

Guo-Bo Chen

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,993
citations

346980

22
h-index

312153

41
g-index

49
all docs

49
docs citations

49
times ranked

9261
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
2	A Generalized Combinatorial Approach for Detecting Gene-by-Gene and Gene-by-Environment Interactions with Application to Nicotine Dependence. <i>American Journal of Human Genetics</i> , 2007, 80, 1125-1137.	2.6	533
3	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. <i>Lancet, The</i> , 2016, 387, 1085-1093.	6.3	306
4	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. <i>PLoS Genetics</i> , 2014, 10, e1004269.	1.5	303
5	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. <i>American Journal of Human Genetics</i> , 2015, 96, 283-294.	2.6	225
6	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	9.4	215
7	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. <i>Human Molecular Genetics</i> , 2014, 23, 4710-4720.	1.4	110
8	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	3.3	110
9	Estimation of SNP Heritability from Dense Genotype Data. <i>American Journal of Human Genetics</i> , 2013, 93, 1151-1155.	2.6	103
10	A Combinatorial Approach to Detecting Gene-Gene and Gene-Environment Interactions in Family Studies. <i>American Journal of Human Genetics</i> , 2008, 83, 457-467.	2.6	90
11	Bitter taste receptor gene polymorphisms are an important factor in the development of nicotine dependence in African Americans. <i>Journal of Medical Genetics</i> , 2008, 45, 578-582.	1.5	74
12	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. <i>Heredity</i> , 2016, 117, 51-61.	1.2	69
13	Estimating heritability of complex traits from genome-wide association studies using IBS-based Haseman-Elston regression. <i>Frontiers in Genetics</i> , 2014, 5, 107.	1.1	68
14	Gene-Gene Interactions Among CHRNA4, CHRN2, BDNF, and NTRK2 in Nicotine Dependence. <i>Biological Psychiatry</i> , 2008, 64, 951-957.	0.7	60
15	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730.	2.6	60
16	Practical and Theoretical Considerations in Study Design for Detecting Gene-Gene Interactions Using MDR and GMDR Approaches. <i>PLoS ONE</i> , 2011, 6, e16981.	1.1	45
17	GMDR: Versatile Software for Detecting Gene-Gene and Gene-Environment Interactions Underlying Complex Traits. <i>Current Genomics</i> , 2016, 17, 396-402.	0.7	44
18	Susceptibility Locus in Neurokinin-1 Receptor Gene Associated with Alcohol Dependence. <i>Neuropsychopharmacology</i> , 2009, 34, 2442-2449.	2.8	41

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19	Association and Interaction Analyses of GABBR1 and GABBR2 with Nicotine Dependence in European- and African-American Populations. <i>PLoS ONE</i> , 2009, 4, e7055.	1.1	40
20	Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. <i>BMC Medical Genetics</i> , 2017, 18, 94.	2.1	36
21	Identifying loci with breeding potential across temperate and tropical adaptation via EigenGWAS and EnvGWAS. <i>Molecular Ecology</i> , 2019, 28, 3544-3560.	2.0	32
22	Analysis of the Influence of microRNAs in Lithium Response in Bipolar Disorder. <i>Frontiers in Psychiatry</i> , 2018, 9, 207.	1.3	28
23	Genome-scale identification of resistance gene analogs and the development of their intron length polymorphism markers in maize. <i>Molecular Breeding</i> , 2012, 29, 437-447.	1.0	23
24	A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. <i>Human Genetics</i> , 2014, 133, 139-150.	1.8	23
25	Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , 2017, 25, 137-146.	1.4	18
26	Associations of Obesity Genes with Obesity-related Outcomes in Multiethnic Children. <i>Archives of Medical Research</i> , 2011, 42, 509-514.	1.5	15
27	Quantitative genetic analysis station for the genetic analysis of complex traits. <i>Science Bulletin</i> , 2012, 57, 2721-2726.	1.7	13
28	A fast genomic selection approach for large genomic data. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1277-1284.	1.8	12
29	ProteomeExpert: a Docker image-based web server for exploring, modeling, visualizing and mining quantitative proteomic datasets. <i>Bioinformatics</i> , 2021, 37, 273-275.	1.8	12
30	Association of amyloid precursor protein-binding protein, family B, member 1 with nicotine dependence in African and European American smokers. <i>Human Genetics</i> , 2008, 124, 393-398.	1.8	11
31	On the reconciliation of missing heritability for genome-wide association studies. <i>European Journal of Human Genetics</i> , 2016, 24, 1810-1816.	1.4	11
32	A new genomic prediction method with additive-dominance effects in the least-squares framework. <i>Heredity</i> , 2018, 121, 196-204.	1.2	11
33	A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. <i>Statistics and Its Interface</i> , 2011, 4, 295-304.	0.2	11
34	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021, 20, 1079-1086.	1.8	10
35	Development of universal genetic markers based on single-copy orthologous (COSII) genes in Poaceae. <i>Plant Cell Reports</i> , 2013, 32, 379-388.	2.8	9
36	Where is the friend's home?. <i>Frontiers in Genetics</i> , 2014, 5, 400.	1.1	4

#	ARTICLE	IF	CITATIONS
37	Reproduction and In-Depth Evaluation of Genome-Wide Association Studies and Genome-Wide Meta-analyses Using Summary Statistics. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 943-952.	0.8	3
38	EigenGWAS: An online visualizing and interactive application for detecting genomic signatures of natural selection. <i>Molecular Ecology Resources</i> , 2021, 21, 1732-1744.	2.2	2
39	A novel genomic prediction method combining randomized Haseman-Elston regression with a modified algorithm for Proven and Young for large genomic data. <i>Crop Journal</i> , 2021, , .	2.3	2
40	A hidden Markov model for haplotype inference for present-absent data of clustered genes using identified haplotypes and haplotype patterns. <i>Frontiers in Genetics</i> , 2014, 5, 267.	1.1	1
41	A rapid genomic selection method combining Haseman-Elston (HE) model and algorithm for proven and young (APY). <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	1
42	Sun et al.'s study led to the underperformance of EigenGWAS. <i>Heredity</i> , 2019, 123, 283-284.	1.2	0
43	Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612045.	1.1	0