Xiaofeng Zhu

List of Publications by Citations

200 papers	8,672 citations	50 h-index	88 g-index
223 ext. papers	10,212 ext. citations	7.3 avg, IF	5.35 L-index

#	Paper	IF	Citations
200	A common genetic variant is associated with adult and childhood obesity. *Science*, **2006**, 312, 279-83	33.3	584
199	Genetic structure, self-identified race/ethnicity, and confounding in case-control association studies. *American Journal of Human Genetics*, **2005**, 76, 268-75	11	446
198	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
197	The landscape of recombination in African Americans. *Nature*, **2011**, 476, 170-5	50.4	243
196	Admixture mapping for hypertension loci with genome-scan markers. *Nature Genetics*, **2005**, 37, 177-81	36.3	224
195	Linkage and association analysis of angiotensin I-converting enzyme (ACE)-gene polymorphisms with ACE concentration and blood pressure. *American Journal of Human Genetics*, **2001**, 68, 1139-48	11	222
194	Reconstructing genetic ancestry blocks in admixed individuals. *American Journal of Human Genetics*, **2006**, 79, 1-12	11	210
193	Transferability of tag SNPs in genetic association studies in multiple populations. *Nature Genetics*, **2006**, 38, 1298-303	36.3	198
192	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. *Nature Genetics*, **2013**, 45, 690-6	36.3	192
191	Meta-analysis of correlated traits via summary statistics from GWASs with an application in hypertension. *American Journal of Human Genetics*, **2015**, 96, 21-36	11	186
190	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. *Nature Genetics*, **2017**, 49, 274-281	36.3	182
189	Corin gene minor allele defined by 2 missense mutations is common in blacks and associated with high blood pressure and hypertension. *Circulation*, **2005**, 112, 2403-10	16.7	166
188	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
187	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. *American Journal of Human Genetics*, **2013**, 93, 545-54	11	145
186	A combined analysis of genomewide linkage scans for body mass index from the National Heart, Lung, and Blood Institute Family Blood Pressure Program. *American Journal of Human Genetics*, **2002**, 70, 1247-56	11	132
185	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
184	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119

183	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
182	The association of a SNP upstream of INSIG2 with body mass index is reproduced in several but not all cohorts. *PLoS Genetics*, **2007**, 3, e61	6	119
181	Association mapping, using a mixture model for complex traits. *Genetic Epidemiology*, **2002**, 23, 181-96	2.6	119
180	A unified association analysis approach for family and unrelated samples correcting for stratification. *American Journal of Human Genetics*, **2008**, 82, 352-65	11	109
179	Associations between hypertension and genes in the renin-angiotensin system. *Hypertension*, **2003**, 41, 1027-34	8.5	105
178	Detecting rare variants for complex traits using family and unrelated data. *Genetic Epidemiology*, **2010**, 34, 171-87	2.6	103
177	The meaning of interaction. *Human Heredity*, **2010**, 70, 269-77	1.1	100
176	Genome-wide characterization of shared and distinct genetic components that influence blood lipid levels in ethnically diverse human populations. *American Journal of Human Genetics*, **2013**, 92, 904-16	11	97
175	Localization of a small genomic region associated with elevated ACE. *American Journal of Human Genetics*, **2000**, 67, 1144-53	11	97
174	Diminished induction of skin fibrosis in mice with MCP-1 deficiency. *Journal of Investigative Dermatology*, **2006**, 126, 1900-8	4.3	92
173	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium. *PLoS Genetics*, **2011**, 7, e1001371	6	86
172	Genome scan among Nigerians linking blood pressure to chromosomes 2, 3, and 19. *Hypertension*, **2002**, 40, 629-33	8.5	83
171	Genome-wide association of anthropometric traits in African- and African-derived populations. *Human Molecular Genetics*, **2010**, 19, 2725-38	5.6	81
170	On a semiparametric test to detect associations between quantitative traits and candidate genes using unrelated individuals. *Genetic Epidemiology*, **2003**, 24, 44-56	2.6	79
169	A candidate gene study of obstructive sleep apnea in European Americans and African Americans. *American Journal of Respiratory and Critical Care Medicine*, **2010**, 182, 947-53	10.2	77
168	Identification, replication, and fine-mapping of Loci associated with adult height in individuals of african ancestry. *PLoS Genetics*, **2011**, 7, e1002298	6	77
167	A test of transmission/disequilibrium for quantitative traits in pedigree data, by multiple regression. *American Journal of Human Genetics*, **1999**, 65, 236-45	11	75
166	Fine mapping of the association with obesity at the FTO locus in African-derived populations. *Human Molecular Genetics*, **2010**, 19, 2907-16	5.6	72

165	Racial admixture and its impact on BMI and blood pressure in African and Mexican Americans. *Human Genetics*, **2006**, 119, 624-33	6.3	72
164	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 194, 886-897	10.2	70
163	Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARe consortium. *Human Molecular Genetics*, **2011**, 20, 2285-95	5.6	70
162	Common variants in the ENPP1 gene are not reproducibly associated with diabetes or obesity. *Diabetes*, **2006**, 55, 3180-4	0.9	69
161	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. *Human Genetics*, **2011**, 130, 725-33	6.3	67
160	Linkage analysis of a complex disease through use of admixed populations. *American Journal of Human Genetics*, **2004**, 74, 1136-53	11	67
159	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
158	Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection. *American Journal of Human Genetics*, **2011**, 89, 368-81	11	63
157	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. *PLoS Genetics*, **2017**, 13, e1006719	6	60
156	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
155	Linkage disequilibrium and haplotype diversity in the genes of the renin-angiotensin system: findings from the family blood pressure program. *Genome Research*, **2003**, 13, 173-81	9.7	59
154	Interrogating local population structure for fine mapping in genome-wide association studies. *Bioinformatics*, **2010**, 26, 2961-8	7.2	58
153	A genome-wide scan for obesity in African-Americans. *Diabetes*, **2002**, 51, 541-4	0.9	58
152	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genetics*, **2017**, 13, e1006728	6	58
151	Genome-wide association studies: implications for multiethnic samples. *Human Molecular Genetics*, **2008**, 17, R151-5	5.6	55
150	Adjustment for local ancestry in genetic association analysis of admixed populations. *Bioinformatics* , **2011**, 27, 670-7	7.2	50
149	Admixture mapping and the role of population structure for localizing disease genes. *Advances in Genetics*, **2008**, 60, 547-69	3.3	49
148	Association of genetic loci with sleep apnea in European Americans and African-Americans: the Candidate Gene Association Resource (CARe). *PLoS ONE*, **2012**, 7, e48836	3.7	48

147	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. *Nature Communications*, **2019**, 10, 3503	17.4	47
146	Genome-wide searching of rare genetic variants in WTCCC data. *Human Genetics*, **2010**, 128, 269-80	6.3	45
145	Pathway-based analysis for genome-wide association studies using supervised principal components. *Genetic Epidemiology*, **2010**, 34, 716-24	2.6	45
144	Association studies of BMI and type 2 diabetes in the neuropeptide Y pathway: a possible role for NPY2R as a candidate gene for type 2 diabetes in men. *Diabetes*, **2007**, 56, 1460-7	0.9	45
143	A genome-wide scan for body mass index among Nigerian families. *Obesity*, **2003**, 11, 266-73		44
142	GEE-based SNP set association test for continuous and discrete traits in family-based association studies. *Genetic Epidemiology*, **2013**, 37, 778-86	2.6	43
141	Genetic background of patients from a university medical center in Manhattan: implications for personalized medicine. *PLoS ONE*, **2011**, 6, e19166	3.7	43
140	Detecting rare and common variants for complex traits: sibpair and odds ratio weighted sum statistics (SPWSS, ORWSS). *Genetic Epidemiology*, **2011**, 35, 398-409	2.6	43
139	Admixture mapping provides evidence of association of the VNN1 gene with hypertension. *PLoS ONE*, **2007**, 2, e1244	3.7	43
138	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
137	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. *American Journal of Human Genetics*, **2016**, 99, 56-75	11	41
136	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
135	A classical likelihood based approach for admixture mapping using EM algorithm. *Human Genetics*, **2006**, 120, 431-45	6.3	38
134	Common variants in DRD2 are associated with sleep duration: the CARe consortium. *Human Molecular Genetics*, **2016**, 25, 167-79	5.6	37
133	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. *American Journal of Respiratory Cell and Molecular Biology*, **2018**, 58, 391-401	5.7	37
132	Improving power in contrasting linkage-disequilibrium patterns between cases and controls. *American Journal of Human Genetics*, **2007**, 80, 911-20	11	36
131	Combined analysis of genomewide scans for adult height: results from the NHLBI Family Blood Pressure Program. *European Journal of Human Genetics*, **2003**, 11, 271-4	5.3	36
130	Linkage for BMI at 3q27 region confirmed in an African-American population. *Diabetes*, **2003**, 52, 1284-7	0.9	35

129	Gene, pathway and network frameworks to identify epistatic interactions of single nucleotide polymorphisms derived from GWAS data. *BMC Systems Biology*, **2012**, 6 Suppl 3, S15	3.5	34
128	Statistical interaction in human genetics: how should we model it if we are looking for biological interaction?. *Nature Reviews Genetics*, **2011**, 12, 74	30.1	34
127	Rapid assessment of genetic ancestry in populations of unknown origin by genome-wide genotyping of pooled samples. *PLoS Genetics*, **2010**, 6, e1000866	6	33
126	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
125	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. *Nature Communications*, **2019**, 10, 5121	17.4	31
124	Admixture mapping of quantitative trait loci for BMI in African Americans: evidence for loci on chromosomes 3q, 5q, and 15q. *Obesity*, **2009**, 17, 1226-31	8	31
123	What is the significance of difference in phenotypic variability across SNP genotypes?. *American Journal of Human Genetics*, **2013**, 93, 390-7	11	29
122	Two major QTLs and several others relate to factors of metabolic syndrome in the family blood pressure program. *Hypertension*, **2005**, 46, 751-7	8.5	29
121	Transmission/disequilibrium tests for quantitative traits. *Genetic Epidemiology*, **2001**, 20, 57-74	2.6	29
120	Admixture mapping of quantitative trait loci for blood lipids in African-Americans. *Human Molecular Genetics*, **2009**, 18, 2091-8	5.6	27
119	Angiotensin I-converting enzyme polymorphisms, ACE level and blood pressure among Nigerians, Jamaicans and African-Americans. *European Journal of Human Genetics*, **2004**, 12, 460-8	5.3	27
118	Determinants of hypertension in a young adult Ugandan population in epidemiological transition-the MEPI-CVD survey. *BMC Public Health*, **2015**, 15, 830	4.1	26
117	Haplotypes produced from rare variants in the promoter and coding regions of angiotensinogen contribute to variation in angiotensinogen levels. *Human Molecular Genetics*, **2005**, 14, 639-43	5.6	25
116	Analysis of Genetic Association Studies **2012**,		24
115	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
114	Variants in CXADR and F2RL1 are associated with blood pressure and obesity in African-Americans in regions identified through admixture mapping. *Journal of Hypertension*, **2012**, 30, 1970-6	1.9	23
113	Genome-wide distribution of ancestry in Mexican Americans. *Human Genetics*, **2008**, 124, 207-14	6.3	23
112	Heterogeneity in older people: examining physiologic failure, age, and comorbidity. *Journal of the American Geriatrics Society*, **2002**, 50, 1955-61	5.6	23

111	Gene-gene and gene-environment interactions in ulcerative colitis. *Human Genetics*, **2014**, 133, 547-58	6.3	22
110	Finding dense and connected subgraphs in dual networks **2015**,		21
109	Systems biology analyses of gene expression and genome wide association study data in obstructive sleep apnea. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2011**, 14-25	1.3	21
108	Power comparison of admixture mapping and direct association analysis in genome-wide association studies. *Genetic Epidemiology*, **2012**, 36, 235-43	2.6	20
107	An association study of angiotensinogen polymorphisms with serum level and hypertension in an African-American population. *Journal of Hypertension*, **2003**, 21, 1847-52	1.9	20
106	A genome scan among Nigerians linking resting energy expenditure to chromosome 16. *Obesity*, **2004**, 12, 577-81		20
105	Erythrocyte sodium-lithium countertransport and blood pressure: a genome-wide linkage study. *Hypertension*, **2003**, 41, 842-6	8.5	20
104	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. *Genetic Epidemiology*, **2016**, 40, 222-32	2.6	20
103	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. *Human Molecular Genetics*, **2019**, 28, 675-687	5.6	20
102	A variance component based multi-marker association test using family and unrelated data. *BMC Genetics*, **2013**, 14, 17	2.6	19
101	Angiotensin-converting enzyme gene polymorphisms and obesity: an examination of three black populations. *Obesity*, **2005**, 13, 823-8		19
100	A genome-wide linkage and association study using COGA data. *BMC Genetics*, **2005**, 6 Suppl 1, S128	2.6	18
99	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. *Sleep*, **2019**, 42,	1.1	16
98	Discovery of common sequences absent in the human reference genome using pooled samples from next generation sequencing. *BMC Genomics*, **2014**, 15, 685	4.5	16
97	Analytical correction for multiple testing in admixture mapping. *Human Heredity*, **2006**, 62, 55-63	1.1	16
96	Racial differences and the genetics of hypertension. *Current Hypertension Reports*, **2001**, 3, 19-24	4.7	16
95	Identification of PIEZO1 polymorphisms for human bone mineral density. *Bone*, **2020**, 133, 115247	4.7	15
94	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. *Human Molecular Genetics*, **2016**, 25, 5244-5253	5.6	15

93	A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. *Human Genetics*, **2014**, 133, 139-50	6.3	15
92	Five blood pressure loci identified by an updated genome-wide linkage scan: meta-analysis of the Family Blood Pressure Program. *American Journal of Hypertension*, **2011**, 24, 347-54	2.3	15
91	An Empirical Comparison of Joint and Stratified Frameworks for Studying G E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
90	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. *Human Genetics*, **2019**, 138, 199-210	6.3	14
89	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. *PLoS Genetics*, **2019**, 15, e1007739	6	14
88	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
87	The association of the vanin-1 N131S variant with blood pressure is mediated by endoplasmic reticulum-associated degradation and loss of function. *PLoS Genetics*, **2014**, 10, e1004641	6	14
86	Association of regions on chromosomes 6 and 7 with blood pressure in Nigerian families. *Circulation: Cardiovascular Genetics*, **2009**, 2, 38-45		14
85	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. *PLoS ONE*, **2016**, 11, e0163912	3.7	14
84	Mining Dual Networks. *ACM Transactions on Knowledge Discovery From Data*, **2016**, 10, 1-37	4	14
83	Assessing the impact of global versus local ancestry in association studies. *BMC Proceedings*, **2009**, 3 Suppl 7, S107	2.3	13
82	A novel approach to detect cumulative genetic effects and genetic interactions in Crohn disease. *Inflammatory Bowel Diseases*, **2013**, 19, 1799-808	4.5	12
81	Using the optimal robust receiver operating characteristic (ROC) curve for predictive genetic tests. *Biometrics*, **2010**, 66, 586-93	1.8	12
80	Study of the relationship between the interleukin-6 gene and obstructive sleep apnea. *Clinical and Translational Science*, **2010**, 3, 337-9	4.9	12
79	Variants for HDL-C, LDL-C, and triglycerides identified from admixture mapping and fine-mapping analysis in African American families. *Circulation: Cardiovascular Genetics*, **2015**, 8, 106-13		11
78	Capability of common SNPs to tag rare variants. *BMC Proceedings*, **2011**, 5 Suppl 9, S88	2.3	11
77	A combinatorial searching method for detecting a set of interacting loci associated with complex traits. *Annals of Human Genetics*, **2006**, 70, 677-92	2.2	11
76	Refinement of the DFNA41 locus and candidate genes analysis. *Journal of Human Genetics*, **2005**, 50, 516-522	4.3	11

75	Power comparison of regression methods to test quantitative traits for association and linkage. *Genetic Epidemiology*, **2000**, 18, 322-30	2.6	11
74	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. *PLoS Genetics* , **2017**, 13, e1006678	6	11
73	A genome-wide scan of loci linked to serum adiponectin in two populations of African descent. *Obesity*, **2007**, 15, 1207-14	8	10
72	Genetic effects on blood pressure localized to chromosomes 6 and 7. *Journal of Hypertension*, **2005**, 23, 1367-73	1.9	10
71	Height associated variants demonstrate assortative mating in human populations. *Scientific Reports* , **2017**, 7, 15689	4.9	9
70	Model-free age-of-onset methods applied to the linkage of bipolar disorder. *Genetic Epidemiology*, **1997**, 14, 711-6	2.6	9
69	A genome-wide search replicates evidence of a quantitative trait locus for circulating angiotensin I-converting enzyme (ACE) unlinked to the ACE gene. *BMC Medical Genomics*, **2008**, 1, 23	3.7	9
68	Association between evolutionary history of angiotensinogen haplotypes and plasma levels. *Human Genetics*, **2004**, 115, 310-8	6.3	9
67	Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. *Genetic Epidemiology*, **2017**, 41, 122-135	2.6	8
66	FAM222A encodes a protein which accumulates in plaques in Alzheimer℞ disease. *Nature Communications*, **2020**, 11, 411	17.4	8
65	De novo mutations discovered in 8 Mexican American families through whole genome sequencing. *BMC Proceedings*, **2014**, 8, S24	2.3	8
64	EINVis: a visualization tool for analyzing and exploring genetic interactions in large-scale association studies. *Genetic Epidemiology*, **2013**, 37, 675-85	2.6	8
63	An iterative approach to detect pleiotropy and perform Mendelian Randomization analysis using GWAS summary statistics. *Bioinformatics*, **2021**, 37, 1390-1400	7.2	8
62	VarExp: estimating variance explained by genome-wide GxE summary statistics. *Bioinformatics*, **2018**, 34, 3412-3414	7.2	7
61	Linkage disequilibrium analysis of the renin-angiotensin system genes. *Current Hypertension Reports*, **2003**, 5, 40-6	4.7	7
60	Testing quantitative traits for association and linkage in the presence or absence of parental data. *Human Heredity*, **2001**, 51, 183-91	1.1	7
59	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S157-61	2.6	7
58	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. *American Journal of Human Genetics*, **2021**, 108, 564-582	11	7

57	Cross-Phenotype Association Analysis Using Summary Statistics from GWAS. *Methods in Molecular Biology*, **2017**, 1666, 455-467	1.4	6
56	Extracellular matrix derived by human umbilical cord-deposited mesenchymal stem cells accelerates chondrocyte proliferation and differentiation potential in vitro. *Cell and Tissue Banking*, **2019**, 20, 351-365	2.2	6
55	Whole genome sequencing data from pedigrees suggests linkage disequilibrium among rare variants created by population admixture. *BMC Proceedings*, **2014**, 8, S44	2.3	6
54	Genomic regions associated with susceptibility to Barrett's esophagus and esophageal adenocarcinoma in African Americans: The cross BETRNet admixture study. *PLoS ONE*, **2017**, 12, e0184962	2.7	5
53	Detecting rare variants. *Methods in Molecular Biology*, **2012**, 850, 453-64	1.4	5
52	Identifying rare variants from exome scans: the GAW17 experience. *BMC Proceedings*, **2011**, 5 Suppl 9, S1	2.3	5
51	Rare variant density across the genome and across populations. *BMC Proceedings*, **2011**, 5 Suppl 9, S39	2.3	5
50	Analysis of exome sequences with and without incorporating prior biological knowledge. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S48-55	2.6	5
49	Mendelian randomization and pleiotropy analysis. *Quantitative Biology*, **2021**, 9, 122-132	3.9	5
48	and Study on an Injectable Glycol Chitosan/Dibenzaldehyde-Terminated Polyethylene Glycol Hydrogel in Repairing Articular Cartilage Defects. *Frontiers in Bioengineering and Biotechnology*, **2021**, 9, 607709	5.8	5
47	A Generalized Sequential Bonferroni Procedure for GWAS in Admixed Populations Incorporating Admixture Mapping Information into Association Tests. *Human Heredity*, **2015**, 79, 80-92	1.1	4
46	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. *American Journal of Human Genetics*, **2019**, 105, 1057-1068	11	4
45	Identifying Rare Variant Associations in Admixed Populations. *Scientific Reports*, **2019**, 9, 5458	4.9	3
44	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
43	Gene Mapping in Admixed Families: A Cautionary Note on the Interpretation of the Transmission Disequilibrium Test and a Possible Solution. *Human Heredity*, **2016**, 81, 106-116	1.1	3
42	The efficacy of detecting variants with small effects on the Affymetrix 6.0 platform using pooled DNA. *Human Genetics*, **2011**, 130, 607-21	6.3	3
41	Evaluation of a LASSO regression approach on the unrelated samples of Genetic Analysis Workshop 17. *BMC Proceedings*, **2011**, 5 Suppl 9, S12	2.3	3
40	Interrogating population structure and its impact on association tests. *BMC Proceedings*, **2011**, 5 Suppl 9, S25	2.3	3

39	Testing gene-environment interactions in gene-based association studies. *BMC Proceedings*, **2011**, 5 Suppl 9, S26	2.3	3
38	A novel method to detect rare variants using both family and unrelated case-control data. *BMC Proceedings*, **2011**, 5 Suppl 9, S80	2.3	3
37	Identifying genetic variation affecting a complex trait in simulated data: a comparison of meta-analysis with pooled data analysis. *BMC Genetics*, **2005**, 6 Suppl 1, S97	2.6	3
36	Association and linkage analysis of ICD-10 diagnosis for alcoholism. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S343-7	2.6	3
35	The analysis of ethnic mixtures. *Methods in Molecular Biology*, **2012**, 850, 465-81	1.4	3
34	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
33	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. *European Journal of Human Genetics*, **2019**, 27, 269-277	5.3	3
32	Adjustment for covariates using summary statistics of genome-wide association studies. *Genetic Epidemiology*, **2018**, 42, 812-825	2.6	3
31	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. *Genome Medicine*, **2021**, 13, 136	14.4	3
30	The Analysis of Ethnic Mixtures. *Methods in Molecular Biology*, **2017**, 1666, 505-525	1.4	2
29	A method to correct for population structure using a segregation model. *BMC Proceedings*, **2009**, 3 Suppl 7, S104	2.3	2
28	A genome-wide linkage study of GAW15 gene expression data. *BMC Proceedings*, **2007**, 1 Suppl 1, S87	2.3	2
27	Localization of the Q1 mutation by cladistic analysis. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S594-9	2.6	2
26	Detecting association with rare variants for common diseases using haplotype-based methods. *Statistics and Its Interface*, **2011**, 4, 273-283	0.4	2
25	Cardiometabolic risks of SARS-CoV-2 hospitalization using Mendelian Randomization. *Scientific Reports*, **2021**, 11, 7848	4.9	2
24	Calibrating Population Stratification in Association Analysis. *Methods in Molecular Biology*, **2017**, 1666, 441-453	1.4	1
23	Linkage-disequilibrium-based binning misleads the interpretation of genome-wide association studies. *American Journal of Human Genetics*, **2012**, 91, 965-8; author reply 969-70	11	1
22	Comparison of a unified analysis approach for family and unrelated samples with the transmission-disequilibrium test to study associations of hypertension in the Framingham Heart Study. *BMC Proceedings*, **2009**, 3 Suppl 7, S22	2.3	1

21	Population-Based Association Studies **2009**, 171-190		1
20	An integrated genome-wide association analysis on rheumatoid arthritis data. *BMC Proceedings*, **2007**, 1 Suppl 1, S35	2.3	1
19	Replication of European hypertension associations in a case-control study of 9,534 African Americans. *PLoS ONE*, **2021**, 16, e0259962	3.7	1
18	Allowing for population stratification in association analysis. *Methods in Molecular Biology*, **2012**, 850, 399-409	1.4	1
17	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile		1
16	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits		1
15	Detecting fitness epistasis in recently admixed populations with genome-wide data. *BMC Genomics*, **2020**, 21, 476	4.5	1
14	Local Ancestry Inference in Large Pedigrees. *Scientific Reports*, **2020**, 10, 189	4.9	0
13	Finding susceptible and protective interaction patterns in large-scale genetic association study. *Frontiers of Computer Science*, **2017**, 11, 541-554	2.2	0
12	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study.. *Scientific Reports*, **2022**, 12, 1472	4.9	0
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