Degui Zhi

List of Publications by Citations

101 papers	3,386 citations	28 h-index	56 g-index
119 ext. papers	4,382 ext. citations	6.3 avg, IF	5.04 L-index

#	Paper	IF	Citations
101	Epigenetic Signatures of Cigarette Smoking. *Circulation: Cardiovascular Genetics*, **2016**, 9, 436-447		442
100	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. *Human Molecular Genetics*, **2015**, 24, 4464-79	5.6	219
99	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. *PLoS Medicine*, **2017**, 14, e1002215	11.6	162
98	Epigenome-wide association study of fasting blood lipids in the Genetics of Lipid-lowering Drugs and Diet Network study. *Circulation*, **2014**, 130, 565-72	16.7	161
97	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. *Obesity*, **2015**, 23, 1493-501	8	122
96	Epigenome-wide association study of fasting measures of glucose, insulin, and HOMA-IR in the Genetics of Lipid Lowering Drugs and Diet Network study. *Diabetes*, **2014**, 63, 801-7	0.9	120
95	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	40.4	119
94	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. *Nature Genetics*, **2014**, 46, 1233-8	36.3	108
93	SNPs located at CpG sites modulate genome-epigenome interaction. *Epigenetics*, **2013**, 8, 802-6	5.7	106
92	Social media and outbreaks of emerging infectious diseases: A systematic review of literature. *American Journal of Infection Control*, **2018**, 46, 962-972	3.8	104
91	Expression signature of IFN/STAT1 signaling genes predicts poor survival outcome in glioblastoma multiforme in a subtype-specific manner. *PLoS ONE*, **2012**, 7, e29653	3.7	88
90	A novel method for multiple alignment of sequences with repeated and shuffled elements. *Genome Research*, **2004**, 14, 2336-46	9.7	83
89	A genome-wide association study in catfish reveals the presence of functional hubs of related genes within QTLs for columnaris disease resistance. *BMC Genomics*, **2015**, 16, 196	4.5	82
88	Genome-wide association study identifies five susceptibility loci for follicular lymphoma outside the HLA region. *American Journal of Human Genetics*, **2014**, 95, 462-71	11	74
87	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. *Circulation: Cardiovascular Genetics*, **2017**, 10,		72
86	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
85	Bayesian analysis of rare variants in genetic association studies. *Genetic Epidemiology*, **2011**, 35, 57-69	2.6	58

84	Sickle Cell Trait and the Risk of ESRD in Blacks. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 2180-2187	12.7	53
83	Methylation at CPT1A locus is associated with lipoprotein subfraction profiles. *Journal of Lipid Research*, **2014**, 55, 1324-30	6.3	50
82	Hierarchical generalized linear models for multiple groups of rare and common variants: jointly estimating group and individual-variant effects. *PLoS Genetics*, **2011**, 7, e1002382	6	50
81	Gene2vec: distributed representation of genes based on co-expression. *BMC Genomics*, **2019**, 20, 82	4.5	42
80	The Bioenergetic Health Index is a sensitive measure of oxidative stress in human monocytes. *Redox Biology*, **2016**, 8, 43-50	11.3	41
79	Med-BERT: pretrained contextualized embeddings on large-scale structured electronic health records for disease prediction. *Npj Digital Medicine*, **2021**, 4, 86	15.7	41
78	Association of DNA Methylation at CPT1A Locus with Metabolic Syndrome in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. *PLoS ONE*, **2016**, 11, e0145789	3.7	40
77	A Genome-Wide Association Study Identifies Multiple Regions Associated with Head Size in Catfish. *G3: Genes, Genomes, Genetics*, **2016**, 6, 3389-3398	3.2	40
76	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. *Human Molecular Genetics*, **2016**, 25, 1663-76	5.6	39
75	A study of generalizability of recurrent neural network-based predictive models for heart failure onset risk using a large and heterogeneous EHR data set. *Journal of Biomedical Informatics*, **2018**, 84, 11-16	10.2	36
74	Public Perception Analysis of Tweets During the 2015 Measles Outbreak: Comparative Study Using Convolutional Neural Network Models. *Journal of Medical Internet Research*, **2018**, 20, e236	7.6	30
73	Haplotype-based methods for detecting uncommon causal variants with common SNPs. *Genetic Epidemiology*, **2012**, 36, 572-82	2.6	28
72	Vitronectin inhibits neutrophil apoptosis through activation of integrin-associated signaling pathways. *American Journal of Respiratory Cell and Molecular Biology*, **2012**, 46, 790-6	5.7	28
71	Tweeting about measles during stages of an outbreak: A semantic network approach to the framing of an emerging infectious disease. *American Journal of Infection Control*, **2018**, 46, 1375-1380	3.8	28
70	A Genome-Wide Association Study Reveals That Genes with Functions for Bone Development Are Associated with Body Conformation in Catfish. *Marine Biotechnology*, **2017**, 19, 570-578	3.4	26
69	Oxidative Modifications of Protein Tyrosyl Residues Are Increased in Plasma of Human Subjects with Interstitial Lung Disease. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 193, 861-8	10.2	26
68	Cyclosporine-mediated allograft fibrosis is associated with micro-RNA-21 through AKT signaling. *Transplant International*, **2015**, 28, 232-45	3	25
67	Vaginal Microbiota in Pregnancy: Evaluation Based on Vaginal Flora, Birth Outcome, and Race. *American Journal of Perinatology*, **2016**, 33, 401-8	3.3	24

66	Identifying repeat domains in large genomes. *Genome Biology*, **2006**, 7, R7	18.3	23
65	Haplotype kernel association test as a powerful method to identify chromosomal regions harboring uncommon causal variants. *Genetic Epidemiology*, **2013**, 37, 560-70	2.6	22
64	Interaction of methylation-related genetic variants with circulating fatty acids on plasma lipids: a meta-analysis of 7 studies and methylation analysis of 3 studies in the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. *American Journal of Clinical Nutrition*, **2016**, 103, 567-78	7	21
63	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. *Genome Biology*, **2019**, 20, 143	18.3	21
62	Statistical guidance for experimental design and data analysis of mutation detection in rare monogenic mendelian diseases by exome sequencing. *PLoS ONE*, **2012**, 7, e31358	3.7	20
61	Lipid changes due to fenofibrate treatment are not associated with changes in DNA methylation patterns in the GOLDN study. *Frontiers in Genetics*, **2015**, 6, 304	4.5	19
60	PCSK9 variation and association with blood pressure in African Americans: preliminary findings from the HyperGEN and REGARDS studies. *Frontiers in Genetics*, **2015**, 6, 136	4.5	19
59	Practical Consideration of Genotype Imputation: Sample Size, Window Size, Reference Choice, and Untyped Rate. *Statistics and Its Interface*, **2011**, 4, 339-352	0.4	19
58	APOL1 nephropathy risk variants are associated with altered high-density lipoprotein profiles in African Americans. *Nephrology Dialysis Transplantation*, **2016**, 31, 602-8	4.3	18
57	Pathway-based approaches for sequencing-based genome-wide association studies. *Genetic Epidemiology*, **2013**, 37, 478-94	2.6	18
56	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. *PLoS ONE*, **2016**, 11, e0165488	3.7	18
55	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor . *JAMA Cardiology*, **2018**, 3, 463-472	16.2	17
54	Differential Gene Expression Landscape of Co-Existing Cervical Pre-Cancer Lesions Using RNA-seq. *Frontiers in Oncology*, **2014**, 4, 339	5.3	17
53	Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. *Gene*, **2006**, 365, 48-56	3.8	17
52	Genomics of post-prandial lipidomic phenotypes in the Genetics of Lipid lowering Drugs and Diet Network (GOLDN) study. *PLoS ONE*, **2014**, 9, e99509	3.7	16
51	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
50	Predicting gene expression using DNA methylation in three human populations. *PeerJ*, **2019**, 7, e6757	3.1	13
49	Statistical quantification of methylation levels by next-generation sequencing. *PLoS ONE*, **2011**, 6, e21034	3.7	12

48	Genotype calling from next-generation sequencing data using haplotype information of reads. *Bioinformatics*, **2012**, 28, 938-46	7.2	11
47	Time-sensitive clinical concept embeddings learned from large electronic health records. *BMC Medical Informatics and Decision Making*, **2019**, 19, 58	3.6	10
46	Influence of common and rare genetic variation on warfarin dose among African-Americans and European-Americans using the exome array. *Pharmacogenomics*, **2017**, 18, 1059-1073	2.6	10
45	PRKCZ methylation is associated with sunlight exposure in a North American but not a Mediterranean population. *Chronobiology International*, **2014**, 31, 1034-40	3.6	10
44	Comprehensive comparative analysis and identification of RNA-binding protein domains: multi-class classification and feature selection. *Journal of Theoretical Biology*, **2012**, 312, 65-75	2.3	10
43	A genome-wide study of lipid response to fenofibrate in Caucasians: a combined analysis of the GOLDN and ACCORD studies. *Pharmacogenetics and Genomics*, **2016**, 26, 324-33	1.9	10
42	Network context matters: graph convolutional network model over social networks improves the detection of unknown HIV infections among young men who have sex with men. *Journal of the American Medical Informatics Association: JAMIA*, **2019**, 26, 1263-1271	8.6	9
41	Recombination-associated sequence homogenization of neighboring Alu elements: signature of nonallelic gene conversion. *Molecular Biology and Evolution*, **2010**, 27, 2300-11	8.3	9
40	Representing and comparing protein structures as paths in three-dimensional space. *BMC Bioinformatics*, **2006**, 7, 460	3.6	9
39	Sequence correlation between neighboring Alu instances suggests post-retrotransposition sequence exchange due to Alu gene conversion. *Gene*, **2007**, 390, 117-21	3.8	9
38	Genome-wide admixture and association study of subclinical atherosclerosis in the WomenS Interagency HIV Study (WIHS). *PLoS ONE*, **2017**, 12, e0188725	3.7	8
37	Asthma Exacerbation Prediction and Risk Factor Analysis Based on a Time-Sensitive, Attentive Neural Network: Retrospective Cohort Study. *Journal of Medical Internet Research*, **2020**, 22, e16981	7.6	8
36	Vasopressor treatment and mortality following nontraumatic subarachnoid hemorrhage: a nationwide electronic health record analysis. *Neurosurgical Focus*, **2020**, 48, E4	4.2	8
35	Joint haplotype phasing and genotype calling of multiple individuals using haplotype informative reads. *Bioinformatics*, **2013**, 29, 2427-34	7.2	7
34	Texas Public AgenciesSTweets and Public Engagement During the COVID-19 Pandemic: Natural Language Processing Approach. *JMIR Public Health and Surveillance*, **2021**, 7, e26720	11.4	7
33	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
32	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. *Pharmacogenomics*, **2017**, 18, 1333-1341	2.6	6
31	Use of ECMO in the Management of Severe Acute Respiratory Distress Syndrome: A Survey of Academic Medical Centers in the United States. *ASAIO Journal*, **2015**, 61, 556-63	3.6	6

30	Correcting base-assignment errors in repeat regions of shotgun assembly. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2007**, 4, 54-64	3	6
29	Representation of EHR data for predictive modeling: a comparison between UMLS and other terminologies. *Journal of the American Medical Informatics Association: JAMIA*, **2020**, 27, 1593-1599	8.6	6
28	Efficient haplotype matching between a query and a panel for genealogical search. *Bioinformatics*, **2019**, 35, i233-i241	7.2	5
27	RYR3 gene variants in subclinical atherosclerosis among HIV-infected women in the Women's Interagency HIV Study (WIHS). *Atherosclerosis*, **2014**, 233, 666-672	3.1	5
26	All pins are not created equal: communicating skin cancer visually on Pinterest. *Translational Behavioral Medicine*, **2019**, 9, 336-346	3.2	5
25	Genome-wide Association Studies of Performance Traits **2017**, 415-433		4
24	An exome-wide sequencing study of lipid response to high-fat meal and fenofibrate in Caucasians from the GOLDN cohort. *Journal of Lipid Research*, **2018**, 59, 722-729	6.3	4
23	Systematic investigation of predicted effect of nonsynonymous SNPs in human prion protein gene: a molecular modeling and molecular dynamics study. *Journal of Biomolecular Structure and Dynamics*, **2014**, 32, 289-300	3.6	4
22	A PheWAS study of a large observational epidemiological cohort of African Americans from the REGARDS study. *BMC Medical Genomics*, **2019**, 12, 26	3.7	3
21	Collective effects of long-range DNA methylations predict gene expressions and estimate phenotypes in cancer. *Scientific Reports*, **2020**, 10, 3920	4.9	3
20	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. *Pharmacogenomics Journal*, **2019**, 19, 97-108	3.5	3
19	Genome-wide meta-analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e00788	2.3	3
18	Gravidas with class III obesity: evaluating the abdominal skin microbiota above and below the panniculus (.). *Journal of Maternal-Fetal and Neonatal Medicine*, **2016**, 29, 3312-6	2	3
17	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. *JAMA Network Open*, **2021**, 4, e2030435	10.4	3
16	Multi-allelic positional Burrows-Wheeler transform. *BMC Bioinformatics*, **2019**, 20, 279	3.6	2
15	Deep sequencing of RYR3 gene identifies rare and common variants associated with increased carotid intima-media thickness (cIMT) in HIV-infected individuals. *Journal of Human Genetics*, **2015**, 60, 63-7	4.3	2
14	Evaluation of association tests for rare variants using simulated data sets in the Genetic Analysis Workshop 17 data. *BMC Proceedings*, **2011**, 5 Suppl 9, S86	2.3	2
13	Association of Sickle Cell Trait with Risk of Coronary Heart Disease in African Americans. *Blood*, **2016**, 128, 11-11	2.2	2

List of Publications

12	Ultra-fast Identity by Descent Detection in Biobank-Scale Cohorts using Positional Burrows-Wheeler Transform		2
11	d-PBWT: dynamic positional Burrows-Wheeler transform. *Bioinformatics*, **2021**,	7.2	2
10	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. *BMC Biology*, **2021**, 19, 32	7.3	2
9	An Exome-Wide Sequencing Study of the GOLDN Cohort Reveals Novel Associations of Coding Variants and Fasting Plasma Lipids. *Frontiers in Genetics*, **2019**, 10, 158	4.5	1
8	On the design and analysis of next-generation sequencing genotyping for a cohort with haplotype-informative reads. *Methods*, **2015**, 79-80, 41-6	4.6	1
7	A hidden Markov model for haplotype inference for present-absent data of clustered genes using identified haplotypes and haplotype patterns. *Frontiers in Genetics*, **2014**, 5, 267	4.5	1
6	RAFFI: Accurate and fast familial relationship inference in large scale biobank studies using RaPID. *PLoS Genetics*, **2021**, 17, e1009315	6	1
5	Genealogical search using whole-genome genotype profiles **2020**, 51-94		0
4	An Optimal Bahadur-Efficient Method in Detection of Sparse Signals with Applications to Pathway Analysis in Sequencing Association Studies. *PLoS ONE*, **2016**, 11, e0152667	3.7	0
3	Real World Long-term Assessment of The Efficacy of Tocilizumab in Patients with COVID-19: Results From A Large De-identified Multicenter Electronic Health Record Dataset in the United States. *International Journal of Infectious Diseases*, **2021**, 113, 148-154	10.5	0
2	Statistics for next generation sequencing - meeting report. *Frontiers in Genetics*, **2012**, 3, 128	4.5	
1	Association of Hemoglobin S and C Traits with Kidney Disease in African Americans in the Reasons for Geographic and Racial Differences in Stroke (REGARDS) Study. *Blood*, **2015**, 126, 70-70	2.2	