Xiaowei Zhan

List of Publications by Year
in descending order

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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	A Bayesian zero-inflated negative binomial regression model for the integrative analysis of microbiome data. Biostatistics, 2021, 22, 522-540.	1.5	17
2	Dominant atopy risk mutations identified by mouse forward genetic analysis. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 1095-1108.	5.7	7
3	Overcoming Expressional Drop-outs in Lineage Reconstruction from Single-Cell RNA-Sequencing Data. Cell Reports, 2021, 34, 108589.	6.4	13
4	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	1
5	Inferring genes that escape X-Chromosome inactivation reveals important contribution of variable escape genes to sex-biased diseases. Genome Research, 2021, 31, 1629-1637.	5.5	25
6	GIANA allows computationally-efficient TCR clustering and multi-disease repertoire classification by isometric transformation. Nature Communications, 2021, 12, 4699.	12.8	30
7	MB-GAN: Microbiome Simulation via Generative Adversarial Network. GigaScience, 2021, 10, .	6.4	14
8	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
9	Investigation of Antigen-Specific T-Cell Receptor Clusters in Human Cancers. Clinical Cancer Research, 2020, 26, 1359-1371.	7.0	90
10	Integrating germline and somatic genetics to identify genes associated with lung cancer. Genetic Epidemiology, 2020, 44, 233-247.	1.3	2
11	Seqminer2: an efficient tool to query and retrieve genotypes for statistical genetics analyses from biobank scale sequence dataset. Bioinformatics, 2020, 36, 4951-4954.	4.1	0
12	Association Analysis and Meta-Analysis of Multi-Allelic Variants for Large-Scale Sequence Data. Genes, 2020, 11, 586.	2.4	3
13	HARMONIES: A Hybrid Approach for Microbiome Networks Inference via Exploiting Sparsity. Frontiers in Genetics, 2020, 11, 445.	2.3	12
14	VAMPr: VAriant Mapping and Prediction of antibiotic resistance via explainable features and machine learning. PLoS Computational Biology, 2020, 16, e1007511.	3.2	50
15	Computational Staining of Pathology Images to Study the Tumor Microenvironment in Lung Cancer. Cancer Research, 2020, 80, 2056-2066.	0.9	88
16	eIF5B drives integrated stress response-dependent translation of PD-L1 in lung cancer. Nature Cancer, 2020, 1, 533-545.	13.2	73
17	The landscape of RNA polymerase IIâ€“associated chromatin interactions in prostate cancer. Journal of Clinical Investigation, 2020, 130, 3987-4005.	8.2	37
18	Gut Microbiota Dysbiosis and Elevated Lipopolysaccharide Serum Levels Are Associated with Venous Thromboembolism in Pediatric Patients. Blood, 2020, 136, 6-7.	1.4	1

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19	Artificial Intelligence in Lung Cancer Pathology Image Analysis. Cancers, 2019, 11, 1673.	3.7	152
20	Type and case volume of health care facility influences survival and surgery selection in cases with earlyâ€stage nonâ€“small cell lung cancer. Cancer, 2019, 125, 4252-4259.	4.1	19
21	Transforming activity of an oncoprotein-encoding circular RNA from human papillomavirus. Nature Communications, 2019, 10, 2300.	12.8	218
22	Pathology Image Analysis Using Segmentation Deep Learning Algorithms. American Journal of Pathology, 2019, 189, 1686-1698.	3.8	232
23	Forward Genetic Screen Reveals Genetic Causes of Atopy. Journal of Allergy and Clinical Immunology, 2019, 143, AB204.	2.9	1
24	DEFOR: depth- and frequency-based somatic copy number alteration detector. Bioinformatics, 2019, 35, 3824-3825.	4.1	4
25	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
26	2682. Prophylaxis-Driven Molecular Epidemiology of Pseudomonas aeruginosa Bloodstream Infections in Adults With Leukemia. Open Forum Infectious Diseases, 2019, 6, S942-S942.	0.9	0
27	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	21.4	1,307
28	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
29	Assessment of circularized E7 RNA, GLUT1, and PD-L1 in anal squamous cell carcinoma. Oncotarget, 2019, 10, 5958-5969.	1.8	23
30	Serum Citrulline As a Biomarker for Blood Stream Infections in Pediatric Hematopoietic Stem Cell Transplant Patients. Blood, 2019, 134, 3268-3268.	1.4	0
31	Usefulness of a Simple Algorithm to Identify Hypertensive Patients Who Benefit from Intensive Blood Pressure Lowering. American Journal of Cardiology, 2018, 122, 248-254.	1.6	5
32	Metaâ€anâ€analysis approaches to combine multiple gene set enrichment studies. Statistics in Medicine, 2018, 37, 659-672.	1.6	5
33	Large-scale forward genetics screening identifies Trpa1 as a chemosensor for predator odor-evoked innate fear behaviors. Nature Communications, 2018, 9, 2041.	12.8	71
34	Proper conditional analysis in the presence of missing data: Application to large scale meta-analysis of tobacco use phenotypes. PLoS Genetics, 2018, 14, e1007452.	3.5	18
35	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
36	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544

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37	IgD class switching is initiated by microbiota and limited to mucosa-associated lymphoid tissue in mice. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1196-E1204.	7.1	50
38	Creatine maintains intestinal homeostasis and protects against colitis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1273-E1281.	7.1	56
39	Antibiotic-Induced Depletion of Anti-inflammatory Clostridia Is Associated with the Development of Graft-versus-Host Disease in Pediatric Stem Cell Transplantation Patients. Biology of Blood and Marrow Transplantation, 2017, 23, 820-829.	2.0	130
40	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. Nucleic Acids Research, 2017, 45, gkx019.	14.5	36
41	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
42	A mixed-effects model approach for the statistical analysis of vocal fold viscoelastic shear properties. Journal of the Mechanical Behavior of Biomedical Materials, 2017, 75, 477-485.	3.1	3
43	Severe Gut Microbiota Dysbiosis Is Associated With Poor Growth in Patients With Short Bowel Syndrome. Journal of Parenteral and Enteral Nutrition, 2017, 41, 1202-1212.	2.6	58
44	FMAP: Functional Mapping and Analysis Pipeline for metagenomics and metatranscriptomics studies. BMC Bioinformatics, 2016, 17, 420.	2.6	98
45	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
46	RVTESTS: an efficient and comprehensive tool for rare variant association analysis using sequence data. Bioinformatics, 2016, 32, 1423-1426.	4.1	366
47	SEQMINER: An Râ€Package to Facilitate the Functional Interpretation of Sequenceâ€Based Associations. Genetic Epidemiology, 2015, 39, 619-623.	1.3	31
48	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS Genetics, 2015, 11, e1005271.	3.5	3
49	Improved Ancestry Estimation for both Genotyping and Sequencing Data using Projection Procrustes Analysis and Genotype Imputation. American Journal of Human Genetics, 2015, 96, 926-937.	6.2	137
50	Activation of HIF-1Î± and LL-37 by commensal bacteria inhibits Candida albicans colonization. Nature Medicine, 2015, 21, 808-814.	30.7	333
51	Real-time resolution of point mutations that cause phenovariance in mice. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E440-9.	7.1	75
52	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	4.1	14
53	A Bayesian framework for de novo mutation calling in parents-offspring trios. Bioinformatics, 2015, 31, 1375-1381.	4.1	87
54	RAREMETAL: fast and powerful meta-analysis for rare variants. Bioinformatics, 2014, 30, 2828-2829.	4.1	108

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55	In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. Psychophysiology, 2014, 51, 1309-1320.	2.4	25
56	Ancestry estimation and control of population stratification for sequence-based association studies. Nature Genetics, 2014, 46, 409-415.	21.4	136
57	Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204.	21.4	178
58	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	21.4	158
59	A Survey of Statistical Methods for Microbiome Data Analysis. Frontiers in Applied Mathematics and Statistics, 0, 8, .	1.3	5