Xiaofeng Zhu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7199030/publications.pdf

Version: 2024-02-01

203 papers	11,394 citations	28190 55 h-index	35952 97 g-index
223 all docs	223 docs citations	223 times ranked	14746 citing authors

#	Article	IF	Citations
1	Genomeâ€wide pleiotropy analysis identifies novel blood pressure variants and improves its polygenic risk scores. Genetic Epidemiology, 2022, 46, 105-121.	0.6	6
2	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	1.6	2
3	Threeâ€dimensional highâ€resolution T₁ and T₂ mapping of whole macaque brain at 9.4 T using magnetic resonance fingerprinting. Magnetic Resonance in Medicine, 2022, 87, 2901-2913.	1.9	3
4	Habitual Dietary Fiber Intake, Fecal Microbiota, and Hemoglobin A1c Level in Chinese Patients with Type 2 Diabetes. Nutrients, 2022, 14, 1003.	1.7	10
5	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
6	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
7	Mendelian randomization and pleiotropy analysis. Quantitative Biology, 2021, 9, 122-132.	0.3	28
8	An iterative approach to detect pleiotropy and perform Mendelian Randomization analysis using GWAS summary statistics. Bioinformatics, 2021, 37, 1390-1400.	1.8	22
9	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
10	In vitro and in vivo Study on an Injectable Glycol Chitosan/Dibenzaldehyde-Terminated Polyethylene Glycol Hydrogel in Repairing Articular Cartilage Defects. Frontiers in Bioengineering and Biotechnology, 2021, 9, 607709.	2.0	12
11	Cardiometabolic risks of SARS-CoV-2 hospitalization using Mendelian Randomization. Scientific Reports, 2021, 11, 7848.	1.6	9
12	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
13	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.	2.6	18
14	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
15	Replication of European hypertension associations in a case-control study of 9,534 African Americans. PLoS ONE, 2021, 16, e0259962.	1.1	4
16	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
17	Detecting fitness epistasis in recently admixed populations with genome-wide data. BMC Genomics, 2020, 21, 476.	1.2	4
18	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17

#	Article	IF	Citations
19	Identification of PIEZO1 polymorphisms for human bone mineral density. Bone, 2020, 133, 115247.	1.4	30
20	Local Ancestry Inference in Large Pedigrees. Scientific Reports, 2020, 10, 189.	1.6	3
21	FAM222A encodes a protein which accumulates in plaques in Alzheimerâ€™s disease. Nature Communications, 2020, 11, 411.	5.8	16
22	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	5.8	117
23	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	5.8	62
24	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.	2.6	10
25	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
26	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
27	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.	1.8	29
28	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.	0.5	12
29	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. Sleep, 2019, 42, .	0.6	27
30	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
31	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
32	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
33	Identifying Rare Variant Associations in Admixed Populations. Scientific Reports, 2019, 9, 5458.	1.6	3
34	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
35	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.	1.4	5
36	VarExp: estimating variance explained by genome-wide GxE summary statistics. Bioinformatics, 2018, 34, 3412-3414.	1.8	13

#	Article	IF	Citations
37	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	1.4	65
38	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
39	Adjustment for covariates using summary statistics of genomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 812-825.	0.6	5
40	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
41	Rare Variant Analysis in Unrelated Individuals. Translational Bioinformatics, 2018, , 27-44.	0.0	0
42	Genomeâ€wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. Genetic Epidemiology, 2017, 41, 122-135.	0.6	9
43	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.	9.4	280
44	Calibrating Population Stratification in Association Analysis. Methods in Molecular Biology, 2017, 1666, 441-453.	0.4	1
45	Cross-Phenotype Association Analysis Using Summary Statistics from GWAS. Methods in Molecular Biology, 2017, 1666, 455-467.	0.4	22
46	The Analysis of Ethnic Mixtures. Methods in Molecular Biology, 2017, 1666, 505-525.	0.4	2
47	Detecting Multiethnic Rare Variants. Methods in Molecular Biology, 2017, 1666, 527-538.	0.4	0
48	Height associated variants demonstrate assortative mating in human populations. Scientific Reports, 2017, 7, 15689.	1.6	15
49	Finding susceptible and protective interaction patterns in large-scale genetic association study. Frontiers of Computer Science, 2017, 11, 541-554.	1.6	1
50	Genomic regions associated with susceptibility to Barrettâ€™s esophagus and esophageal adenocarcinoma in African Americans: The cross BETRNet admixture study. PLoS ONE, 2017, 12, e0184962.	1.1	6
51	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
52	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.	1.5	98
53	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
54	Abstract P530: Pleiotropic Effects on Blood Pressure Traits Using Genome-wide Analysis of Gene-alcohol Interactions. Hypertension, 2017, 70, .	1.3	0

#	Article	IF	Citations
55	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	0.6	18
56	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. Genetic Epidemiology, 2016, 40, 222-232.	0.6	32
57	Mining Dual Networks. ACM Transactions on Knowledge Discovery From Data, 2016, 10, 1-37.	2.5	19
58	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
59	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	1.4	21
60	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.	0.4	3
61	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	2.6	55
62	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	2.5	107
63	Common variants inDRD2are associated with sleep duration: the CARe consortium. Human Molecular Genetics, 2016, 25, 167-179.	1.4	40
64	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. PLoS ONE, 2016, 11, e0163912.	1.1	19
65	Meta-analysis of Correlated Traits via Summary Statistics from GWASs with an Application in Hypertension. American Journal of Human Genetics, 2015, 96, 21-36.	2.6	321
66	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
67	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, 106-113.	5.1	18
68	Determinants of hypertension in a young adult Ugandan population in epidemiological transitionâ€”the MEPI-CVD survey. BMC Public Health, 2015, 15, 830.	1.2	42
69	Finding dense and connected subgraphs in dual networks. , 2015, , .		23
70	A Generalized Sequential Bonferroni Procedure for GWAS in Admixed Populations Incorporating Admixture Mapping Information into Association Tests. Human Heredity, 2015, 79, 80-92.	0.4	9
71	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.	1.5	16
72	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158

#	Article	IF	Citations
73	A unified GMDR method for detecting geneâ€“gene interactions in family and unrelated samples with application to nicotine dependence. Human Genetics, 2014, 133, 139-150.	1.8	23
74	Discovery of common sequences absent in the human reference genome using pooled samples from next generation sequencing. BMC Genomics, 2014, 15, 685.	1.2	24
75	De novo mutations discovered in 8 Mexican American families through whole genome sequencing. BMC Proceedings, 2014, 8, S24.	1.8	11
76	Whole genome sequencing data from pedigrees suggests linkage disequilibrium among rare variants created by population admixture. BMC Proceedings, 2014, 8, S44.	1.8	6
77	Geneâ€“gene and geneâ€“environment interactions in ulcerative colitis. Human Genetics, 2014, 133, 547-558.	1.8	29
78	A variance component based multi-marker association test using family and unrelated data. BMC Genetics, 2013, 14, 17.	2.7	22
79	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, 545-554.	2.6	189
80	What Is the Significance of Difference in Phenotypic Variability across SNP Genotypes?. American Journal of Human Genetics, 2013, 93, 390-397.	2.6	39
81	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
82	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, 904-916.	2.6	113
83	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
84	GEEâ€Based SNP Set Association Test for Continuous and Discrete Traits in Familyâ€Based Association Studies. Genetic Epidemiology, 2013, 37, 778-786.	0.6	55
85	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 3394-3395.	1.4	1
86	EINVis: A Visualization Tool for Analyzing and Exploring Genetic Interactions in Largeâ€Scale Association Studies. Genetic Epidemiology, 2013, 37, 675-685.	0.6	9
87	A Novel Approach to Detect Cumulative Genetic Effects and Genetic Interactions in Crohnâ€™s Disease. Inflammatory Bowel Diseases, 2013, 19, 1.	0.9	15
88	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, 1970-1976.	0.3	30
89	Linkage-Disequilibrium-Based Binning Misleads the Interpretation of Genome-wide Association Studies. American Journal of Human Genetics, 2012, 91, 965-968.	2.6	1
90	Analysis of Genetic Association Studies. Statistics in the Health Sciences, 2012, , .	0.2	26

#	Article	IF	Citations
91	Detecting Rare Variants. Methods in Molecular Biology, 2012, 850, 453-464.	0.4	7
92	Gene, pathway and network frameworks to identify epistatic interactions of single nucleotide polymorphisms derived from GWAS data. BMC Systems Biology, 2012, 6, S15.	3.0	41
93	Power Comparison of Admixture Mapping and Direct Association Analysis in Genomeâ€Wide Association Studies. Genetic Epidemiology, 2012, 36, 235-243.	0.6	23
94	Allowing for Population Stratification in Association Analysis. Methods in Molecular Biology, 2012, 850, 399-409.	0.4	2
95	The Analysis of Ethnic Mixtures. Methods in Molecular Biology, 2012, 850, 465-481.	0.4	5
96	Association of Genetic Loci with Sleep Apnea in European Americans and African-Americans: The Candidate Gene Association Resource (CARe). PLoS ONE, 2012, 7, e48836.	1.1	64
97	Haplotype Analysis for Case-Control Data. Statistics in the Health Sciences, 2012, , 209-233.	0.2	0
98	Population Structure. Statistics in the Health Sciences, 2012, , 259-286.	0.2	0
99	Rare Variants Analysis in Unrelated Individuals. Translational Bioinformatics, 2012, , 121-138.	0.0	0
100	Gene-Gene Interactions. Statistics in the Health Sciences, 2012, , 235-256.	0.2	0
101	Analysis of Family Data. Statistics in the Health Sciences, 2012, , 353-387.	0.2	0
102	Genetic Background of Patients from a University Medical Center in Manhattan: Implications for Personalized Medicine. PLoS ONE, 2011, 6, e19166.	1.1	56
103	The CRPandGDNFGenes Do Not Contribute to Apneaâ€“Hypopnea Index or Risk of Obstructive Sleep Apnea. American Journal of Respiratory and Critical Care Medicine, 2011, 184, 144-145.	2.5	1
104	Statistical interaction in human genetics: how should we model it if we are looking for biological interaction?. Nature Reviews Genetics, 2011, 12, 74-74.	7.7	35
105	Genome-wide Comparison of African-Ancestry Populations from CARe and Other Cohorts Reveals Signals of Natural Selection. American Journal of Human Genetics, 2011, 89, 368-381.	2.6	79
106	The efficacy of detecting variants with small effects on the Affymetrix 6.0 platform using pooled DNA. Human Genetics, 2011, 130, 607-621.	1.8	3
107	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. Human Genetics, 2011, 130, 725-733.	1.8	79
108	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6

#	Article	IF	Citations
109	Evaluation of a LASSO regression approach on the unrelated samples of Genetic Analysis Workshop 17. BMC Proceedings, 2011, 5, S12.	1.8	4
110	Interrogating population structure and its impact on association tests. BMC Proceedings, 2011, 5, S25.	1.8	5
111	Testing gene-environment interactions in gene-based association studies. BMC Proceedings, 2011, 5, S26.	1.8	3
112	Rare variant density across the genome and across populations. BMC Proceedings, 2011, 5, S39.	1.8	5
113	A novel method to detect rare variants using both family and unrelated case-control data. BMC Proceedings, 2011, 5, S80.	1.8	3
114	Capability of common SNPs to tag rare variants. BMC Proceedings, 2011, 5, S88.	1.8	13
115	Detecting rare and common variants for complex traits: sibpair and odds ratio weighted sum statistics (SPWSS, ORWSS). Genetic Epidemiology, 2011, 35, 398-409.	0.6	48
116	Analysis of exome sequences with and without incorporating prior biological knowledge. Genetic Epidemiology, 2011, 35, S48-55.	0.6	6
117	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, 2285-2295.	1.4	77
118	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
119	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
120	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, 347-354.	1.0	17
121	Adjustment for local ancestry in genetic association analysis of admixed populations. Bioinformatics, 2011, 27, 670-677.	1.8	59
122	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genetics, 2011, 7, e1001371.	1.5	110
123	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298.	1.5	93
124	Detecting association with rare variants for common diseases using haplotype-based methods. Statistics and Its Interface, 2011, 4, 273-283.	0.2	2
125	Genome-wide searching of rare genetic variants in WTCCC data. Human Genetics, 2010, 128, 269-280.	1.8	49
126	A Study of The Relationship between The Interleukinâ€6 Gene and Obstructive Sleep Apnea. Clinical and Translational Science, 2010, 3, 337-339.	1.5	14

#	Article	IF	Citations
127	Detecting rare variants for complex traits using family and unrelated data. Genetic Epidemiology, 2010, 34, 171-187.	0.6	114
128	Pathwayâ€based analysis for genomeâ€wide association studies using supervised principal components. Genetic Epidemiology, 2010, 34, 716-724.	0.6	48
129	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. Biometrics, 2010, 66, 586-593.	0.8	12
130	Genome-wide association of anthropometric traits in African- and African-derived populations. Human Molecular Genetics, 2010, 19, 2725-2738.	1.4	90
131	Rapid Assessment of Genetic Ancestry in Populations of Unknown Origin by Genome-Wide Genotyping of Pooled Samples. PLoS Genetics, 2010, 6, e1000866.	1.5	47
132	The Meaning of Interaction. Human Heredity, 2010, 70, 269-277.	0.4	115
133	Interrogating local population structure for fine mapping in genome-wide association studies. Bioinformatics, 2010, 26, 2961-2968.	1.8	65
134	Fine mapping of the association with obesity at the FTO locus in African-derived populations. Human Molecular Genetics, 2010, 19, 2907-2916.	1.4	82
135	A Candidate Gene Study of Obstructive Sleep Apnea in European Americans and African Americans. American Journal of Respiratory and Critical Care Medicine, 2010, 182, 947-953.	2.5	96
136	SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDE ASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA. , 2010, , 14-25.		25
137	Admixture mapping of quantitative trait loci for blood lipids in African-Americans. Human Molecular Genetics, 2009, 18, 2091-2098.	1.4	29
138	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, S22.	1.8	2
139	A method to correct for population structure using a segregation model. BMC Proceedings, 2009, 3, S104.	1.8	7
140	Assessing the impact of global versus local ancestry in association studies. BMC Proceedings, 2009, 3, S107.	1.8	21
141	Association of Regions on Chromosomes 6 and 7 With Blood Pressure in Nigerian Families. Circulation: Cardiovascular Genetics, 2009, 2, 38-45.	5.1	17
142	Population-Based Association Studies. , 2009, , 171-190.		1
143	Admixture Mapping of Quantitative Trait Loci for BMI in African Americans: Evidence for Loci on Chromosomes 3q, 5q, and 15q. Obesity, 2009, 17, 1226-1231.	1.5	35
144	Genome-wide distribution of ancestry in Mexican Americans. Human Genetics, 2008, 124, 207-214.	1.8	27

#	Article	IF	Citations
145	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.	0.7	9
146	A Unified Association Analysis Approach for Family and Unrelated Samples Correcting for Stratification. American Journal of Human Genetics, 2008, 82, 352-365.	2.6	124
147	Admixture Mapping and the Role of Population Structure for Localizing Disease Genes. Advances in Genetics, 2008, 60, 547-569.	0.8	57
148	Genome-wide association studies: implications for multiethnic samples. Human Molecular Genetics, 2008, 17, R151-R155.	1.4	62
149	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.	1.5	134
150	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, 1460-1467.	0.3	52
151	An integrated genome-wide association analysis on rheumatoid arthritis data. BMC Proceedings, 2007, 1, S35.	1.8	1
152	Improving Power in Contrasting Linkage-Disequilibrium Patterns between Cases and Controls. American Journal of Human Genetics, 2007, 80, 911-920.	2.6	38
153	Admixture Mapping Provides Evidence of Association of the VNN1 Gene with Hypertension. PLoS ONE, 2007, 2, e1244.	1.1	46
154	A genome-wide linkage study of GAW15 gene expression data. BMC Proceedings, 2007, 1, S87.	1.8	3
155	A Genomeâ€wide Scan of Loci Linked to Serum Adiponectin in Two Populations of African Descent. Obesity, 2007, 15, 1207-1214.	1.5	11
156	A Common Genetic Variant Is Associated with Adult and Childhood Obesity. Science, 2006, 312, 279-283.	6.0	652
157	Reconstructing Genetic Ancestry Blocks in Admixed Individuals. American Journal of Human Genetics, 2006, 79, 1-12.	2.6	240
158	A Combinatorial Searching Method for Detecting a Set of Interacting Loci Associated with Complex Traits. Annals of Human Genetics, 2006, 70, 677-692.	0.3	14
159	Transferability of tag SNPs in genetic association studies in multiple populations. Nature Genetics, 2006, 38, 1298-1303.	9.4	224
160	Diminished Induction of Skin Fibrosis in Mice with MCP-1 Deficiency. Journal of Investigative Dermatology, 2006, 126, 1900-1908.	0.3	101
161	Racial admixture and its impact on BMI and blood pressure in African and Mexican Americans. Human Genetics, 2006, 119, 624-633.	1.8	81
162	A classical likelihood based approach for admixture mapping using EM algorithm. Human Genetics, 2006, 120, 431-445.	1.8	38

#	Article	IF	Citations
163	Analytical Correction for Multiple Testing in Admixture Mapping. Human Heredity, 2006, 62, 55-63.	0.4	16
164	Common Variants in the ENPP1 Gene Are Not Reproducibly Associated With Diabetes or Obesity. Diabetes, 2006, 55, 3180-3184.	0.3	76
165	Genetic effects on blood pressure localized to chromosomes 6 and 7. Journal of Hypertension, 2005, 23, 1367-1373.	0.3	14
166	Angiotensinâ€Converting Enzyme Gene Polymorphisms and Obesity: An Examination of Three Black Populations. Obesity, 2005, 13, 823-828.	4.0	26
167	Admixture mapping for hypertension loci with genome-scan markers. Nature Genetics, 2005, 37, 177-181.	9.4	246
168	Refinement of the DFNA41 locus and candidate genes analysis. Journal of Human Genetics, 2005, 50, 516-522.	1.1	11
169	A genome-wide linkage and association study using COGA data. BMC Genetics, 2005, 6, S128.	2.7	18
170	Identifying genetic variation affecting a complex trait in simulated data: a comparison of meta-analysis with pooled data analysis. BMC Genetics, 2005, 6, S97.	2.7	4
171	Two Major QTLs and Several Others Relate to Factors of Metabolic Syndrome in the Family Blood Pressure Program. Hypertension, 2005, 46, 751-757.	1.3	35
172	Haplotypes produced from rare variants in the promoter and coding regions of angiotensinogen contribute to variation in angiotensinogen levels. Human Molecular Genetics, 2005, 14, 639-643.	1.4	29
173	Corin Gene Minor Allele Defined by 2 Missense Mutations Is Common in Blacks and Associated With High Blood Pressure and Hypertension. Circulation, 2005, 112, 2403-2410.	1.6	189
174	Genetic Structure, Self-Identified Race/Ethnicity, and Confounding in Case-Control Association Studies. American Journal of Human Genetics, 2005, 76, 268-275.	2.6	513
175	Angiotensin I-converting enzyme polymorphisms, ACE level and blood pressure among Nigerians, Jamaicans and African-Americans. European Journal of Human Genetics, 2004, 12, 460-468.	1.4	28
176	A Genome Scan among Nigerians Linking Resting Energy Expenditure to Chromosome 16. Obesity, 2004, 12, 577-581.	4.0	21
177	Association between evolutionary history of angiotensinogen haplotypes and plasma levels. Human Genetics, 2004, 115, 310-8.	1.8	10
178	Linkage Analysis of a Complex Disease through Use of Admixed Populations. American Journal of Human Genetics, 2004, 74, 1136-1153.	2.6	73
179	Linkage disequilibrium analysis of the renin-angiotensin system genes. Current Hypertension Reports, 2003, 5, 40-46.	1.5	7
180	On a semiparametric test to detect associations between quantitative traits and candidate genes using unrelated individuals. Genetic Epidemiology, 2003, 24, 44-56.	0.6	95

#	Article	IF	Citations
181	A Genomeâ€Wide Scan for Body Mass Index among Nigerian Families. Obesity, 2003, 11, 266-273.	4.0	57
182	Combined analysis of genomewide scans for adult height: results from the NHLBI Family Blood Pressure Program. European Journal of Human Genetics, 2003, 11, 271-274.	1.4	39
183	Erythrocyte Sodium-Lithium Countertransport and Blood Pressure. Hypertension, 2003, 41, 842-846.	1.3	21
184	Linkage for BMI at 3q27 Region Confirmed in an African-American Population. Diabetes, 2003, 52, 1284-1287.	0.3	38
185	Linkage Disequilibrium and Haplotype Diversity in the Genes of the Renin-Angiotensin System: Findings From the Family Blood Pressure Program. Genome Research, 2003, 13, 173-181.	2.4	71
186	Associations Between Hypertension and Genes in the Renin-Angiotensin System. Hypertension, 2003, 41, 1027-1034.	1.3	116
187	An association study of angiotensinogen polymorphisms with serum level and hypertension in an African-American population. Journal of Hypertension, 2003, 21, 1847-1852.	0.3	23
188	Genome Scan Among Nigerians Linking Blood Pressure to Chromosomes 2, 3, and 19. Hypertension, 2002, 40, 629-633.	1.3	88
189	A Genome-Wide Scan for Obesity in African-Americans. Diabetes, 2002, 51, 541-544.	0.3	60
190	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, 1247-1256.	2.6	145
191	Association mapping, using a mixture model for complex traits. Genetic Epidemiology, 2002, 23, 181-196.	0.6	128
192	Heterogeneity in Older People: Examining Physiologic Failure, Age, and Comorbidity. Journal of the American Geriatrics Society, 2002, 50, 1955-1961.	1.3	29
193	Linkage and Association Analysis of Angiotensin Iâ€“Converting Enzyme (ACE)â€“Gene Polymorphisms with ACE Concentration and Blood Pressure. American Journal of Human Genetics, 2001, 68, 1139-1148.	2.6	241
194	Testing Quantitative Traits for Association and Linkage in the Presence or Absence of Parental Data. Human Heredity, 2001, 51, 183-191.	0.4	7
195	Localization of the Q1 Mutation by Cladistic Analysis. Genetic Epidemiology, 2001, 21, S594-9.	0.6	4
196	Racial differences and the genetics of hypertension. Current Hypertension Reports, 2001, 3, 19-24.	1.5	18
197	Transmission/disequilibrium tests for quantitative traits. Genetic Epidemiology, 2001, 20, 57-74.	0.6	93
198	Power comparison of regression methods to test quantitative traits for association and linkage. , 2000, 18, 322-330.		15

#	Article	IF	Citations
199	Localization of a Small Genomic Region Associated with Elevated ACE. American Journal of Human Genetics, 2000, 67, 1144-1153.	2.6	104
200	A Test of Transmission/Disequilibrium for Quantitative Traits in Pedigree Data, by Multiple Regression. American Journal of Human Genetics, 1999, 65, 236-245.	2.6	85
201	Association and linkage analysis of ICDâ€10 diagnosis for alcoholism. Genetic Epidemiology, 1999, 17, S343-7.	0.6	3
202	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. Genetic Epidemiology, 1999, 17, S157-S161.	0.6	7
203	Model-free age-of-onset methods applied to the linkage of bipolar disorder. Genetic Epidemiology, 1997, 14, 711-716.	0.6	9