Xin Wang

List of Publications by Year in descending order

69 papers	7,748 citations	159573 30 h-index	85537 71 g-index
73 all docs	73 docs citations	73 times ranked	13741 citing authors

#	Article	IF	Citations
1	The consensus molecular subtypes of colorectal cancer. Nature Medicine, 2015, 21, 1350-1356.	30.7	3,596
2	Poor-prognosis colon cancer is defined by a molecularly distinct subtype and develops from serrated precursor lesions. Nature Medicine, 2013, 19, 614-618.	30.7	656
3	Transcription factors LRF and BCL11A independently repress expression of fetal hemoglobin. Science, 2016, 351, 285-289.	12.6	260
4	Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 2013, 4, 2464.	12.8	180
5	Colorectal Cancer Heterogeneity and Targeted Therapy: A Case for Molecular Disease Subtypes. Cancer Research, 2015, 75, 245-249.	0.9	163
6	The oncogenic BRD4-NUT chromatin regulator drives aberrant transcription within large topological domains. Genes and Development, 2015, 29, 1507-1523.	5.9	160
7	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. Cell, 2016, 167, 1310-1322.e17.	28.9	153
8	Diverse epigenetic strategies interact to control epidermal differentiation. Nature Cell Biology, 2012, 14, 753-763.	10.3	139
9	DeepCC: a novel deep learning-based framework for cancer molecular subtype classification. Oncogenesis, 2019, 8, 44.	4.9	138
10	Consensus molecular subtypes of colorectal cancer are recapitulated in in vitro and in vivo models. Cell Death and Differentiation, 2018, 25, 616-633.	11.2	137
11	HTSanalyzeR: an R/Bioconductor package for integrated network analysis of high-throughput screens. Bioinformatics, 2011, 27, 879-880.	4.1	131
12	Practical and Robust Identification of Molecular Subtypes in Colorectal Cancer by Immunohistochemistry. Clinical Cancer Research, 2017, 23, 387-398.	7.0	128
13	Molecular subtyping of colorectal cancer: Recent progress, new challenges and emerging opportunities. Seminars in Cancer Biology, 2019, 55, 37-52.	9.6	125
14	TGFÎ² signaling directs serrated adenomas to the mesenchymal colorectal cancer subtype. EMBO Molecular Medicine, 2016, 8, 745-760.	6.9	119
15	An integrated genomic regulatory network of virulence-related transcriptional factors in Pseudomonas aeruginosa. Nature Communications, 2019, 10, 2931.	12.8	112
16	RedeR: R/Bioconductor package for representing modular structures, nested networks and multiple levels of hierarchical associations.. Genome Biology, 2012, 13, R29.	9.6	91
17	A MicroRNA Signature Associated With Metastasis of T1 Colorectal Cancers to Lymph Nodes. Gastroenterology, 2018, 154, 844-848.e7.	1.3	91
18	Tetherless near-infrared control of brain activity in behaving animals using fully implantable upconversion microdevices. Biomaterials, 2017, 142, 136-148.	11.4	74

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19	Reconciliation of classification systems defining molecular subtypes of colorectal cancer. Cell Cycle, 2014, 13, 353-357.	2.6	69
20	The RNA binding protein SORBS2 suppresses metastatic colonization of ovarian cancer by stabilizing tumor-suppressive immunomodulatory transcripts. Genome Biology, 2018, 19, 35.	8.8	68
21	Pharmacological activation of estrogen receptor beta augments innate immunity to suppress cancer metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3673-E3681.	7.1	56
22	Defining super-enhancer landscape in triple-negative breast cancer by multiomic profiling. Nature Communications, 2021, 12, 2242.	12.8	56
23	Diagnosis and prognosis of breast cancer by high-performance serum metabolic fingerprints. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2122245119.	7.1	53
24	A multidimensional network approach reveals microRNAs as determinants of the mesenchymal colorectal cancer subtype. Oncogene, 2016, 35, 6026-6037.	5.9	49
25	Genome-wide Discovery and Identification of a Novel miRNA Signature for Recurrence Prediction in Stage II and III Colorectal Cancer. Clinical Cancer Research, 2018, 24, 3867-3877.	7.0	47
26	Unsupervised class discovery in pancreatic ductal adenocarcinoma reveals cell-intrinsic mesenchymal features and high concordance between existing classification systems. Scientific Reports, 2020, 10, 337.	3.3	46
27	Integrative network biology analysis identifies miR-508-3p as the determinant for the mesenchymal identity and a strong prognostic biomarker of ovarian cancer. Oncogene, 2019, 38, 2305-2319.	5.9	41
28	c-myc regulates the sensitivity of breast cancer cells to palbociclib via c-myc/miR-29b-3p/CDK6 axis. Cell Death and Disease, 2020, 11, 760.	6.3	39
29	Gene Expression Signature in Surgical Tissues and Endoscopic Biopsies Identifies High-Risk T1 Colorectal Cancers. Gastroenterology, 2019, 156, 2338-2341.e3.	1.3	37
30	High-throughput brain activity mapping and machine learning as a foundation for systems neuropharmacology. Nature Communications, 2018, 9, 5142.	12.8	34
31	High-throughput three-dimensional chemotactic assays reveal steepness-dependent complexity in neuronal sensation to molecular gradients. Nature Communications, 2018, 9, 4745.	12.8	33
32	Single-cell EMT-related transcriptional analysis revealed intra-cluster heterogeneity of tumor cell clusters in epithelial ovarian cancer ascites. Oncogene, 2020, 39, 4227-4240.	5.9	30
33	Dissecting cancer heterogeneity â€“ An unsupervised classification approach. International Journal of Biochemistry and Cell Biology, 2013, 45, 2574-2579.	2.8	28
34	Regeneration of cortical tissue from brain injury by implantation of defined molecular gradient of semaphorin 3A. Biomaterials, 2018, 157, 125-135.	11.4	28
35	Novel therapeutic strategies for treatingPseudomonas aeruginosainfection. Expert Opinion on Drug Discovery, 2020, 15, 1403-1423.	5.0	26
36	Plasma cells shape the mesenchymal identity of ovarian cancers through transfer of exosome-derived microRNAs. Science Advances, 2021, 7, .	10.3	25

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37	Targeting m6A modification inhibits herpes virus 1 infection. Genes and Diseases, 2022, 9, 1114-1128.	3.4	24
38	RNAMethyPro: a biologically conserved signature of N6-methyladenosine regulators for predicting survival at pan-cancer level. Npj Precision Oncology, 2019, 3, 13.	5.4	23
39	Single-cell RNA-seq recognized the initiator of epithelial ovarian cancer recurrence. Oncogene, 2022, 41, 895-906.	5.9	22
40	High-throughput intracellular biopsy of microRNAs for dissecting the temporal dynamics of cellular heterogeneity. Science Advances, 2020, 6, eaba4971.	10.3	20
41	Demyelination Regulates the Circadian Transcription Factor BMAL1 to Signal Adult Neural Stem Cells to Initiate Oligodendrogenesis. Cell Reports, 2020, 33, 108394.	6.4	19
42	Integrated regulatory network in Pseudomonas syringae reveals dynamics of virulence. Cell Reports, 2021, 34, 108920.	6.4	19
43	Posterior Association Networks and Functional Modules Inferred from Rich Phenotypes of Gene Perturbations. PLoS Computational Biology, 2012, 8, e1002566.	3.2	18
44	A genomewide transcriptomic approach identifies a novel gene expression signature for the detection of lymph node metastasis in patients with early stage gastric cancer. EBioMedicine, 2019, 41, 268-275.	6.1	18
45	Cancer-associated histone mutation H2BG53D disrupts DNAâ€“histone octamer interaction and promotes oncogenic phenotypes. Signal Transduction and Targeted Therapy, 2020, 5, 27.	17.1	17
46	The elevated transcription of ADAM19 by the oncohistone H2BE76K contributes to oncogenic properties in breast cancer. Journal of Biological Chemistry, 2021, 296, 100374.	3.4	17
47	Reconstructing evolving signalling networks by hidden Markov nested effects models. Annals of Applied Statistics, 2014, 8, .	1.1	16
48	Pseudomonas syringae dualâ€function protein Lon switches between virulence and metabolism by acting as both <scp>DNA</scp>â€binding transcriptional regulator and protease in different environments. Environmental Microbiology, 2020, 22, 2968-2988.	3.8	16
49	Dissecting cancer heterogeneity based on dimension reduction of transcriptomic profiles using extreme learning machines. PLoS ONE, 2018, 13, e0203824.	2.5	14
50	OCaMIRâ€”A Noninvasive, Diagnostic Signature for Early-Stage Ovarian Cancer: A Multi-cohort Retrospective and Prospective Study. Clinical Cancer Research, 2021, 27, 4277-4286.	7.0	14
51	The H2BG53D oncohistone directly upregulates ANXA3 transcription and enhances cell migration in pancreatic ductal adenocarcinoma. Signal Transduction and Targeted Therapy, 2020, 5, 106.	17.1	12
52	Structural mechanism of bivalent histone H3K4me3K9me3 recognition by the Spindlin1/C11orf84 complex in rRNA transcription activation. Nature Communications, 2021, 12, 949.	12.8	11
53	TCOF1 upregulation in triple-negative breast cancer promotes stemness and tumour growth and correlates with poor prognosis. British Journal of Cancer, 2022, 126, 57-71.	6.4	11
54	Profiling MicroRNAs with Associated Spatial Dynamics in Acute Tissue Slices. ACS Nano, 2021, 15, 4881-4892.	14.6	10

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55	Weighted Gene Co-expression Network Analysis Identifies CALD1 as a Biomarker Related to M2 Macrophages Infiltration in Stage III and IV Mismatch Repair-Proficient Colorectal Carcinoma. Frontiers in Molecular Biosciences, 2021, 8, 649363.	3.5	10
56	Multi-Omics Data Fusion for Cancer Molecular Subtyping Using Sparse Canonical Correlation Analysis. Frontiers in Genetics, 2021, 12, 607817.	2.3	10
57	An integrated workflow for biomarker development using microRNAs in extracellular vesicles for cancer precision medicine. Seminars in Cancer Biology, 2021, 74, 134-155.	9.6	9
58	A Network-Based Approach for Identification of Subtype-Specific Master Regulators in Pancreatic Ductal Adenocarcinoma. Genes, 2020, 11, 155.	2.4	8
59	HSP90 Inhibition Synergizes with Cisplatin to Eliminate Basal-like Pancreatic Ductal Adenocarcinoma Cells. Cancers, 2021, 13, 6163.	3.7	8
60	Identification of prognostic spatial organization features in colorectal cancer microenvironment using deep learning on histopathology images. Medicine in Omics, 2021, 2, 100008.	1.3	6
61	Inhibition of Vascular Growth by Modulation of the Anandamide/Fatty Acid Amide Hydrolase Axis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2974-2989.	2.4	6
62	Development of a miRNAâ€based classifier for detection of colorectal cancer molecular subtypes. Molecular Oncology, 2022, 16, 2693-2709.	4.6	6
63	A modified particle swarm optimization algorithm for reliability problems. , 2010, , .		4
64	Dissecting super-enhancer heterogeneity: time to re-examine cancer subtypes?. Trends in Genetics, 2022, 38, 1199-1203.	6.7	3
65	Attention to time-of-day variability improves the reproducibility of gene expression patterns in multiple sclerosis. IScience, 2021, 24, 103247.	4.1	2
66	Colorectal cancer subtype identification from differential gene expression levels using minimalist deep learning. BioData Mining, 2022, 15, 12.	4.0	2
67	Postnatal eye size in mice is controlled by SREBP2-mediated transcriptional repression of Lrp2 and Bmp2. Development (Cambridge), 2022, 149, .	2.5	2
68	NEM-Tar: A Probabilistic Graphical Model for Cancer Regulatory Network Inference and Prioritization of Potential Therapeutic Targets From Multi-Omics Data. Frontiers in Genetics, 2021, 12, 608042.	2.3	1
69	Joining the dots: network analysis of gene perturbation data. , 0, , 83-107.		0