

Xiaowei Zhan

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

5,789
citations

172457

29
h-index

133252

59
g-index

67
all docs

67
docs citations

67
times ranked

14081
citing authors

#	ARTICLE	IF	CITATIONS
1	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	21.4	1,307
2	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
3	RVTESTS: an efficient and comprehensive tool for rare variant association analysis using sequence data. <i>Bioinformatics</i> , 2016, 32, 1423-1426.	4.1	366
4	Activation of HIF-1 α and LL-37 by commensal bacteria inhibits <i>Candida albicans</i> colonization. <i>Nature Medicine</i> , 2015, 21, 808-814.	30.7	333
5	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
6	Pathology Image Analysis Using Segmentation Deep Learning Algorithms. <i>American Journal of Pathology</i> , 2019, 189, 1686-1698.	3.8	232
7	Transforming activity of an oncoprotein-encoding circular RNA from human papillomavirus. <i>Nature Communications</i> , 2019, 10, 2300.	12.8	218
8	Meta-analysis of gene-level tests for rare variant association. <i>Nature Genetics</i> , 2014, 46, 200-204.	21.4	178
9	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. <i>Nature Genetics</i> , 2013, 45, 1375-1379.	21.4	158
10	Artificial Intelligence in Lung Cancer Pathology Image Analysis. <i>Cancers</i> , 2019, 11, 1673.	3.7	152
11	Improved Ancestry Estimation for both Genotyping and Sequencing Data using Projection Procrustes Analysis and Genotype Imputation. <i>American Journal of Human Genetics</i> , 2015, 96, 926-937.	6.2	137
12	Ancestry estimation and control of population stratification for sequence-based association studies. <i>Nature Genetics</i> , 2014, 46, 409-415.	21.4	136
13	Antibiotic-Induced Depletion of Anti-inflammatory Clostridia Is Associated with the Development of Graft-versus-Host Disease in Pediatric Stem Cell Transplantation Patients. <i>Biology of Blood and Marrow Transplantation</i> , 2017, 23, 820-829.	2.0	130
14	RAREMETAL: fast and powerful meta-analysis for rare variants. <i>Bioinformatics</i> , 2014, 30, 2828-2829.	4.1	108
15	FMAP: Functional Mapping and Analysis Pipeline for metagenomics and metatranscriptomics studies. <i>BMC Bioinformatics</i> , 2016, 17, 420.	2.6	98
16	Investigation of Antigen-Specific T-Cell Receptor Clusters in Human Cancers. <i>Clinical Cancer Research</i> , 2020, 26, 1359-1371.	7.0	90
17	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
18	Computational Staining of Pathology Images to Study the Tumor Microenvironment in Lung Cancer. <i>Cancer Research</i> , 2020, 80, 2056-2066.	0.9	88

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19	A Bayesian framework for <i>de novo</i> mutation calling in parents-offspring trios. <i>Bioinformatics</i> , 2015, 31, 1375-1381.	4.1	87
20	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83
21	Real-time resolution of point mutations that cause phenovariance in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E440-9.	7.1	75
22	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
23	eIF5B drives integrated stress response-dependent translation of PD-L1 in lung cancer. <i>Nature Cancer</i> , 2020, 1, 533-545.	13.2	73
24	Large-scale forward genetics screening identifies <i>Trpa1</i> as a chemosensor for predator odor-evoked innate fear behaviors. <i>Nature Communications</i> , 2018, 9, 2041.	12.8	71
25	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019, 85, 946-955.	1.3	69
26	Severe Gut Microbiota Dysbiosis Is Associated With Poor Growth in Patients With Short Bowel Syndrome. <i>Journal of Parenteral and Enteral Nutrition</i> , 2017, 41, 1202-1212.	2.6	58
27	Creatine maintains intestinal homeostasis and protects against colitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1273-E1281.	7.1	56
28	IgD class switching is initiated by microbiota and limited to mucosa-associated lymphoid tissue in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1196-E1204.	7.1	50
29	VAMPr: VARIant Mapping and Prediction of antibiotic resistance via explainable features and machine learning. <i>PLoS Computational Biology</i> , 2020, 16, e1007511.	3.2	50
30	The landscape of RNA polymerase II-associated chromatin interactions in prostate cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 3987-4005.	8.2	37
31	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. <i>Nucleic Acids Research</i> , 2017, 45, gkx019.	14.5	36
32	SEQMINER: An R Package to Facilitate the Functional Interpretation of Sequence-Based Associations. <i>Genetic Epidemiology</i> , 2015, 39, 619-623.	1.3	31
33	GIANA allows computationally-efficient TCR clustering and multi-disease repertoire classification by isometric transformation. <i>Nature Communications</i> , 2021, 12, 4699.	12.8	30
34	In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. <i>Psychophysiology</i> , 2014, 51, 1309-1320.	2.4	25
35	Inferring genes that escape X-Chromosome inactivation reveals important contribution of variable escape genes to sex-biased diseases. <i>Genome Research</i> , 2021, 31, 1629-1637.	5.5	25
36	Assessment of circularized E7 RNA, GLUT1, and PD-L1 in anal squamous cell carcinoma.	1.8	23

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37	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017, 5, 485-497.e3.	6.2	19
38	Type and case volume of health care facility influences survival and surgery selection in cases with early-stage non-small cell lung cancer. <i>Cancer</i> , 2019, 125, 4252-4259.	4.1	19
39	Proper conditional analysis in the presence of missing data: Application to large scale meta-analysis of tobacco use phenotypes. <i>PLoS Genetics</i> , 2018, 14, e1007452.	3.5	18
40	A Bayesian zero-inflated negative binomial regression model for the integrative analysis of microbiome data. <i>Biostatistics</i> , 2021, 22, 522-540.	1.5	17
41	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. <i>Bioinformatics</i> , 2015, 31, 1452-1459.	4.1	14
42	MB-GAN: Microbiome Simulation via Generative Adversarial Network. <i>GigaScience</i> , 2021, 10, .	6.4	14
43	Overcoming Expressional Drop-outs in Lineage Reconstruction from Single-Cell RNA-Sequencing Data. <i>Cell Reports</i> , 2021, 34, 108589.	6.4	13
44	HARMONIES: A Hybrid Approach for Microbiome Networks Inference via Exploiting Sparsity. <i>Frontiers in Genetics</i> , 2020, 11, 445.	2.3	12
45	Dominant atopy risk mutations identified by mouse forward genetic analysis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1095-1108.	5.7	7
46	Usefulness of a Simple Algorithm to Identify Hypertensive Patients Who Benefit from Intensive Blood Pressure Lowering. <i>American Journal of Cardiology</i> , 2018, 122, 248-254.	1.6	5
47	Meta-analysis approaches to combine multiple gene set enrichment studies. <i>Statistics in Medicine</i> , 2018, 37, 659-672.	1.6	5
48	A Survey of Statistical Methods for Microbiome Data Analysis. <i>Frontiers in Applied Mathematics and Statistics</i> , 0, 8, .	1.3	5
49	DEFOR: depth- and frequency-based somatic copy number alteration detector. <i>Bioinformatics</i> , 2019, 35, 3824-3825.	4.1	4
50	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. <i>PLoS Genetics</i> , 2015, 11, e1005271.	3.5	3
51	A mixed-effects model approach for the statistical analysis of vocal fold viscoelastic shear properties. <i>Journal of the Mechanical Behavior of Biomedical Materials</i> , 2017, 75, 477-485.	3.1	3
52	Association Analysis and Meta-Analysis of Multi-Allelic Variants for Large-Scale Sequence Data. <i>Genes</i> , 2020, 11, 586.	2.4	3
53	Integrating germline and somatic genetics to identify genes associated with lung cancer. <i>Genetic Epidemiology</i> , 2020, 44, 233-247.	1.3	2
54	Forward Genetic Screen Reveals Genetic Causes of Atopy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, AB204.	2.9	1

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55	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	1
56	Gut Microbiota Dysbiosis and Elevated Lipopolysaccharide Serum Levels Are Associated with Venous Thromboembolism in Pediatric Patients. <i>Blood</i> , 2020, 136, 6-7.	1.4	1
57	2682. Prophylaxis-Driven Molecular Epidemiology of <i>Pseudomonas aeruginosa</i> Bloodstream Infections in Adults With Leukemia. <i>Open Forum Infectious Diseases</i> , 2019, 6, S942-S942.	0.9	0
58	Seqminer2: an efficient tool to query and retrieve genotypes for statistical genetics analyses from biobank scale sequence dataset. <i>Bioinformatics</i> , 2020, 36, 4951-4954.	4.1	0
59	Serum Citrulline As a Biomarker for Blood Stream Infections in Pediatric Hematopoietic Stem Cell Transplant Patients. <i>Blood</i> , 2019, 134, 3268-3268.	1.4	0