Nancy R Zhang

List of Publications by Year
in descending order

48 papers	3,951 citations	218677 26 h-index	214800 47 g-index
64 all docs	64 docs citations	64 times ranked	7329 citing authors

#	Article	IF	Citations
1	Distribution-Free Multisample Tests Based on Optimal Matchings With Applications to Single Cell Genomics. Journal of the American Statistical Association, 2022, 117, 627-638.	3.1	5
2	The interferon-stimulated gene RIPK1 regulates cancer cell intrinsic and extrinsic resistance to immune checkpoint blockade. Immunity, 2022, 55, 671-685.e10.	14.3	35
3	A Mendelian randomization study of the role of lipoprotein subfractions in coronary artery disease. ELife, 2021, 10, .	6.0	25
4	Integrative single-cell analysis of allele-specific copy number alterations and chromatin accessibility in cancer. Nature Biotechnology, 2021, 39, 1259-1269.	17.5	31
5	Causal inference for heritable phenotypic risk factors using heterogeneous genetic instruments. PLoS Genetics, 2021, 17, e1009575.	3.5	36
6	Single cell biologyâ€”a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
7	DENDRO: genetic heterogeneity profiling and subclone detection by single-cell RNA sequencing. Genome Biology, 2020, 21, 10.	8.8	35
8	Surface protein imputation from single cell transcriptomes by deep neural networks. Nature Communications, 2020, 11, 651.	12.8	47
9	Data Denoising and Post-Denoising Corrections in Single Cell RNA Sequencing. Statistical Science, 2020, 35, .	2.8	6
10	Online Single-cell RNA-seq Data Denoising with Transfer Learning. , 2020, , .		0
11	Opposing Functions of Interferon Coordinate Adaptive and Innate Immune Responses to Cancer Immune Checkpoint Blockade. Cell, 2019, 178, 933-948.e14.	28.9	301
12	Data denoising with transfer learning in single-cell transcriptomics. Nature Methods, 2019, 16, 875-878.	19.0	152
13	Bulk tissue cell type deconvolution with multi-subject single-cell expression reference. Nature Communications, 2019, 10, 380.	12.8	526
14	Elite control of HIV is associated with distinct functional and transcriptional signatures in lymphoid tissue CD8 ⁺ T cells. Science Translational Medicine, 2019, 11, .	12.4	81
15	Cell-Type-Specific Complement Expression in the Healthy and Diseased Retina. Cell Reports, 2019, 29, 2835-2848.e4.	6.4	81
16	Semblance: An empirical similarity kernel on probability spaces. Science Advances, 2019, 5, eaau9630.	10.3	4
17	Integrative pipeline for profiling DNA copy number and inferring tumor phylogeny. Bioinformatics, 2018, 34, 2126-2128.	4.1	28
18	Learning-dependent chromatin remodeling highlights noncoding regulatory regions linked to autism. Science Signaling, 2018, 11, .	3.6	25

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19	Identification of large rearrangements in cancer genomes with barcode linked reads. Nucleic Acids Research, 2018, 46, e19-e19.	14.5	33
20	DNA copy number profiling using single-cell sequencing. Briefings in Bioinformatics, 2018, 19, 731-736.	6.5	38
21	CODEX2: full-spectrum copy number variation detection by high-throughput DNA sequencing. Genome Biology, 2018, 19, 202.	8.8	62
22	SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. GigaScience, 2018, 7, .	6.4	15
23	Gene expression distribution deconvolution in single-cell RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6437-E6446.	7.1	93
24	SAVER: gene expression recovery for single-cell RNA sequencing. Nature Methods, 2018, 15, 539-542.	19.0	574
25	First Giant Steps Toward a Cell Atlas of Atherosclerosis. Circulation Research, 2018, 122, 1632-1634.	4.5	6
26	SCALE: modeling allele-specific gene expression by single-cell RNA sequencing. Genome Biology, 2017, 18, 74.	8.8	89
27	Accounting for technical noise in differential expression analysis of single-cell RNA sequencing data. Nucleic Acids Research, 2017, 45, 10978-10988.	14.5	73
28	BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. Nature Communications, 2017, 8, 319.	12.8	212
29	Allele-specific copy number estimation by whole exome sequencing. Annals of Applied Statistics, 2017, 11, 1169-1192.	1.1	8
30	Functional germline variants as potential co-oncogenes. Npj Breast Cancer, 2017, 3, 46.	5.2	14
31	Genetic and Genomic Characterization of 462 Melanoma Patient-Derived Xenografts, Tumor Biopsies, and Cell Lines. Cell Reports, 2017, 21, 1936-1952.	6.4	72
32	A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic Acids Research, 2016, 44, gkw481.	14.5	14
33	Assessing intratumor heterogeneity and tracking longitudinal and spatial clonal evolutionary history by next-generation sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5528-37.	7.1	200
34	Scan statistics on Poisson random fields with applications in genomics. Annals of Applied Statistics, 2016, 10, .	1.1	11
35	Global copy number profiling of cancer genomes. Bioinformatics, 2016, 32, 926-928.	4.1	4
36	Allelic variation contributes to bacterial host specificity. Nature Communications, 2015, 6, 8754.	12.8	100

#	ARTICLE	IF	CITATIONS
37	Emergence of Hemagglutinin Mutations During the Course of Influenza Infection. Scientific Reports, 2015, 5, 16178.	3.3	13
38	Allele-specific copy number profiling by next-generation DNA sequencing. Nucleic Acids Research, 2015, 43, e23-e23.	14.5	47
39	CODEX: a normalization and copy number variation detection method for whole exome sequencing. Nucleic Acids Research, 2015, 43, e39-e39.	14.5	126
40	Identification of Insertion Deletion Mutations from Deep Targeted Resequencing. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	2
41	Multiple hypothesis testing adjusted for latent variables, with an application to the AGEMAP gene expression data. Annals of Applied Statistics, 2012, 6, .	1.1	35
42	Change-point model on nonhomogeneous Poisson processes with application in copy number profiling by next-generation DNA sequencing. Annals of Applied Statistics, 2012, 6, .	1.1	46
43	False discovery rates and copy number variation. Biometrika, 2011, 98, 251-271.	2.4	19
44	Estimation of Parent Specific DNA Copy Number in Tumors using High-Density Genotyping Arrays. PLoS Computational Biology, 2011, 7, e1001060.	3.2	35
45	Joint estimation of DNA copy number from multiple platforms. Bioinformatics, 2010, 26, 153-160.	4.1	18
46	Detecting simultaneous changepoints in multiple sequences. Biometrika, 2010, 97, 631-645.	2.4	123
47	Bayesian Variable Selection in Structured High-Dimensional Covariate Spaces With Applications in Genomics. Journal of the American Statistical Association, 2010, 105, 1202-1214.	3.1	128
48	A Modified Bayes Information Criterion with Applications to the Analysis of Comparative Genomic Hybridization Data. Biometrics, 2007, 63, 22-32.	1.4	274