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	SAVER: gene expression recovery for single-cell RNA sequencing. Nature Methods, 2018, 15, 539-542.	19.0	574
2	Bulk tissue cell type deconvolution with multi-subject single-cell expression reference. Nature Communications, 2019, 10, 380.	12.8	526
3	Opposing Functions of Interferon Coordinate Adaptive and Innate Immune Responses to Cancer Immune Checkpoint Blockade. Cell, 2019, 178, 933-948.e14.	28.9	301
4	A Modified Bayes Information Criterion with Applications to the Analysis of Comparative Genomic Hybridization Data. Biometrics, 2007, 63, 22-32.	1.4	274
5	BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. Nature Communications, 2017, 8, 319.	12.8	212
6	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
7	Data denoising with transfer learning in single-cell transcriptomics. Nature Methods, 2019, 16, 875-878.	19.0	152
8	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
9	CODEX: a normalization and copy number variation detection method for whole exome sequencing. Nucleic Acids Research, 2015, 43, e39-e39.	14.5	126
10	Detecting simultaneous changepoints in multiple sequences. Biometrika, 2010, 97, 631-645.	2.4	123
11	Allelic variation contributes to bacterial host specificity. Nature Communications, 2015, 6, 8754.	12.8	100
12	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
13	SCALE: modeling allele-specific gene expression by single-cell RNA sequencing. Genome Biology, 2017, 18, 74.	8.8	89
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	Accounting for technical noise in differential expression analysis of single-cell RNA sequencing data. Nucleic Acids Research, 2017, 45, 10978-10988.	14.5	73
17	Genetic and Genomic Characterization of 462 Melanoma Patient-Derived Xenografts, Tumor Biopsies, and Cell Lines. Cell Reports, 2017, 21, 1936-1952.	6.4	72
18	CODEX2: full-spectrum copy number variation detection by high-throughput DNA sequencing. Genome Biology, 2018, 19, 202.	8.8	62

#	Article	IF	Citations
19	Allele-specific copy number profiling by next-generation DNA sequencing. Nucleic Acids Research, 2015, 43, e23-e23.	14.5	47
20	Surface protein imputation from single cell transcriptomes by deep neural networks. Nature Communications, 2020, 11, 651.	12.8	47
21	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
22	DNA copy number profiling using single-cell sequencing. Briefings in Bioinformatics, 2018, 19, 731-736.	6.5	38
23	Causal inference for heritable phenotypic risk factors using heterogeneous genetic instruments. PLoS Genetics, 2021, 17, e1009575.	3.5	36
24	Estimation of Parent Specific DNA Copy Number in Tumors using High-Density Genotyping Arrays. PLoS Computational Biology, 2011, 7, e1001060.	3.2	35
25	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
26	DENDRO: genetic heterogeneity profiling and subclone detection by single-cell RNA sequencing. Genome Biology, 2020, 21, 10.	8.8	35
27	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
28	Identification of large rearrangements in cancer genomes with barcode linked reads. Nucleic Acids Research, 2018, 46, e19-e19.	14.5	33
29	Integrative single-cell analysis of allele-specific copy number alterations and chromatin accessibility in cancer. Nature Biotechnology, 2021, 39, 1259-1269.	17.5	31
30	Integrative pipeline for profiling DNA copy number and inferring tumor phylogeny. Bioinformatics, 2018, 34, 2126-2128.	4.1	28
31	Learning-dependent chromatin remodeling highlights noncoding regulatory regions linked to autism. Science Signaling, 2018, 11, .	3.6	25
32	A Mendelian randomization study of the role of lipoprotein subfractions in coronary artery disease. ELife, 2021, 10, .	6.0	25
33	False discovery rates and copy number variation. Biometrika, 2011, 98, 251-271.	2.4	19
34	Joint estimation of DNA copy number from multiple platforms. Bioinformatics, 2010, 26, 153-160.	4.1	18
35	SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. GigaScience, 2018, 7, .	6.4	15
36	A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic Acids Research, 2016, 44, gkw481.	14.5	14

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37	Functional germline variants as potential co-oncogenes. Npj Breast Cancer, 2017, 3, 46.	5.2	14
38	Emergence of Hemagglutinin Mutations During the Course of Influenza Infection. Scientific Reports, 2015, 5, 16178.	3.3	13
39	Scan statistics on Poisson random fields with applications in genomics. Annals of Applied Statistics, 2016, 10, .	1.1	11
40	Allele-specific copy number estimation by whole exome sequencing. Annals of Applied Statistics, 2017, 11, 1169-1192.	1.1	8
41	First Giant Steps Toward a Cell Atlas of Atherosclerosis. Circulation Research, 2018, 122, 1632-1634.	4.5	6
42	Data Denoising and Post-Denoising Corrections in Single Cell RNA Sequencing. Statistical Science, 2020, 35, .	2.8	6
43	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
44	Global copy number profiling of cancer genomes. Bioinformatics, 2016, 32, 926-928.	4.1	4
45	Semblance: An empirical similarity kernel on probability spaces. Science Advances, 2019, 5, eaau9630.	10.3	4
46	Single cell biologyâ€”a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
47	Identification of Insertion Deletion Mutations from Deep Targeted Resequencing. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	2
48	Online Single-cell RNA-seq Data Denoising with Transfer Learning. , 2020, , .		0