Degui Zhi

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1318898/publications.pdf

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101	5,096	147726	102432
papers	citations	31 h-index	66 g-index

119	119	119	9682
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
2	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, 4464-4479.	1.4	289
3	Med-BERT: pretrained contextualized embeddings on large-scale structured electronic health records for disease prediction. Npj Digital Medicine, 2021, 4, 86.	5.7	248
4	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.	3.9	246
5	Epigenome-Wide Association Study of Fasting Blood Lipids in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Circulation, 2014, 130, 565-572.	1.6	190
6	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
7	Social media and outbreaks of emerging infectious diseases: A systematic review of literature. American Journal of Infection Control, 2018, 46, 962-972.	1.1	173
8	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. Obesity, 2015, 23, 1493-1501.	1.5	152
9	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, 801-807.	0.3	149
10	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
11	SNPs located at CpG sites modulate genome-epigenome interaction. Epigenetics, 2013, 8, 802-806.	1.3	131
12	Expression Signature of IFN/STAT1 Signaling Genes Predicts Poor Survival Outcome in Glioblastoma Multiforme in a Subtype-Specific Manner. PLoS ONE, 2012, 7, e29653.	1.1	118
13	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.	1.2	117
14	A novel method for multiple alignment of sequences with repeated and shuffled elements. Genome Research, 2004, 14, 2336-2346.	2.4	106
15	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, .	5.1	104
16	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
17	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
18	Gene2vec: distributed representation of genes based on co-expression. BMC Genomics, 2019, 20, 82.	1.2	87

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19	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.	2.5	80
20	Sickle Cell Trait and the Risk of ESRD in Blacks. Journal of the American Society of Nephrology: JASN, 2017, 28, 2180-2187.	3.0	79
21	A Genome-Wide Association Study Identifies Multiple Regions Associated with Head Size in Catfish. G3: Genes, Genomes, Genetics, 2016, 6, 3389-3398.	0.8	70
22	Methylation at CPT1A locus is associated with lipoprotein subfraction profiles. Journal of Lipid Research, 2014, 55, 1324-1330.	2.0	65
23	Bayesian analysis of rare variants in genetic association studies. Genetic Epidemiology, 2011, 35, 57-69.	0.6	62
24	Hierarchical Generalized Linear Models for Multiple Groups of Rare and Common Variants: Jointly Estimating Group and Individual-Variant Effects. PLoS Genetics, 2011, 7, e1002382.	1.5	54
25	The Bioenergetic Health Index is a sensitive measure of oxidative stress in human monocytes. Redox Biology, 2016, 8, 43-50.	3.9	54
26	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.	1.1	54
27	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.	1.1	53
28	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
29	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.	2.1	49
30	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. Genome Biology, 2019, 20, 143.	3.8	48
31	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.	1.1	46
32	Recurrent neural network models (CovRNN) for predicting outcomes of patients with COVID-19 on admission to hospital: model development and validation using electronic health record data. The Lancet Digital Health, 2022, 4, e415-e425.	5.9	35
33	Vaginal Microbiota in Pregnancy: Evaluation Based on Vaginal Flora, Birth Outcome, and Race. American Journal of Perinatology, 2016, 33, 401-408.	0.6	34
34	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.	2.1	34
35	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor Î±. JAMA Cardiology, 2018, 3, 463.	3.0	33
36	Identifying repeat domains in large genomes. Genome Biology, 2006, 7, R7.	13.9	31

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37	Vitronectin Inhibits Neutrophil Apoptosis through Activation of Integrin-Associated Signaling Pathways. American Journal of Respiratory Cell and Molecular Biology, 2012, 46, 790-796.	1.4	31
38	Haplotypeâ€Based Methods for Detecting Uncommon Causal Variants With Common SNPs. Genetic Epidemiology, 2012, 36, 572-582.	0.6	30
39	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, 861-868.	2.5	30
40	Predicting gene expression using DNA methylation in three human populations. PeerJ, 2019, 7, e6757.	0.9	28
41	Cyclosporine-mediated allograft fibrosis is associated with micro-RNA-21 through AKT signaling. Transplant International, 2015, 28, 232-245.	0.8	27
42	Practical consideration of genotype imputation: Sample size, window size, reference choice, and untyped rate. Statistics and Its Interface, 2011, 4, 339-351.	0.2	26
43	PCSK9 variation and association with blood pressure in African Americans: preliminary findings from the HyperGEN and REGARDS studies. Frontiers in Genetics, 2015, 6, 136.	1.1	25
44	Haplotype Kernel Association Test as a Powerful Method to Identify Chromosomal Regions Harboring Uncommon Causal Variants. Genetic Epidemiology, 2013, 37, 560-570.	0.6	24
45	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, 567-578.	2.2	24
46	Statistical Guidance for Experimental Design and Data Analysis of Mutation Detection in Rare Monogenic Mendelian Diseases by Exome Sequencing. PLoS ONE, 2012, 7, e31358.	1.1	24
47	Differential Gene Expression Landscape of Co-Existing Cervical Pre-Cancer Lesions Using RNA-seq. Frontiers in Oncology, 2014, 4, 339.	1.3	23
48	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
49	APOL1nephropathy risk variants are associated with altered high-density lipoprotein profiles in African Americans. Nephrology Dialysis Transplantation, 2016, 31, 602-608.	0.4	23
50	Texas Public Agenciesâ€™ Tweets and Public Engagement During the COVID-19 Pandemic: Natural Language Processing Approach. JMIR Public Health and Surveillance, 2021, 7, e26720.	1.2	22
51	Genomics of Post-Prandial Lipidomic Phenotypes in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. PLoS ONE, 2014, 9, e99509.	1.1	21
52	Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. Gene, 2006, 365, 48-56.	1.0	20
53	Pathwayâ€Based Approaches for Sequencingâ€Based Genomeâ€Wide Association Studies. Genetic Epidemiology, 2013, 37, 478-494.	0.6	20
54	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.	1.1	20

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55	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.	2.2	19
56	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. PLoS ONE, 2016, 11, e0165488.	1.1	19
57	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
58	Time-sensitive clinical concept embeddings learned from large electronic health records. BMC Medical Informatics and Decision Making, 2019, 19, 58.	1.5	17
59	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.	0.6	16
60	Efficient haplotype matching between a query and a panel for genealogical search. Bioinformatics, 2019, 35, i233-i241.	1.8	14
61	Statistical Quantification of Methylation Levels by Next-Generation Sequencing. PLoS ONE, 2011, 6, e21034.	1.1	14
62	Genotype calling from next-generation sequencing data using haplotype information of reads. Bioinformatics, 2012, 28, 938-946.	1.8	13
63	Sequence correlation between neighboring Alu instances suggests post-retrotransposition sequence exchange due to Alu gene conversion. Gene, 2007, 390, 117-121.	1.0	12
64	PRKCZmethylation is associated with sunlight exposure in a North American but not a Mediterranean population. Chronobiology International, 2014, 31, 1034-1040.	0.9	12
65	A genome-wide study of lipid response to fenofibrate in Caucasians. Pharmacogenetics and Genomics, 2016, 26, 324-333.	0.7	12
66	Influence of common and rare genetic variation on warfarin dose among Africanâ€“Americans and Europeanâ€“Americans using the exome array. Pharmacogenomics, 2017, 18, 1059-1073.	0.6	12
67	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. BMC Biology, 2021, 19, 32.	1.7	12
68	Vasopressor treatment and mortality following nontraumatic subarachnoid hemorrhage: a nationwide electronic health record analysis. Neurosurgical Focus, 2020, 48, E4.	1.0	12
69	Representing and comparing protein structures as paths in three-dimensional space. BMC Bioinformatics, 2006, 7, 460.	1.2	11
70	Genome-wide admixture and association study of subclinical atherosclerosis in the Womenâ€™s Interagency HIV Study (WIHS). PLoS ONE, 2017, 12, e0188725.	1.1	11
71	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.	2.2	11
72	Recombination-Associated Sequence Homogenization of Neighboring Alu Elements: Signature of Nonallelic Gene Conversion. Molecular Biology and Evolution, 2010, 27, 2300-2311.	3.5	10

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73	Comprehensive comparative analysis and identification of RNA-binding protein domains: Multi-class classification and feature selection. Journal of Theoretical Biology, 2012, 312, 65-75.	0.8	10
74	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.	2.0	10
75	Collective effects of long-range DNA methylations predict gene expressions and estimate phenotypes in cancer. Scientific Reports, 2020, 10, 3920.	1.6	10
76	d-PBWT: dynamic positional Burrowsâ€“Wheeler transform. Bioinformatics, 2021, 37, 2390-2397.	1.8	10
77	Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 54-64.	1.9	9
78	A PheWAS study of a large observational epidemiological cohort of African Americans from the REGARDS study. BMC Medical Genomics, 2019, 12, 26.	0.7	9
79	Joint haplotype phasing and genotype calling of multiple individuals using haplotype informative reads. Bioinformatics, 2013, 29, 2427-2434.	1.8	8
80	All pins are not created equal: communicating skin cancer visually on Pinterest. Translational Behavioral Medicine, 2019, 9, 336-346.	1.2	8
81	RYR3 gene variants in subclinical atherosclerosis among HIV-infected women in the Women's Interagency HIV Study (WIHS). Atherosclerosis, 2014, 233, 666-672.	0.4	7
82	Use of ECMO in the Management of Severe Acute Respiratory Distress Syndrome. ASAIO Journal, 2015, 61, 556-563.	0.9	7
83	Multi-allelic positional Burrows-Wheeler transform. BMC Bioinformatics, 2019, 20, 279.	1.2	7
84	RAFFI: Accurate and fast familial relationship inference in large scale biobank studies using RaPID. PLoS Genetics, 2021, 17, e1009315.	1.5	7
85	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.	2.0	6
86	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. JAMA Network Open, 2021, 4, e2030435.	2.8	5
87	Genomeâ€wide metaâ€analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	0.6	4
88	Gravidas with class III obesity: evaluating the abdominal skin microbiota above and below the panniculus. Journal of Maternal-Fetal and Neonatal Medicine, 2016, 29, 1-5.	0.7	3
89	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, 63-67.	1.1	3
90	On the design and analysis of next-generation sequencing genotyping for a cohort with haplotype-informative reads. Methods, 2015, 79-80, 41-46.	1.9	3

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91	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.	0.9	3
92	Association of Sickle Cell Trait with Risk of Coronary Heart Disease in African Americans. Blood, 2016, 128, 11-11.	0.6	3
93	Evaluation of association tests for rare variants using simulated data sets in the Genetic Analysis Workshop 17 data. BMC Proceedings, 2011, 5, S86.	1.8	2
94	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.	1.1	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. International Journal of Infectious Diseases, 2021, 113, 148-154.	1.5	2
96	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.	1.1	1
97	The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications. BMC Bioinformatics, 2018, 19, 492.	1.2	1
98	Genealogical search using whole-genome genotype profiles. , 2020, , 51-94.		1
99	An Optimal Bahadur-Efficient Method in Detection of Sparse Signals with Applications to Pathway Analysis in Sequencing Association Studies. PLoS ONE, 2016, 11, e0152667.	1.1	1
100	Statistics for Next Generation Sequencing â€“ Meeting Report. Frontiers in Genetics, 2012, 3, 128.	1.1	0
101	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.	0.6	0