

# 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	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
2	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021, 20, 1079-1086.	1.8	10
3	Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612045.	1.1	0
4	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
5	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
6	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
7	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
8	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
9	Sun et al.'s study led to the underperformance of EigenGWAS. <i>Heredity</i> , 2019, 123, 283-284.	1.2	0
10	Analysis of the Influence of microRNAs in Lithium Response in Bipolar Disorder. <i>Frontiers in Psychiatry</i> , 2018, 9, 207.	1.3	28
11	A new genomic prediction method with additive-dominance effects in the least-squares framework. <i>Heredity</i> , 2018, 121, 196-204.	1.2	11
12	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
13	A fast genomic selection approach for large genomic data. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1277-1284.	1.8	12
14	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
15	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
16	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
17	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
18	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

#	ARTICLE	IF	CITATIONS
19	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
20	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. Lancet, The, 2016, 387, 1085-1093.	6.3	306
21	GMDR: Versatile Software for Detecting Gene-Gene and Gene-Environment Interactions Underlying Complex Traits. Current Genomics, 2016, 17, 396-402.	0.7	44
22	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	2.6	225
23	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
24	Estimating heritability of complex traits from genome-wide association studies using IBS-based Haseman-Elston regression. Frontiers in Genetics, 2014, 5, 107.	1.1	68
25	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. Human Molecular Genetics, 2014, 23, 4710-4720.	1.4	110
26	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303
27	A hidden Markov model for haplotype inference for present-absent data of clustered genes using identified haplotypes and haplotype patterns. Frontiers in Genetics, 2014, 5, 267.	1.1	1
28	Where is the friend's home?. Frontiers in Genetics, 2014, 5, 400.	1.1	4
29	A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. Human Genetics, 2014, 133, 139-150.	1.8	23
30	Development of universal genetic markers based on single-copy orthologous (COSII) genes in Poaceae. Plant Cell Reports, 2013, 32, 379-388.	2.8	9
31	Estimation of SNP Heritability from Dense Genotype Data. American Journal of Human Genetics, 2013, 93, 1151-1155.	2.6	103
32	Quantitative genetic analysis station for the genetic analysis of complex traits. Science Bulletin, 2012, 57, 2721-2726.	1.7	13
33	Genome-scale identification of resistance gene analogs and the development of their intron length polymorphism markers in maize. Molecular Breeding, 2012, 29, 437-447.	1.0	23
34	Practical and Theoretical Considerations in Study Design for Detecting Gene-Gene Interactions Using MDR and GMDR Approaches. PLoS ONE, 2011, 6, e16981.	1.1	45
35	Associations of Obesity Genes with Obesity-related Outcomes in Multiethnic Children. Archives of Medical Research, 2011, 42, 509-514.	1.5	15
36	A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. Statistics and Its Interface, 2011, 4, 295-304.	0.2	11

#	ARTICLE	IF	CITATIONS
37	Association and Interaction Analyses of GABBR1 and GABBR2 with Nicotine Dependence in European- and African-American Populations. PLoS ONE, 2009, 4, e7055.	1.1	40
38	Susceptibility Locus in Neurokinin-1 Receptor Gene Associated with Alcohol Dependence. Neuropsychopharmacology, 2009, 34, 2442-2449.	2.8	41
39	Association of amyloid precursor protein-binding protein, family B, member 1 with nicotine dependence in African and European American smokers. Human Genetics, 2008, 124, 393-398.	1.8	11
40	A Combinatorial Approach to Detecting Gene-Gene and Gene-Environment Interactions in Family Studies. American Journal of Human Genetics, 2008, 83, 457-467.	2.6	90
41	Gene-Gene Interactions Among CHRNA4, CHRN2, BDNF, and NTRK2 in Nicotine Dependence. Biological Psychiatry, 2008, 64, 951-957.	0.7	60
42	Bitter taste receptor gene polymorphisms are an important factor in the development of nicotine dependence in African Americans. Journal of Medical Genetics, 2008, 45, 578-582.	1.5	74
43	A Generalized Combinatorial Approach for Detecting Gene-by-Gene and Gene-by-Environment Interactions with Application to Nicotine Dependence. American Journal of Human Genetics, 2007, 80, 1125-1137.	2.6	533