Omics for Precision Medicine (TOPMed) program. PLoS ONE, 2020, 15, e0242364.	2.5	16
25	Influence of Alzheimer's disease genes on cognitive decline: the Guangzhou Biobank Cohort Study. Neurobiology of Aging, 2014, 35, 2422.e3-2422.e8.	3.1	15
26	Race and Betaâ€Blocker Survival Benefit in Patients With Heart Failure: An Investigation of Selfâ€Reported Race and Proportion of African Genetic Ancestry. Journal of the American Heart Association, 2018, 7, .	3.7	15
27	Depletion of theIKBKAPortholog in zebrafish leads to hirschsprung disease-like phenotype. World Journal of Gastroenterology, 2015, 21, 2040-2046.	3.3	15
28	Association of BDNF Polymorphisms with the Risk of Epilepsy: a Multicenter Study. Molecular Neurobiology, 2016, 53, 2869-2877.	4.0	13
29	A Three-Stage Genome-Wide Association Study Combining Multilocus Test and Gene Expression Analysis for Young-Onset Hypertension in Taiwan Han Chinese. American Journal of Hypertension, 2014, 27, 819-827.	2.0	12
30	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT LigandKITLG/SCFand Gene-By-Air-Pollution Interaction. Genetics, 2020, 215, 869-886.	2.9	11
31	Plasma Proteomic Profile Predicts Survival in Heart Failure With Reduced Ejection Fraction. Circulation Genomic and Precision Medicine, 2021, 14, e003140.	3.6	11
32	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
33	SNP-based HLA allele tagging, imputation and association with antiepileptic drug-induced cutaneous reactions in Hong Kong Han Chinese. Pharmacogenomics Journal, 2018, 18, 340-346.	2.0	10
34	Genetics of heart rate in heart failure patients (GenHRate). Human Genomics, 2019, 13, 22.	2.9	9
35	Targeted Next-Generation Sequencing on Hirschsprung Disease: A Pilot Study Exploits DNA Pooling. Annals of Human Genetics, 2014, 78, 381-387.	0.8	8
36	The Contribution of Genetic Diversity to Subdivide Populations Living in the Silk Road of China. PLoS ONE, 2014, 9, e97344.	2.5	8

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37	Sharing of Genes and Pathways Across Complex Phenotypes: A Multilevel Genome-Wide Analysis. Genetics, 2017, 206, 1601-1609.	2.9	7
38	Performance of the Meta-Analysis Global Group in Chronic Heart Failure Score in Black Patients Compared With Whites. Circulation: Cardiovascular Quality and Outcomes, 2019, 12, e004714.	2.2	6
39	Suppression tumorigenicity 2 (ST2) turbidimetric immunoassay compared to enzyme-linked immunosorbent assay in predicting survival in heart failure patients with reduced ejection fraction. Clinica Chimica Acta, 2020, 510, 767-771.	1.1	6
40	Genetic overlap between epilepsy and schizophrenia: Evidence from cross phenotype analysis in Hong Kong Chinese population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 86-92.	1.7	5
41	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
42	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. Epilepsia, 2021, 62, 1518-1527.	5.1	5
43	Screening of the RET gene of Vietnamese Hirschsprung patients identifies 2 novel missense mutations. Journal of Pediatric Surgery, 2012, 47, 1859-1864.	1.6	4
44	Detecting and distinguishing indicators of risk for suicide using clinical records. Translational Psychiatry, 2022, 12, .	4.8	1
45	A Cardiac-Specific Regulatory Genetic Variant for Protein Kinase C Î± is Significantly Associated with Mortality in Patients with Heart Failure. Journal of Cardiac Failure, 2018, 24, S2.	1.7	0
46	Improving Mitochondrial Function Improves the Plasma Metabolite Profile in Experimental Heart Failure. Journal of Cardiac Failure, 2018, 24, S79-S80.	1.7	0
47	Association of Regulatory Genetic Variants for Protein Kinase CÎ± with Mortality and Drug Efficacy in Patients with Heart Failure. Cardiovascular Drugs and Therapy, 2019, 33, 693-700.	2.6	0
48	Survival Association of Angiotensin Inhibitors in Heart Failure With Reduced Ejection Fraction: Comparisons Using Self-Identified Race and Genomic Ancestry. Journal of Cardiac Failure, 2022, 28, 215-225.	1.7	0