Xiaofeng Zhu

List of Publications by Year
in descending order

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203	11,394	28242	36008
papers	citations	55 h-index	97 g-index

223	223	223	14746
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Common Genetic Variant Is Associated with Adult and Childhood Obesity. Science, 2006, 312, 279-283.	6.0	652
2	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
3	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
4	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
5	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
6	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
7	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
8	Admixture mapping for hypertension loci with genome-scan markers. Nature Genetics, 2005, 37, 177-181.	9.4	246
9	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
10	Reconstructing Genetic Ancestry Blocks in Admixed Individuals. American Journal of Human Genetics, 2006, 79, 1-12.	2.6	240
11	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
12	Transferability of tag SNPs in genetic association studies in multiple populations. Nature Genetics, 2006, 38, 1298-1303.	9.4	224
13	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
14	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
15	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
16	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
17	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
18	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

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19	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
20	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
21	Association mapping, using a mixture model for complex traits. Genetic Epidemiology, 2002, 23, 181-196.	0.6	128
22	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
23	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
24	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	5.8	117
25	Associations Between Hypertension and Genes in the Renin-Angiotensin System. Hypertension, 2003, 41, 1027-1034.	1.3	116
26	The Meaning of Interaction. Human Heredity, 2010, 70, 269-277.	0.4	115
27	Detecting rare variants for complex traits using family and unrelated data. Genetic Epidemiology, 2010, 34, 171-187.	0.6	114
28	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
29	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
30	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
31	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
32	Localization of a Small Genomic Region Associated with Elevated ACE. American Journal of Human Genetics, 2000, 67, 1144-1153.	2.6	104
33	Diminished Induction of Skin Fibrosis in Mice with MCP-1 Deficiency. Journal of Investigative Dermatology, 2006, 126, 1900-1908.	0.3	101
34	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
35	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
36	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

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37	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
38	Transmission/disequilibrium tests for quantitative traits. Genetic Epidemiology, 2001, 20, 57-74.	0.6	93
39	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298.	1.5	93
40	Genome-wide association of anthropometric traits in African- and African-derived populations. Human Molecular Genetics, 2010, 19, 2725-2738.	1.4	90
41	Genome Scan Among Nigerians Linking Blood Pressure to Chromosomes 2, 3, and 19. Hypertension, 2002, 40, 629-633.	1.3	88
42	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
43	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
44	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
45	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
46	Racial admixture and its impact on BMI and blood pressure in African and Mexican Americans. Human Genetics, 2006, 119, 624-633.	1.8	81
47	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
48	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. Human Genetics, 2011, 130, 725-733.	1.8	79
49	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
50	Common Variants in the ENPP1 Gene Are Not Reproducibly Associated With Diabetes or Obesity. Diabetes, 2006, 55, 3180-3184.	0.3	76
51	Linkage Analysis of a Complex Disease through Use of Admixed Populations. American Journal of Human Genetics, 2004, 74, 1136-1153.	2.6	73
52	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
53	Interrogating local population structure for fine mapping in genome-wide association studies. Bioinformatics, 2010, 26, 2961-2968.	1.8	65
54	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

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55	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
56	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
57	Genome-wide association studies: implications for multiethnic samples. Human Molecular Genetics, 2008, 17, R151-R155.	1.4	62
58	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
59	A Genome-Wide Scan for Obesity in African-Americans. Diabetes, 2002, 51, 541-544.	0.3	60
60	Adjustment for local ancestry in genetic association analysis of admixed populations. Bioinformatics, 2011, 27, 670-677.	1.8	59
61	A Genomeâ€Wide Scan for Body Mass Index among Nigerian Families. Obesity, 2003, 11, 266-273.	4.0	57
62	Admixture Mapping and the Role of Population Structure for Localizing Disease Genes. Advances in Genetics, 2008, 60, 547-569.	0.8	57
63	Genetic Background of Patients from a University Medical Center in Manhattan: Implications for Personalized Medicine. PLoS ONE, 2011, 6, e19166.	1.1	56
64	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
65	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
66	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
67	Genome-wide searching of rare genetic variants in WTCCC data. Human Genetics, 2010, 128, 269-280.	1.8	49
68	Pathwayâ€based analysis for genomeâ€wide association studies using supervised principal components. Genetic Epidemiology, 2010, 34, 716-724.	0.6	48
69	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
70	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
71	Admixture Mapping Provides Evidence of Association of the VNN1 Gene with Hypertension. PLoS ONE, 2007, 2, e1244.	1.1	46
72	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

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73	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
74	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
75	Common variants inDRD2are associated with sleep duration: the CARe consortium. Human Molecular Genetics, 2016, 25, 167-179.	1.4	40
76	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
77	What Is the Significance of Difference in Phenotypic Variability across SNP Genotypes?. American Journal of Human Genetics, 2013, 93, 390-397.	2.6	39
78	Linkage for BMI at 3q27 Region Confirmed in an African-American Population. Diabetes, 2003, 52, 1284-1287.	0.3	38
79	A classical likelihood based approach for admixture mapping using EM algorithm. Human Genetics, 2006, 120, 431-445.	1.8	38
80	Improving Power in Contrasting Linkage-Disequilibrium Patterns between Cases and Controls. American Journal of Human Genetics, 2007, 80, 911-920.	2.6	38
81	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
82	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
83	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
84	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. Genetic Epidemiology, 2016, 40, 222-232.	0.6	32
85	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
86	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
87	Identification of PIEZO1 polymorphisms for human bone mineral density. Bone, 2020, 133, 115247.	1.4	30
88	Heterogeneity in Older People: Examining Physiologic Failure, Age, and Comorbidity. Journal of the American Geriatrics Society, 2002, 50, 1955-1961.	1.3	29
89	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
90	Admixture mapping of quantitative trait loci for blood lipids in African-Americans. Human Molecular Genetics, 2009, 18, 2091-2098.	1.4	29

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91	Geneâ€“gene and geneâ€“environment interactions in ulcerative colitis. Human Genetics, 2014, 133, 547-558.	1.8	29
92	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
93	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
94	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
95	Mendelian randomization and pleiotropy analysis. Quantitative Biology, 2021, 9, 122-132.	0.3	28
96	Genome-wide distribution of ancestry in Mexican Americans. Human Genetics, 2008, 124, 207-214.	1.8	27
97	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
98	Angiotensinâ€Converting Enzyme Gene Polymorphisms and Obesity: An Examination of Three Black Populations. Obesity, 2005, 13, 823-828.	4.0	26
99	Analysis of Genetic Association Studies. Statistics in the Health Sciences, 2012, , .	0.2	26
100	SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDE ASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA. , 2010, , 14-25.		25
101	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
102	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
103	Power Comparison of Admixture Mapping and Direct Association Analysis in Genomeâ€Wide Association Studies. Genetic Epidemiology, 2012, 36, 235-243.	0.6	23
104	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
105	Finding dense and connected subgraphs in dual networks. , 2015, , .		23
106	A variance component based multi-marker association test using family and unrelated data. BMC Genetics, 2013, 14, 17.	2.7	22
107	Cross-Phenotype Association Analysis Using Summary Statistics from GWAS. Methods in Molecular Biology, 2017, 1666, 455-467.	0.4	22
108	An iterative approach to detect pleiotropy and perform Mendelian Randomization analysis using GWAS summary statistics. Bioinformatics, 2021, 37, 1390-1400.	1.8	22

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109	Erythrocyte Sodium-Lithium Countertransport and Blood Pressure. Hypertension, 2003, 41, 842-846.	1.3	21
110	A Genome Scan among Nigerians Linking Resting Energy Expenditure to Chromosome 16. Obesity, 2004, 12, 577-581.	4.0	21
111	Assessing the impact of global versus local ancestry in association studies. BMC Proceedings, 2009, 3, S107.	1.8	21
112	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	1.4	21
113	Mining Dual Networks. ACM Transactions on Knowledge Discovery From Data, 2016, 10, 1-37.	2.5	19
114	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. PLoS ONE, 2016, 11, e0163912.	1.1	19
115	Racial differences and the genetics of hypertension. Current Hypertension Reports, 2001, 3, 19-24.	1.5	18
116	A genome-wide linkage and association study using COGA data. BMC Genetics, 2005, 6, S128.	2.7	18
117	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
118	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
119	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
120	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
121	Association of Regions on Chromosomes 6 and 7 With Blood Pressure in Nigerian Families. Circulation: Cardiovascular Genetics, 2009, 2, 38-45.	5.1	17
122	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
123	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
124	Analytical Correction for Multiple Testing in Admixture Mapping. Human Heredity, 2006, 62, 55-63.	0.4	16
125	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
126	FAM222A encodes a protein which accumulates in plaques in Alzheimerâ€™s disease. Nature Communications, 2020, 11, 411.	5.8	16

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127	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
128	Power comparison of regression methods to test quantitative traits for association and linkage. , 2000, 18, 322-330.		15
129	A Novel Approach to Detect Cumulative Genetic Effects and Genetic Interactions in Crohnâ€™s Disease. Inflammatory Bowel Diseases, 2013, 19, 1.	0.9	15
130	Height associated variants demonstrate assortative mating in human populations. Scientific Reports, 2017, 7, 15689.	1.6	15
131	Genetic effects on blood pressure localized to chromosomes 6 and 7. Journal of Hypertension, 2005, 23, 1367-1373.	0.3	14
132	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
133	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
134	Capability of common SNPs to tag rare variants. BMC Proceedings, 2011, 5, S88.	1.8	13
135	VarExp: estimating variance explained by genome-wide GxE summary statistics. Bioinformatics, 2018, 34, 3412-3414.	1.8	13
136	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
137	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. Biometrics, 2010, 66, 586-593.	0.8	12
138	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
139	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
140	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
141	Refinement of the DFNA41 locus and candidate genes analysis. Journal of Human Genetics, 2005, 50, 516-522.	1.1	11
142	A Genomeâ€wide Scan of Loci Linked to Serum Adiponectin in Two Populations of African Descent. Obesity, 2007, 15, 1207-1214.	1.5	11
143	De novo mutations discovered in 8 Mexican American families through whole genome sequencing. BMC Proceedings, 2014, 8, S24.	1.8	11
144	Association between evolutionary history of angiotensinogen haplotypes and plasma levels. Human Genetics, 2004, 115, 310-8.	1.8	10

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145	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
146	Habitual Dietary Fiber Intake, Fecal Microbiota, and Hemoglobin A1c Level in Chinese Patients with Type 2 Diabetes. Nutrients, 2022, 14, 1003.	1.7	10
147	Model-free age-of-onset methods applied to the linkage of bipolar disorder. Genetic Epidemiology, 1997, 14, 711-716.	0.6	9
148	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
149	EINVis: A Visualization Tool for Analyzing and Exploring Genetic Interactions in Largeâ€Scale Association Studies. Genetic Epidemiology, 2013, 37, 675-685.	0.6	9
150	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
151	Genomeâ€wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. Genetic Epidemiology, 2017, 41, 122-135.	0.6	9
152	Cardiometabolic risks of SARS-CoV-2 hospitalization using Mendelian Randomization. Scientific Reports, 2021, 11, 7848.	1.6	9
153	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. Genetic Epidemiology, 1999, 17, S157-S161.	0.6	7
154	Testing Quantitative Traits for Association and Linkage in the Presence or Absence of Parental Data. Human Heredity, 2001, 51, 183-191.	0.4	7
155	Linkage disequilibrium analysis of the renin-angiotensin system genes. Current Hypertension Reports, 2003, 5, 40-46.	1.5	7
156	A method to correct for population structure using a segregation model. BMC Proceedings, 2009, 3, S104.	1.8	7
157	Detecting Rare Variants. Methods in Molecular Biology, 2012, 850, 453-464.	0.4	7
158	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6
159	Analysis of exome sequences with and without incorporating prior biological knowledge. Genetic Epidemiology, 2011, 35, S48-55.	0.6	6
160	Whole genome sequencing data from pedigrees suggests linkage disequilibrium among rare variants created by population admixture. BMC Proceedings, 2014, 8, S44.	1.8	6
161	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
162	Genomeâ€wide pleiotropy analysis identifies novel blood pressure variants and improves its polygenic risk scores. Genetic Epidemiology, 2022, 46, 105-121.	0.6	6

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163	Interrogating population structure and its impact on association tests. BMC Proceedings, 2011, 5, S25.	1.8	5
164	Rare variant density across the genome and across populations. BMC Proceedings, 2011, 5, S39.	1.8	5
165	Adjustment for covariates using summary statistics of genomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 812-825.	0.6	5
166	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
167	The Analysis of Ethnic Mixtures. Methods in Molecular Biology, 2012, 850, 465-481.	0.4	5
168	Localization of the Q1 Mutation by Cladistic Analysis. Genetic Epidemiology, 2001, 21, S594-9.	0.6	4
169	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
170	Evaluation of a LASSO regression approach on the unrelated samples of Genetic Analysis Workshop 17. BMC Proceedings, 2011, 5, S12.	1.8	4
171	Detecting fitness epistasis in recently admixed populations with genome-wide data. BMC Genomics, 2020, 21, 476.	1.2	4
172	Replication of European hypertension associations in a case-control study of 9,534 African Americans. PLoS ONE, 2021, 16, e0259962.	1.1	4
173	Association and linkage analysis of ICDâ€10 diagnosis for alcoholism. Genetic Epidemiology, 1999, 17, S343-7.	0.6	3
174	A genome-wide linkage study of GAW15 gene expression data. BMC Proceedings, 2007, 1, S87.	1.8	3
175	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
176	Testing gene-environment interactions in gene-based association studies. BMC Proceedings, 2011, 5, S26.	1.8	3
177	A novel method to detect rare variants using both family and unrelated case-control data. BMC Proceedings, 2011, 5, S80.	1.8	3
178	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
179	Identifying Rare Variant Associations in Admixed Populations. Scientific Reports, 2019, 9, 5458.	1.6	3
180	Local Ancestry Inference in Large Pedigrees. Scientific Reports, 2020, 10, 189.	1.6	3

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181	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
182	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
183	The Analysis of Ethnic Mixtures. Methods in Molecular Biology, 2017, 1666, 505-525.	0.4	2
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