

Guo-Bo Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/227428/publications.pdf>

Version: 2024-02-01

43

papers

3,993

citations

304743

22

h-index

276875

41

g-index

49

all docs

49

docs citations

49

times ranked

8261

citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542. | 27.8 | 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. | 6.2 | 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. | 13.7 | 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. | 3.5 | 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. | 6.2 | 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. | 21.4 | 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. | 2.9 | 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. | 7.1 | 110 |
| 9 | Estimation of SNP Heritability from Dense Genotype Data. <i>American Journal of Human Genetics</i> , 2013, 93, 1151-1155. | 6.2 | 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. | 6.2 | 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. | 3.2 | 74 |
| 12 | EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. <i>Heredity</i> , 2016, 117, 51-61. | 2.6 | 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. | 2.3 | 68 |
| 14 | Gene-Gene Interactions Among CHRNA4, CHRN2, BDNF, and NTRK2 in Nicotine Dependence. <i>Biological Psychiatry</i> , 2008, 64, 951-957. | 1.3 | 60 |
| 15 | Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730. | 6.2 | 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. | 2.5 | 45 |
| 17 | GMDR: Versatile Software for Detecting Gene-Gene and Gene-Environment Interactions Underlying Complex Traits. <i>Current Genomics</i> , 2016, 17, 396-402. | 1.6 | 44 |
| 18 | Susceptibility Locus in Neurokinin-1 Receptor Gene Associated with Alcohol Dependence. <i>Neuropsychopharmacology</i> , 2009, 34, 2442-2449. | 5.4 | 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. | 2.5 | 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. | 3.9 | 32 |
| 22 | Analysis of the Influence of microRNAs in Lithium Response in Bipolar Disorder. <i>Frontiers in Psychiatry</i> , 2018, 9, 207. | 2.6 | 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. | 2.1 | 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. | 3.8 | 23 |
| 25 | Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , 2017, 25, 137-146. | 2.8 | 18 |
| 26 | Associations of Obesity Genes with Obesity-related Outcomes in Multiethnic Children. <i>Archives of Medical Research</i> , 2011, 42, 509-514. | 3.3 | 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. | 3.6 | 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. | 4.1 | 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. | 3.8 | 11 |
| 31 | On the reconciliation of missing heritability for genome-wide association studies. <i>European Journal of Human Genetics</i> , 2016, 24, 1810-1816. | 2.8 | 11 |
| 32 | A new genomic prediction method with additive-dominance effects in the least-squares framework. <i>Heredity</i> , 2018, 121, 196-204. | 2.6 | 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. | 0.3 | 11 |
| 34 | BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021, 20, 1079-1086. | 3.7 | 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. | 5.6 | 9 |
| 36 | Where is the friend's home?. <i>Frontiers in Genetics</i> , 2014, 5, 400. | 2.3 | 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. | 1.8 | 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. | 4.8 | 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, , . | 5.2 | 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. | 2.3 | 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. | 2.1 | 1 |
| 42 | Sun et al.'s study led to the underperformance of EigenGWAS. <i>Heredity</i> , 2019, 123, 283-284. | 2.6 | 0 |
| 43 | Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612045. | 2.3 | 0 |