

# Degui Zhi

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Texas Public Agencies STweets and Public Engagement During the COVID-19 Pandemic: Natural Language Processing Approach. <i>JMIR Public Health and Surveillance</i> , <b>2021</b> , 7, e26720	11.4	7
100	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 564-582	11	7
99	Med-BERT: pretrained contextualized embeddings on large-scale structured electronic health records for disease prediction. <i>Npj Digital Medicine</i> , <b>2021</b> , 4, 86	15.7	41
98	RAFFI: Accurate and fast familial relationship inference in large scale biobank studies using RaPID. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009315	6	1
97	d-PBWT: dynamic positional Burrows-Wheeler transform. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	2
96	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. <i>BMC Biology</i> , <b>2021</b> , 19, 32	7.3	2
95	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. <i>International Journal of Infectious Diseases</i> , <b>2021</b> , 113, 148-154	10.5	0
94	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. <i>JAMA Network Open</i> , <b>2021</b> , 4, e2030435	10.4	3
93	Genealogical search using whole-genome genotype profiles <b>2020</b> , 51-94		0
92	Collective effects of long-range DNA methylations predict gene expressions and estimate phenotypes in cancer. <i>Scientific Reports</i> , <b>2020</b> , 10, 3920	4.9	3
91	Asthma Exacerbation Prediction and Risk Factor Analysis Based on a Time-Sensitive, Attentive Neural Network: Retrospective Cohort Study. <i>Journal of Medical Internet Research</i> , <b>2020</b> , 22, e16981	7.6	8
90	Vasopressor treatment and mortality following nontraumatic subarachnoid hemorrhage: a nationwide electronic health record analysis. <i>Neurosurgical Focus</i> , <b>2020</b> , 48, E4	4.2	8
89	Representation of EHR data for predictive modeling: a comparison between UMLS and other terminologies. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2020</b> , 27, 1593-1599	8.6	6
88	A PheWAS study of a large observational epidemiological cohort of African Americans from the REGARDS study. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 26	3.7	3
87	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. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2019</b> , 26, 1263-1271	8.6	9
86	Multi-allelic positional Burrows-Wheeler transform. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 279	3.6	2
85	Time-sensitive clinical concept embeddings learned from large electronic health records. <i>BMC Medical Informatics and Decision Making</i> , <b>2019</b> , 19, 58	3.6	10

84	Gene2vec: distributed representation of genes based on co-expression. <i>BMC Genomics</i> , <b>2019</b> , 20, 82	4.5	42
83	An Exome-Wide Sequencing Study of the GOLDN Cohort Reveals Novel Associations of Coding Variants and Fasting Plasma Lipids. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 158	4.5	1
82	Genome-wide meta-analysis of SNP-by-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. <i>Pharmacogenomics Journal</i> , <b>2019</b> , 19, 97-108	3.5	3
81	Genome-wide meta-analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2019</b> , 7, e00788	2.3	3
80	Efficient haplotype matching between a query and a panel for genealogical search. <i>Bioinformatics</i> , <b>2019</b> , 35, i233-i241	7.2	5
79	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. <i>Genome Biology</i> , <b>2019</b> , 20, 143	18.3	21
78	Predicting gene expression using DNA methylation in three human populations. <i>PeerJ</i> , <b>2019</b> , 7, e6757	3.1	13
77	All pins are not created equal: communicating skin cancer visually on Pinterest. <i>Translational Behavioral Medicine</i> , <b>2019</b> , 9, 336-346	3.2	5
76	An exome-wide sequencing study of lipid response to high-fat meal and fenofibrate in Caucasians from the GOLDN cohort. <i>Journal of Lipid Research</i> , <b>2018</b> , 59, 722-729	6.3	4
75	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\beta$ . <i>JAMA Cardiology</i> , <b>2018</b> , 3, 463-472	16.2	17
74	Social media and outbreaks of emerging infectious diseases: A systematic review of literature. <i>American Journal of Infection Control</i> , <b>2018</b> , 46, 962-972	3.8	104
73	A study of generalizability of recurrent neural network-based predictive models for heart failure onset risk using a large and heterogeneous EHR data set. <i>Journal of Biomedical Informatics</i> , <b>2018</b> , 84, 11-16	10.2	36
72	Public Perception Analysis of Tweets During the 2015 Measles Outbreak: Comparative Study Using Convolutional Neural Network Models. <i>Journal of Medical Internet Research</i> , <b>2018</b> , 20, e236	7.6	30
71	Tweeting about measles during stages of an outbreak: A semantic network approach to the framing of an emerging infectious disease. <i>American Journal of Infection Control</i> , <b>2018</b> , 46, 1375-1380	3.8	28
70	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , <b>2017</b> , 10,		72
69	Sickle Cell Trait and the Risk of ESRD in Blacks. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 2180-2187	12.7	53
68	Genome-wide Association Studies of Performance Traits <b>2017</b> , 415-433		4
67	A Genome-Wide Association Study Reveals That Genes with Functions for Bone Development Are Associated with Body Conformation in Catfish. <i>Marine Biotechnology</i> , <b>2017</b> , 19, 570-578	3.4	26

66	Genome-wide admixture and association study of subclinical atherosclerosis in the Women's Interagency HIV Study (WIHS). <i>PLoS ONE</i> , <b>2017</b> , 12, e0188725	3.7	8
65	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , <b>2017</b> , 14, e1002215	11.6	162
64	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. <i>Pharmacogenomics</i> , <b>2017</b> , 18, 1333-1341	2.6	6
63	Influence of common and rare genetic variation on warfarin dose among African-Americans and European-Americans using the exome array. <i>Pharmacogenomics</i> , <b>2017</b> , 18, 1059-1073	2.6	10
62	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. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006719	6	60
61	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 436-447		442
60	The Bioenergetic Health Index is a sensitive measure of oxidative stress in human monocytes. <i>Redox Biology</i> , <b>2016</b> , 8, 43-50	11.3	41
59	Vaginal Microbiota in Pregnancy: Evaluation Based on Vaginal Flora, Birth Outcome, and Race. <i>American Journal of Perinatology</i> , <b>2016</b> , 33, 401-8	3.3	24
58	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. <i>American Journal of Clinical Nutrition</i> , <b>2016</b> , 103, 567-78	7	21
57	Oxidative Modifications of Protein Tyrosyl Residues Are Increased in Plasma of Human Subjects with Interstitial Lung Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2016</b> , 193, 861-8	10.2	26
56	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 1663-76	5.6	39
55	APOL1 nephropathy risk variants are associated with altered high-density lipoprotein profiles in African Americans. <i>Nephrology Dialysis Transplantation</i> , <b>2016</b> , 31, 602-8	4.3	18
54	Gravidas with class III obesity: evaluating the abdominal skin microbiota above and below the panniculus (.). <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , <b>2016</b> , 29, 3312-6	2	3
53	Association of Sickle Cell Trait with Risk of Coronary Heart Disease in African Americans. <i>Blood</i> , <b>2016</b> , 128, 11-11	2.2	2
52	Association of DNA Methylation at CPT1A Locus with Metabolic Syndrome in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. <i>PLoS ONE</i> , <b>2016</b> , 11, e0145789	3.7	40
51	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. <i>PLoS ONE</i> , <b>2016</b> , 11, e0165488	3.7	18
50	An Optimal Bahadur-Efficient Method in Detection of Sparse Signals with Applications to Pathway Analysis in Sequencing Association Studies. <i>PLoS ONE</i> , <b>2016</b> , 11, e0152667	3.7	0
49	A genome-wide study of lipid response to fenofibrate in Caucasians: a combined analysis of the GOLDN and ACCORD studies. <i>Pharmacogenetics and Genomics</i> , <b>2016</b> , 26, 324-33	1.9	10

48	A Genome-Wide Association Study Identifies Multiple Regions Associated with Head Size in Catfish. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 3389-3398	3.2	40
47	Deep sequencing of RYR3 gene identifies rare and common variants associated with increased carotid intima-media thickness (cIMT) in HIV-infected individuals. <i>Journal of Human Genetics</i> , <b>2015</b> , 60, 63-7	4.3	2
46	On the design and analysis of next-generation sequencing genotyping for a cohort with haplotype-informative reads. <i>Methods</i> , <b>2015</b> , 79-80, 41-6	4.6	1
45	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , <b>2015</b> , 523, 459-462	5.4	119
44	A genome-wide association study in catfish reveals the presence of functional hubs of related genes within QTLs for columnaris disease resistance. <i>BMC Genomics</i> , <b>2015</b> , 16, 196	4.5	82
43	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 4464-79	5.6	219
42	Cyclosporine-mediated allograft fibrosis is associated with micro-RNA-21 through AKT signaling. <i>Transplant International</i> , <b>2015</b> , 28, 232-45	3	25
41	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. <i>Obesity</i> , <b>2015</b> , 23, 1493-501	8	122
40	Use of ECMO in the Management of Severe Acute Respiratory Distress Syndrome: A Survey of Academic Medical Centers in the United States. <i>ASAIO Journal</i> , <b>2015</b> , 61, 556-63	3.6	6
39	Lipid changes due to fenofibrate treatment are not associated with changes in DNA methylation patterns in the GOLDN study. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 304	4.5	19
38	PCSK9 variation and association with blood pressure in African Americans: preliminary findings from the HyperGEN and REGARDS studies. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 136	4.5	19
37	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. <i>Blood</i> , <b>2015</b> , 126, 70-70	2.2	
36	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , <b>2014</b> , 46, 1233-8	36.3	108
35	Genome-wide association study identifies five susceptibility loci for follicular lymphoma outside the HLA region. <i>American Journal of Human Genetics</i> , <b>2014</b> , 95, 462-71	11	74
34	Epigenome-wide association study of fasting blood lipids in the Genetics of Lipid-lowering Drugs and Diet Network study. <i>Circulation</i> , <b>2014</b> , 130, 565-72	16.7	161
33	Methylation at CPT1A locus is associated with lipoprotein subfraction profiles. <i>Journal of Lipid Research</i> , <b>2014</b> , 55, 1324-30	6.3	50
32	A hidden Markov model for haplotype inference for present-absent data of clustered genes using identified haplotypes and haplotype patterns. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 267	4.5	1
31	Differential Gene Expression Landscape of Co-Existing Cervical Pre-Cancer Lesions Using RNA-seq. <i>Frontiers in Oncology</i> , <b>2014</b> , 4, 339	5.3	17

30	Epigenome-wide association study of fasting measures of glucose, insulin, and HOMA-IR in the Genetics of Lipid Lowering Drugs and Diet Network study. <i>Diabetes</i> , <b>2014</b> , 63, 801-7	0.9	120
29	PRKCZ methylation is associated with sunlight exposure in a North American but not a Mediterranean population. <i>Chronobiology International</i> , <b>2014</b> , 31, 1034-40	3.6	10
28	RYR3 gene variants in subclinical atherosclerosis among HIV-infected women in the Women's Interagency HIV Study (WIHS). <i>Atherosclerosis</i> , <b>2014</b> , 233, 666-672	3.1	5
27	Systematic investigation of predicted effect of nonsynonymous SNPs in human prion protein gene: a molecular modeling and molecular dynamics study. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2014</b> , 32, 289-300	3.6	4
26	A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. <i>Human Genetics</i> , <b>2014</b> , 133, 139-50	6.3	15
25	Genomics of post-prandial lipidomic phenotypes in the Genetics of Lipid lowering Drugs and Diet Network (GOLDN) study. <i>PLoS ONE</i> , <b>2014</b> , 9, e99509	3.7	16
24	Joint haplotype phasing and genotype calling of multiple individuals using haplotype informative reads. <i>Bioinformatics</i> , <b>2013</b> , 29, 2427-34	7.2	7
23	Haplotype kernel association test as a powerful method to identify chromosomal regions harboring uncommon causal variants. <i>Genetic Epidemiology</i> , <b>2013</b> , 37, 560-70	2.6	22
22	Pathway-based approaches for sequencing-based genome-wide association studies. <i>Genetic Epidemiology</i> , <b>2013</b> , 37, 478-94	2.6	18
21	SNPs located at CpG sites modulate genome-epigenome interaction. <i>Epigenetics</i> , <b>2013</b> , 8, 802-6	5.7	106
20	Comprehensive comparative analysis and identification of RNA-binding protein domains: multi-class classification and feature selection. <i>Journal of Theoretical Biology</i> , <b>2012</b> , 312, 65-75	2.3	10
19	Expression signature of IFN/STAT1 signaling genes predicts poor survival outcome in glioblastoma multiforme in a subtype-specific manner. <i>PLoS ONE</i> , <b>2012</b> , 7, e29653	3.7	88
18	Statistics for next generation sequencing - meeting report. <i>Frontiers in Genetics</i> , <b>2012</b> , 3, 128	4.5	
17	Haplotype-based methods for detecting uncommon causal variants with common SNPs. <i>Genetic Epidemiology</i> , <b>2012</b> , 36, 572-82	2.6	28
16	Vitronectin inhibits neutrophil apoptosis through activation of integrin-associated signaling pathways. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2012</b> , 46, 790-6	5.7	28
15	Genotype calling from next-generation sequencing data using haplotype information of reads. <i>Bioinformatics</i> , <b>2012</b> , 28, 938-46	7.2	11
14	Statistical guidance for experimental design and data analysis of mutation detection in rare monogenic mendelian diseases by exome sequencing. <i>PLoS ONE</i> , <b>2012</b> , 7, e31358	3.7	20
13	Evaluation of association tests for rare variants using simulated data sets in the Genetic Analysis Workshop 17 data. <i>BMC Proceedings</i> , <b>2011</b> , 5 Suppl 9, S86	2.3	2

12	Bayesian analysis of rare variants in genetic association studies. <i>Genetic Epidemiology</i> , <b>2011</b> , 35, 57-69	2.6	58
11	Hierarchical generalized linear models for multiple groups of rare and common variants: jointly estimating group and individual-variant effects. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002382	6	50
10	Statistical quantification of methylation levels by next-generation sequencing. <i>PLoS ONE</i> , <b>2011</b> , 6, e210347	3.7	12
9	Practical Consideration of Genotype Imputation: Sample Size, Window Size, Reference Choice, and Untyped Rate. <i>Statistics and Its Interface</i> , <b>2011</b> , 4, 339-352	0.4	19
8	Recombination-associated sequence homogenization of neighboring Alu elements: signature of nonallelic gene conversion. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 2300-11	8.3	9
7	Correcting base-assignment errors in repeat regions of shotgun assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2007</b> , 4, 54-64	3	6
6	Sequence correlation between neighboring Alu instances suggests post-retrotransposition sequence exchange due to Alu gene conversion. <i>Gene</i> , <b>2007</b> , 390, 117-21	3.8	9
5	Representing and comparing protein structures as paths in three-dimensional space. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 460	3.6	9
4	Identifying repeat domains in large genomes. <i>Genome Biology</i> , <b>2006</b> , 7, R7	18.3	23
3	Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. <i>Gene</i> , <b>2006</b> , 365, 48-56	3.8	17
2	A novel method for multiple alignment of sequences with repeated and shuffled elements. <i>Genome Research</i> , <b>2004</b> , 14, 2336-46	9.7	83
1	Ultra-fast Identity by Descent Detection in Biobank-Scale Cohorts using Positional Burrows-Wheeler Transform		2