

# Xiaowo Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

8,724  
citations

236612

25  
h-index

123241

61  
g-index

81  
all docs

81  
docs citations

81  
times ranked

14875  
citing authors

#	ARTICLE	IF	CITATIONS
1	DEGseq: an R package for identifying differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2010, 26, 136-138.	1.8	3,728
2	CRISPR interference (CRISPRi) for sequence-specific control of gene expression. <i>Nature Protocols</i> , 2013, 8, 2180-2196.	5.5	930
3	Control of the senescence-associated secretory phenotype by NF- $\kappa$ B promotes senescence and enhances chemosensitivity. <i>Genes and Development</i> , 2011, 25, 2125-2136.	2.7	720
4	Allelic reprogramming of 3D chromatin architecture during early mammalian development. <i>Nature</i> , 2017, 547, 232-235.	13.7	406
5	Dissecting the Unique Role of the Retinoblastoma Tumor Suppressor during Cellular Senescence. <i>Cancer Cell</i> , 2010, 17, 376-387.	7.7	323
6	MicroRNA identification based on sequence and structure alignment. <i>Bioinformatics</i> , 2005, 21, 3610-3614.	1.8	270
7	Cell-Type-Based Analysis of MicroRNA Profiles in the Mouse Brain. <i>Neuron</i> , 2012, 73, 35-48.	3.8	254
8	DEsingle for detecting three types of differential expression in single-cell RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 3223-3224.	1.8	193
9	CRISPR-ERA: a comprehensive design tool for CRISPR-mediated gene editing, repression and activation: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 3676-3678.	1.8	171
10	H3K4 demethylation by Jarid1a and Jarid1b contributes to retinoblastoma-mediated gene silencing during cellular senescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8971-8976.	3.3	141
11	Model-guided quantitative analysis of microRNA-mediated regulation on competing endogenous RNAs using a synthetic gene circuit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3158-3163.	3.3	117
12	ATRX-mediated chromatin association of histone variant macroH2A1 regulates $\hat{\pm}$ -globin expression. <i>Genes and Development</i> , 2012, 26, 433-438.	2.7	116
13	Genome-wide analyses reveal a role of Polycomb in promoting hypomethylation of DNA methylation valleys. <i>Genome Biology</i> , 2018, 19, 18.	3.8	103
14	The atypical E2F family member E2F7 couples the p53 and RB pathways during cellular senescence. <i>Genes and Development</i> , 2012, 26, 1546-1557.	2.7	100
15	High-resolution human core-promoter prediction with CoreBoost_HM. <i>Genome Research</i> , 2009, 19, 266-275.	2.4	96
16	Synthetic promoter design in <i>Escherichia coli</i> based on a deep generative network. <i>Nucleic Acids Research</i> , 2020, 48, 6403-6412.	6.5	90
17	Long noncoding RNA GSTM3TV2 upregulates LAT2 and OLR1 by competitively sponging let-7 to promote gemcitabine resistance in pancreatic cancer. <i>Journal of Hematology and Oncology</i> , 2019, 12, 97.	6.9	88
18	Integrated omics study delineates the dynamics of lipid droplets in <i>Rhodococcus opacus</i> PD630. <i>Nucleic Acids Research</i> , 2014, 42, 1052-1064.	6.5	79

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19	Calorie restriction is the most reasonable anti-ageing intervention: a meta-analysis of survival curves. <i>Scientific Reports</i> , 2018, 8, 5779.	1.6	75
20	Identification of phylogenetically conserved microRNA <i>cis</i> -regulatory elements across 12 <i>Drosophila</i> species. <i>Bioinformatics</i> , 2008, 24, 165-171.	1.8	60
21	Aging-induced IL27Ra signaling impairs hematopoietic stem cells. <i>Blood</i> , 2020, 136, 183-198.	0.6	53
22	esATAC: an easy-to-use systematic pipeline for ATAC-seq data analysis. <i>Bioinformatics</i> , 2018, 34, 2664-2665.	1.8	50
23	Plasma microRNA panels to diagnose pancreatic cancer: Results from a multicenter study. <i>Oncotarget</i> , 2018, 9, 41575-41583.	0.8	46
24	The loss of heterochromatin is associated with multiscale three-dimensional genome reorganization and aberrant transcription during cellular senescence. <i>Genome Research</i> , 2021, 31, 1121-1135.	2.4	36
25	MICC: an R package for identifying chromatin interactions from ChIA-PET data. <i>Bioinformatics</i> , 2015, 31, 3832-3834.	1.8	34
26	Primary transcripts and expressions of mammal intergenic microRNAs detected by mapping ESTs to their flanking sequences. <i>Mammalian Genome</i> , 2006, 17, 1033-1041.	1.0	33
27	Genome-wide cell-free DNA methylation analyses improve accuracy of non-invasive diagnostic imaging for early-stage breast cancer. <i>Molecular Cancer</i> , 2021, 20, 36.	7.9	30
28	Regulation by competition: a hidden layer of gene regulatory network. <i>Quantitative Biology</i> , 2019, 7, 110-121.	0.3	27
29	DISMIR: Deep learning-based noninvasive cancer detection by integrating DNA sequence and methylation information of individual cell-free DNA reads. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
30	Dynamic transcriptome profiling in DNA damage-induced cellular senescence and transient cell-cycle arrest. <i>Genomics</i> , 2020, 112, 1309-1317.	1.3	21
31	hECA: The cell-centric assembly of a cell atlas. <i>IScience</i> , 2022, 25, 104318.	1.9	21
32	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. <i>Epigenetics</i> , 2011, 6, 1505-1512.	1.3	19
33	Identification and Characterization of Human snoRNA Core Promoters. <i>Genomics</i> , 2010, 96, 50-56.	1.3	18
34	A quantitative understanding of microRNA-mediated competing endogenous RNA regulation. <i>Quantitative Biology</i> , 2016, 4, 47-57.	0.3	18
35	Nucleosome eviction and multiple co-factor binding predict estrogen-receptor-alpha-associated long-range interactions. <i>Nucleic Acids Research</i> , 2014, 42, 6935-6944.	6.5	17
36	Regulatory RNA binding proteins contribute to the transcriptome-wide splicing alterations in human cellular senescence. <i>Aging</i> , 2018, 10, 1489-1505.	1.4	17

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37	OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions. <i>Nucleic Acids Research</i> , 2021, 49, W483-W490.	6.5	17
38	Observations on novel splice junctions from RNA sequencing data. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 299-303.	1.0	16
39	HCSGD: An integrated database of human cellular senescence genes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 227-234.	1.7	15
40	Discovering multiple transcripts of human hepatocytes using massively parallel signature sequencing (MPSS). <i>BMC Genomics</i> , 2007, 8, 207.	1.2	13
41	MIRROR: a method for cell-type specific microRNA occupancy rate prediction. <i>Molecular BioSystems</i> , 2014, 10, 1377-1384.	2.9	11
42	Characterizing microRNA-mediated modulation of gene expression noise and its effect on synthetic gene circuits. <i>Cell Reports</i> , 2021, 36, 109573.	2.9	11
43	YTHDF3 modulates hematopoietic stem cells by recognizing RNA m <sup>6</sup> A modification on <i>Ccnd1</i> . <i>Haematologica</i> , 2022, 107, 2381-2394.	1.7	10
44	CellTracker: an automated toolbox for single-cell segmentation and tracking of time-lapse microscopy images. <i>Bioinformatics</i> , 2021, 37, 285-287.	1.8	9
45	A large-scale CRISPR screen and identification of essential genes in cellular senescence bypass. <i>Aging</i> , 2019, 11, 4011-4031.	1.4	8
46	A Review on The Processing and Analysis of Next-generation RNA-seq Data*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 834-846.	0.3	8
47	ARIC: accurate and robust inference of cell type proportions from bulk gene expression or DNA methylation data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
48	Cell-Type-Based Analysis of MicroRNA Profiles in the Mouse Brain. <i>Neuron</i> , 2012, 73, 620.	3.8	5
49	Advances in computational ChIA-PET data analysis. <i>Quantitative Biology</i> , 2016, 4, 217-225.	0.3	5
50	cfDNApipe: a comprehensive quality control and analysis pipeline for cell-free DNA high-throughput sequencing data. <i>Bioinformatics</i> , 2021, 37, 4251-4252.	1.8	5
51	Single-cell Transcriptomes Reveal Characteristics of MicroRNAs in Gene Expression Noise Reduction. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 394-407.	3.0	5
52	DeSP: a systematic DNA storage error simulation pipeline. <i>BMC Bioinformatics</i> , 2022, 23, 185.	1.2	5
53	Complicated evolutionary patterns of microRNAs in vertebrates. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 552-559.	1.3	4
54	Chromatin state and microRNA determine different gene expression dynamics responsive to TNF stimulation. <i>Genomics</i> , 2012, 100, 297-302.	1.3	4

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55	Basics for Bioinformatics. , 2013, , 1-25.		4
56	Meta-analytic Insights into the Effects of Different Anti-aging Drugs on Survival Curves of <i>Caenorhabditis elegans</i> . <i>Scientia Sinica Vitae</i> , 2015, 45, 479-487.	0.1	4
57	Functional importance of different patterns of correlation between adjacent cassette exons in human and mouse. <i>BMC Genomics</i> , 2008, 9, 191.	1.2	3
58	CRISPR-ERA: A Webserver for Guide RNA Design of Gene Editing and Regulation. <i>Methods in Molecular Biology</i> , 2021, 2189, 65-69.	0.4	3
59	OPâ€Synthetic: identification of optimal genetic manipulations for the overproduction of native and nonâ€native metabolites. <i>Quantitative Biology</i> , 2015, 2, 100-109.	0.3	2
60	Using CRISPR-ERA Webserver for sgRNA Design. <i>Bio-protocol</i> , 2017, 7, e2522.	0.2	2
61	MeConcord: a new metric to quantitatively characterize DNA methylation heterogeneity across reads and CpG sites. <i>Bioinformatics</i> , 2022, 38, i307-i315.	1.8	2
62	Cell-Type-Based Analysis of MicroRNA Profiles in the Mouse Brain. <i>Neuron</i> , 2012, 75, 930-932.	3.8	1
63	Sequence signatures of genes with accompanying antisense transcripts in <i>Saccharomyces cerevisiae</i> . <i>Science China Life Sciences</i> , 2014, 57, 52-58.	2.3	1
64	Regulation by competing: A hidden layer of gene regulatory networks. , 2017, , .		0
65	From big biological data to big discovery: The past decade and the future. <i>Chinese Science Bulletin</i> , 2016, 61, 3869-3877.	0.4	0
66	In silico and in vitro protocols for quantifying gene expression noise modulated by microRNAs. <i>STAR Protocols</i> , 2022, 3, 101205.	0.5	0
67	Evaluating methylation of human ribosomal DNA at each CpG site reveals its utility for cancer detection using cell-free DNA. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	0