Xiaofeng Zhu

List of Publications by Year in Descending Order

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	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study.. *Scientific Reports*, **2022**, 12, 1472	4.9	0
199	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	
198	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
197	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
196	Replication of European hypertension associations in a case-control study of 9,534 African Americans. *PLoS ONE*, **2021**, 16, e0259962	3.7	1
195	Mendelian randomization and pleiotropy analysis. *Quantitative Biology*, **2021**, 9, 122-132	3.9	5
194	An iterative approach to detect pleiotropy and perform Mendelian Randomization analysis using GWAS summary statistics. *Bioinformatics*, **2021**, 37, 1390-1400	7.2	8
193	Cardiometabolic risks of SARS-CoV-2 hospitalization using Mendelian Randomization. *Scientific Reports*, **2021**, 11, 7848	4.9	2
192	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
191	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
190	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
189	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. *Genome Medicine*, **2021**, 13, 136	14.4	3
188	Identification of PIEZO1 polymorphisms for human bone mineral density. *Bone*, **2020**, 133, 115247	4.7	15
187	Local Ancestry Inference in Large Pedigrees. *Scientific Reports*, **2020**, 10, 189	4.9	0
186	FAM222A encodes a protein which accumulates in plaques in Alzheimer's disease. *Nature Communications*, **2020**, 11, 411	17.4	8
185	Detecting fitness epistasis in recently admixed populations with genome-wide data. *BMC Genomics*, **2020**, 21, 476	4.5	1
184	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39

183	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
182	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
181	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
180	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
179	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. *PLoS Genetics*, **2019**, 15, e1007739	6	14
178	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
177	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
176	Identifying Rare Variant Associations in Admixed Populations. *Scientific Reports*, **2019**, 9, 5458	4.9	3
175	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. *Nature Communications*, **2019**, 10, 3503	17.4	47
174	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
173	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
172	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. *Human Molecular Genetics*, **2019**, 28, 675-687	5.6	20
171	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
170	VarExp: estimating variance explained by genome-wide GxE summary statistics. *Bioinformatics*, **2018**, 34, 3412-3414	7.2	7
169	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
168	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
167	Rare Variant Analysis in Unrelated Individuals. *Translational Bioinformatics*, **2018**, 27-44		
166	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64

165	Adjustment for covariates using summary statistics of genome-wide association studies. *Genetic Epidemiology*, **2018**, 42, 812-825	2.6	3
164	Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. *Genetic Epidemiology*, **2017**, 41, 122-135	2.6	8
163	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
162	Calibrating Population Stratification in Association Analysis. *Methods in Molecular Biology*, **2017**, 1666, 441-453	1.4	1
161	Cross-Phenotype Association Analysis Using Summary Statistics from GWAS. *Methods in Molecular Biology*, **2017**, 1666, 455-467	1.4	6
160	The Analysis of Ethnic Mixtures. *Methods in Molecular Biology*, **2017**, 1666, 505-525	1.4	2
159	Detecting Multiethnic Rare Variants. *Methods in Molecular Biology*, **2017**, 1666, 527-538	1.4	
158	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	3.7	5
157	Height associated variants demonstrate assortative mating in human populations. *Scientific Reports*, **2017**, 7, 15689	4.9	9
156	Finding susceptible and protective interaction patterns in large-scale genetic association study. *Frontiers of Computer Science*, **2017**, 11, 541-554	2.2	0
155	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. *PLoS Genetics*, **2017**, 13, e1006678	6	11
154	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
153	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
152	Common variants in DRD2 are associated with sleep duration: the CARe consortium. *Human Molecular Genetics*, **2016**, 25, 167-79	5.6	37
151	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
150	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. *Human Molecular Genetics*, **2016**, 25, 5244-5253	5.6	15
149	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
148	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

147	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
146	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. *PLoS ONE*, **2016**, 11, e0163912	3.7	14
145	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
144	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. *Genetic Epidemiology*, **2016**, 40, 222-32	2.6	20
143	Mining Dual Networks. *ACM Transactions on Knowledge Discovery From Data*, **2016**, 10, 1-37	4	14
142	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119
141	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
140	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
139	Finding dense and connected subgraphs in dual networks **2015**,		21
138	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
137	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
136	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
135	De novo mutations discovered in 8 Mexican American families through whole genome sequencing. *BMC Proceedings*, **2014**, 8, S24	2.3	8
134	Whole genome sequencing data from pedigrees suggests linkage disequilibrium among rare variants created by population admixture. *BMC Proceedings*, **2014**, 8, S44	2.3	6
133	Gene-gene and gene-environment interactions in ulcerative colitis. *Human Genetics*, **2014**, 133, 547-58	6.3	22
132	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
131	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
130	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

129	A variance component based multi-marker association test using family and unrelated data. *BMC Genetics*, **2013**, 14, 17	2.6	19
128	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
127	What is the significance of difference in phenotypic variability across SNP genotypes?. *American Journal of Human Genetics*, **2013**, 93, 390-7	11	29
126	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
125	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
124	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
123	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
122	EINVis: a visualization tool for analyzing and exploring genetic interactions in large-scale association studies. *Genetic Epidemiology*, **2013**, 37, 675-85	2.6	8
121	A novel approach to detect cumulative genetic effects and genetic interactions in Crohn's disease. *Inflammatory Bowel Diseases*, **2013**, 19, 1799-808	4.5	12
120	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
119	Analysis of Genetic Association Studies **2012**,		24
118	Detecting rare variants. *Methods in Molecular Biology*, **2012**, 850, 453-64	1.4	5
117	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
116	Power comparison of admixture mapping and direct association analysis in genome-wide association studies. *Genetic Epidemiology*, **2012**, 36, 235-43	2.6	20
115	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
114	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
113	Allowing for population stratification in association analysis. *Methods in Molecular Biology*, **2012**, 850, 399-409	1.4	1
112	The analysis of ethnic mixtures. *Methods in Molecular Biology*, **2012**, 850, 465-81	1.4	3

111	Gene-Environment Interactions **2012**, 287-308		
110	Haplotype Analysis for Case-Control Data **2012**, 209-233		
109	Population Structure **2012**, 259-286		
108	Rare Variants Analysis in Unrelated Individuals. *Translational Bioinformatics*, **2012**, 121-138		
107	Gene-Gene Interactions **2012**, 235-256		
106	Analysis of Family Data **2012**, 353-387		
105	Introduction to Genetic Epidemiology **2012**, 33-58		
104	Genetic background of patients from a university medical center in Manhattan: implications for personalized medicine. *PLoS ONE*, **2011**, 6, e19166	3.7	43
103	The CRPandGDNFGenes Do Not Contribute to ApneaHypopnea Index or Risk of Obstructive Sleep Apnea. *American Journal of Respiratory and Critical Care Medicine*, **2011**, 184, 144-145	10.2	
102	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
101	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
100	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
99	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. *Human Genetics*, **2011**, 130, 725-33	6.3	67
98	Identifying rare variants from exome scans: the GAW17 experience. *BMC Proceedings*, **2011**, 5 Suppl 9, S1	2.3	5
97	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
96	Interrogating population structure and its impact on association tests. *BMC Proceedings*, **2011**, 5 Suppl 9, S25	2.3	3
95	Testing gene-environment interactions in gene-based association studies. *BMC Proceedings*, **2011**, 5 Suppl 9, S26	2.3	3
94	Rare variant density across the genome and across populations. *BMC Proceedings*, **2011**, 5 Suppl 9, S39	2.3	5

93	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
92	Capability of common SNPs to tag rare variants. *BMC Proceedings*, **2011**, 5 Suppl 9, S88	2.3	11
91	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
90	Analysis of exome sequences with and without incorporating prior biological knowledge. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S48-55	2.6	5
89	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
88	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
87	The landscape of recombination in African Americans. *Nature*, **2011**, 476, 170-5	50.4	243
86	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
85	Adjustment for local ancestry in genetic association analysis of admixed populations. *Bioinformatics* , **2011**, 27, 670-7	7.2	50
84	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
83	Identification, replication, and fine-mapping of Loci associated with adult height in individuals of african ancestry. *PLoS Genetics*, **2011**, 7, e1002298	6	77
82	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
81	Detecting association with rare variants for common diseases using haplotype-based methods. *Statistics and Its Interface*, **2011**, 4, 273-283	0.4	2
80	Using the optimal robust receiver operating characteristic (ROC) curve for predictive genetic tests. *Biometrics*, **2010**, 66, 586-93	1.8	12
79	Genome-wide association of anthropometric traits in African- and African-derived populations. *Human Molecular Genetics*, **2010**, 19, 2725-38	5.6	81
78	Rapid assessment of genetic ancestry in populations of unknown origin by genome-wide genotyping of pooled samples. *PLoS Genetics*, **2010**, 6, e1000866	6	33
77	The meaning of interaction. *Human Heredity*, **2010**, 70, 269-77	1.1	100
76	Interrogating local population structure for fine mapping in genome-wide association studies. *Bioinformatics*, **2010**, 26, 2961-8	7.2	58

75	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
74	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
73	Genome-wide searching of rare genetic variants in WTCCC data. *Human Genetics*, **2010**, 128, 269-80	6.3	45
72	Study of the relationship between the interleukin-6 gene and obstructive sleep apnea. *Clinical and Translational Science*, **2010**, 3, 337-9	4.9	12
71	Detecting rare variants for complex traits using family and unrelated data. *Genetic Epidemiology*, **2010**, 34, 171-87	2.6	103
70	Pathway-based analysis for genome-wide association studies using supervised principal components. *Genetic Epidemiology*, **2010**, 34, 716-24	2.6	45
69	Admixture mapping of quantitative trait loci for blood lipids in African-Americans. *Human Molecular Genetics*, **2009**, 18, 2091-8	5.6	27
68	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
67	A method to correct for population structure using a segregation model. *BMC Proceedings*, **2009**, 3 Suppl 7, S104	2.3	2
66	Assessing the impact of global versus local ancestry in association studies. *BMC Proceedings*, **2009**, 3 Suppl 7, S107	2.3	13
65	Association of regions on chromosomes 6 and 7 with blood pressure in Nigerian families. *Circulation: Cardiovascular Genetics*, **2009**, 2, 38-45		14
64	Population-Based Association Studies **2009**, 171-190		1
63	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
62	Admixture mapping and the role of population structure for localizing disease genes. *Advances in Genetics*, **2008**, 60, 547-69	3.3	49
61	Genome-wide association studies: implications for multiethnic samples. *Human Molecular Genetics*, **2008**, 17, R151-5	5.6	55
60	Genome-wide distribution of ancestry in Mexican Americans. *Human Genetics*, **2008**, 124, 207-14	6.3	23
59	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
58	A unified association analysis approach for family and unrelated samples correcting for stratification. *American Journal of Human Genetics*, **2008**, 82, 352-65	11	109

57	Admixture mapping provides evidence of association of the VNN1 gene with hypertension. *PLoS ONE*, **2007**, 2, e1244	3.7	43
56	A genome-wide linkage study of GAW15 gene expression data. *BMC Proceedings*, **2007**, 1 Suppl 1, S87	2.3	2
55	A genome-wide scan of loci linked to serum adiponectin in two populations of African descent. *Obesity*, **2007**, 15, 1207-14	8	10
54	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
53	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
52	An integrated genome-wide association analysis on rheumatoid arthritis data. *BMC Proceedings*, **2007**, 1 Suppl 1, S35	2.3	1
51	Improving power in contrasting linkage-disequilibrium patterns between cases and controls. *American Journal of Human Genetics*, **2007**, 80, 911-20	11	36
50	Analytical correction for multiple testing in admixture mapping. *Human Heredity*, **2006**, 62, 55-63	1.1	16
49	Common variants in the ENPP1 gene are not reproducibly associated with diabetes or obesity. *Diabetes*, **2006**, 55, 3180-4	0.9	69
48	A common genetic variant is associated with adult and childhood obesity. *Science*, **2006**, 312, 279-83	33.3	584
47	Reconstructing genetic ancestry blocks in admixed individuals. *American Journal of Human Genetics*, **2006**, 79, 1-12	11	210
46	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
45	Transferability of tag SNPs in genetic association studies in multiple populations. *Nature Genetics*, **2006**, 38, 1298-303	36.3	198
44	Diminished induction of skin fibrosis in mice with MCP-1 deficiency. *Journal of Investigative Dermatology*, **2006**, 126, 1900-8	4.3	92
43	Racial admixture and its impact on BMI and blood pressure in African and Mexican Americans. *Human Genetics*, **2006**, 119, 624-33	6.3	72
42	A classical likelihood based approach for admixture mapping using EM algorithm. *Human Genetics*, **2006**, 120, 431-45	6.3	38
41	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
40	Genetic structure, self-identified race/ethnicity, and confounding in case-control association studies. *American Journal of Human Genetics*, **2005**, 76, 268-75	11	446

39	Genetic effects on blood pressure localized to chromosomes 6 and 7. *Journal of Hypertension*, **2005**, 23, 1367-73	1.9	10
38	Angiotensin-converting enzyme gene polymorphisms and obesity: an examination of three black populations. *Obesity*, **2005**, 13, 823-8		19
37	Admixture mapping for hypertension loci with genome-scan markers. *Nature Genetics*, **2005**, 37, 177-81	36.3	224
36	Refinement of the DFNA41 locus and candidate genes analysis. *Journal of Human Genetics*, **2005**, 50, 516-522	4.3	11
35	A genome-wide linkage and association study using COGA data. *BMC Genetics*, **2005**, 6 Suppl 1, S128	2.6	18
34	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
33	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
32	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
31	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
30	A genome scan among Nigerians linking resting energy expenditure to chromosome 16. *Obesity*, **2004**, 12, 577-81		20
29	Association between evolutionary history of angiotensinogen haplotypes and plasma levels. *Human Genetics*, **2004**, 115, 310-8	6.3	9
28	Linkage analysis of a complex disease through use of admixed populations. *American Journal of Human Genetics*, **2004**, 74, 1136-53	11	67
27	Associations between hypertension and genes in the renin-angiotensin system. *Hypertension*, **2003**, 41, 1027-34	8.5	105
26	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
25	Linkage disequilibrium analysis of the renin-angiotensin system genes. *Current Hypertension Reports*, **2003**, 5, 40-6	4.7	7
24	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
23	A genome-wide scan for body mass index among Nigerian families. *Obesity*, **2003**, 11, 266-73		44
22	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

21	Erythrocyte sodium-lithium countertransport and blood pressure: a genome-wide linkage study. *Hypertension*, **2003**, 41, 842-6	8.5	20
20	Linkage for BMI at 3q27 region confirmed in an African-American population. *Diabetes*, **2003**, 52, 1284-7	0.9	35
19	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
18	Association mapping, using a mixture model for complex traits. *Genetic Epidemiology*, **2002**, 23, 181-96	2.6	119
17	Heterogeneity in older people: examining physiologic failure, age, and comorbidity. *Journal of the American Geriatrics Society*, **2002**, 50, 1955-61	5.6	23
16	Genome scan among Nigerians linking blood pressure to chromosomes 2, 3, and 19. *Hypertension*, **2002**, 40, 629-33	8.5	83
15	A genome-wide scan for obesity in African-Americans. *Diabetes*, **2002**, 51, 541-4	0.9	58
14	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
13	Localization of the Q1 mutation by cladistic analysis. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S594-9	2.6	2
12	Racial differences and the genetics of hypertension. *Current Hypertension Reports*, **2001**, 3, 19-24	4.7	16
11	Transmission/disequilibrium tests for quantitative traits. *Genetic Epidemiology*, **2001**, 20, 57-74	2.6	29
10	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
9	Testing quantitative traits for association and linkage in the presence or absence of parental data. *Human Heredity*, **2001**, 51, 183-91	1.1	7
8	Power comparison of regression methods to test quantitative traits for association and linkage. *Genetic Epidemiology*, **2000**, 18, 322-30	2.6	11
7	Localization of a small genomic region associated with elevated ACE. *American Journal of Human Genetics*, **2000**, 67, 1144-53	11	97
6	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
5	Association and linkage analysis of ICD-10 diagnosis for alcoholism. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S343-7	2.6	3
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2	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
1	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits		1