Xiao-Sheng Wang

List of Publications by Year
in descending order

96 papers	4,647 citations	172443 29 h-index	114455 63 g-index
119 all docs	119 docs citations	119 times ranked	7865 citing authors

#	Article	IF	Citations
1	Expression of the SARS-CoV-2 cell receptor gene ACE2 in a wide variety of human tissues. Infectious Diseases of Poverty, 2020, 9, 45.	3.7	1,195
2	Comparative Review of SARS-CoV-2, SARS-CoV, MERS-CoV, and Influenza A Respiratory Viruses. Frontiers in Immunology, 2020, 11, 552909.	4.8	330
3	Classification of triple-negative breast cancers based on Immunogenomic profiling. Journal of Experimental and Clinical Cancer Research, 2018, 37, 327.	8.6	329
4	PLK1, A Potential Target for Cancer Therapy. Translational Oncology, 2017, 10, 22-32.	3.7	291
5	A Comprehensive Immunologic Portrait of Triple-Negative Breast Cancer. Translational Oncology, 2018, 11, 311-329.	3.7	204
6	Correlate tumor mutation burden with immune signatures in human cancers. BMC Immunology, 2019, 20, 4.	2.2	149
7	Increased glycolysis correlates with elevated immune activity in tumor immune microenvironment. EBioMedicine, 2019, 42, 431-442.	6.1	111
8	*TP53* mutations, expression and interaction networks in human cancers. Oncotarget, 2017, 8, 624-643.	1.8	105
9	Cancer type-dependent correlations between TP53 mutations and antitumor immunity. DNA Repair, 2020, 88, 102785.	2.8	100
10	Immunogenomics Analysis Reveals that TP53 Mutations Inhibit Tumor Immunity in Gastric Cancer. Translational Oncology, 2018, 11, 1171-1187.	3.7	94
11	A Bayesian connectivity-based approach to constructing probabilistic gene regulatory networks. Bioinformatics, 2004, 20, 2918-2927.	4.1	90
12	Correlate the TP53 Mutation and the HRAS Mutation with Immune Signatures in Head and Neck Squamous Cell Cancer. Computational and Structural Biotechnology Journal, 2019, 17, 1020-1030.	4.1	86
13	Transcriptional landscape of human cancers. Oncotarget, 2017, 8, 34534-34551.	1.8	74
14	ARID1A Mutations Are Associated with Increased Immune Activity in Gastrointestinal Cancer. Cells, 2019, 8, 678.	4.1	73
15	Identification of potential synthetic lethal genes to p53 using a computational biology approach. BMC Medical Genomics, 2013, 6, 30.	1.5	71
16	Identifying novel factors associated with COVID-19 transmission and fatality using the machine learning approach. Science of the Total Environment, 2021, 764, 142810.	8.0	69
17	PPAR-delta promotes survival of breast cancer cells in harsh metabolic conditions. Oncogenesis, 2016, 5, e232-e232.	4.9	62
18	A Meta Analysis of Pancreatic Microarray Datasets Yields New Targets as Cancer Genes and Biomarkers. PLoS ONE, 2014, 9, e93046.	2.5	60

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19	Classification of breast cancer patients using somatic mutation profiles and machine learning approaches. BMC Systems Biology, 2016, 10, 62.	3.0	54
20	Accurate molecular classification of cancer using simple rules. BMC Medical Genomics, 2009, 2, 64.	1.5	51
21	*TP53* Mutations Promote Immunogenic Activity in Breast Cancer. Journal of Oncology, 2019, 2019, 1-19.	1.3	51
22	Microarray-based cancer prediction using single genes. BMC Bioinformatics, 2011, 12, 391.	2.6	50
23	An algorithm to quantify intratumor heterogeneity based on alterations of gene expression profiles. Communications Biology, 2020, 3, 505.	4.4	50
24	A Robust Gene selection Method for Microarray-based Cancer Classification. Cancer Informatics, 2010, 9, CIN.S3794.	1.9	46
25	A ZEB1/p53 signaling axis in stromal fibroblasts promotes mammary epithelial tumours. Nature Communications, 2019, 10, 3210.	12.8	46
26	PreMSIm: An R package for predicting microsatellite instability from the expression profiling of a gene panel in cancer. Computational and Structural Biotechnology Journal, 2020, 18, 668-675.	4.1	44
27	Microarray-Based Cancer Prediction Using Soft Computing Approach. Cancer Informatics, 2009, 7, CIN.S2655.	1.9	37
28	Combination of DC/CIK adoptive T cell immunotherapy with chemotherapy in advanced non-small-cell lung cancer (NSCLC) patients: a prospective patients' preference-based study (PPPS). Clinical and Translational Oncology, 2019, 21, 721-728.	2.4	32
29	The SARS-CoV-2 host cell receptor ACE2 correlates positively with immunotherapy response and is a potential protective factor for cancer progression. Computational and Structural Biotechnology Journal, 2020, 18, 2438-2444.	4.1	32
30	Identification of molecular features correlating with tumor immunity in gastric cancer by multi-omics data analysis. Annals of Translational Medicine, 2020, 8, 1050-1050.	1.7	31
31	Oroxylin A reverses hypoxia-induced cisplatin resistance through inhibiting HIF-1α mediated XPC transcription. Oncogene, 2020, 39, 6893-6905.	5.9	30
32	Identification of Transcriptional Markers and microRNA–mRNA Regulatory Networks in Colon Cancer by Integrative Analysis of mRNA and microRNA Expression Profiles in Colon Tumor Stroma. Cells, 2019, 8, 1054.	4.1	29
33	Identification of gastric cancer subtypes based on pathway clustering. Npj Precision Oncology, 2021, 5, 46.	5.4	28
34	HIF1A expression correlates with increased tumor immune and stromal signatures and aggressive phenotypes in human cancers. Cellular Oncology (Dordrecht), 2020, 43, 877-888.	4.4	25
35	Integrative exploration of genomic profiles for triple negative breast cancer identifies potential drug targets. Medicine (United States), 2016, 95, e4321.	1.0	24
36	Exploration of the Combination of PLK1 Inhibition with Immunotherapy in Cancer Treatment. Journal of Oncology, 2018, 2018, 1-13.	1.3	22

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37	Identification of Transcriptional Signatures of Colon Tumor Stroma by a Meta-Analysis. Journal of Oncology, 2019, 2019, 1-12.	1.3	22
38	The Cancer Omics Atlas: an integrative resource for cancer omics annotations. BMC Medical Genomics, 2018, 11, 63.	1.5	20
39	PLK1 inhibition in cancer therapy: potentials and challenges. Future Medicinal Chemistry, 2019, 11, 1383-1386.	2.3	20
40	Computational analysis of TMPRSS2 expression in normal and SARS-CoV-2-infected human tissues. Chemico-Biological Interactions, 2021, 346, 109583.	4.0	20
41	Exome Analysis Reveals Differentially Mutated Gene Signatures of Stage, Grade and Subtype in Breast Cancers. PLoS ONE, 2015, 10, e0119383.	2.5	19
42	Identifying Pathways and Networks Associated With the SARS-CoV-2 Cell Receptor ACE2 Based on Gene Expression Profiles in Normal and SARS-CoV-2-Infected Human Tissues. Frontiers in Molecular Biosciences, 2020, 7, 568954.	3.5	18
43	Immunological classification of gliomas based on immunogenomic profiling. Journal of Neuroinflammation, 2020, 17, 360.	7.2	17
44	DITHER: an algorithm for Defining IntraTumor Heterogeneity based on EntRopy. Briefings in Bioinformatics, 2021, 22, .	6.5	16
45	Evaluation of the Current Therapeutic Approaches for COVID-19: A Systematic Review and a Meta-analysis. Frontiers in Pharmacology, 2021, 12, 607408.	3.5	15
46	Identification of genes highly downregulated in pancreatic cancer through a meta-analysis of microarray datasets: implications for discovery of novel tumor-suppressor genes and therapeutic targets. Journal of Cancer Research and Clinical Oncology, 2018, 144, 309-320.	2.5	14
47	Important factors affecting COVID-19 transmission and fatality in metropolises. Public Health, 2021, 190, e21-e23.	2.9	14
48	KALRN mutations promote antitumor immunity and immunotherapy response in cancer. , 2020, 8, e000293.		13
49	Inference of Cancer-specific Gene Regulatory Networks Using Soft Computing Rules. Gene Regulation and Systems Biology, 2010, 4, GRSB.S4509.	2.3	12
50	RNF43 frameshift mutations contribute to tumourigenesis in right-sided colon cancer. Pathology Research and Practice, 2019, 215, 152453.	2.3	12
51	Identification of subtypes correlated with tumor immunity and immunotherapy in cutaneous melanoma. Computational and Structural Biotechnology Journal, 2021, 19, 4472-4485.	4.1	12
52	Identification of key tumor stroma-associated transcriptional signatures correlated with survival prognosis and tumor progression in breast cancer. Breast Cancer, 2022, , 1.	2.9	12
53	Evaluation of the effects of meteorological factors on COVID-19 prevalence by the distributed lag nonlinear model. Journal of Translational Medicine, 2022, 20, 170.	4.4	12
54	Robust two-gene classifiers for cancer prediction. Genomics, 2012, 99, 90-95.	2.9	9

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55	Malignancy of Cancers and Synthetic Lethal Interactions Associated With Mutations of Cancer Driver Genes. Medicine (United States), 2016, 95, e2697.	1.0	9
56	Cell cycle activity correlates with increased anti‐tumor immunity in diverse cancers. Clinical and Translational Medicine, 2020, 10, e98.	4.0	9
57	The landscape of long non-coding RNAs in tumor stroma. Life Sciences, 2021, 264, 118725.	4.3	9
58	Computational analysis of expression of human embryonic stem cell-associated signatures in tumors. BMC Research Notes, 2011, 4, 471.	1.4	8
59	Recent advances targeting C‐C chemokine receptor type 2 for liver diseases in monocyte/macrophage. Liver International, 2020, 40, 2928-2936.	3.9	8
60	Pan-cancer analysis reveals that neurotrophin signaling correlates positively with anti-tumor immunity, clinical outcomes, and response to targeted therapies and immunotherapies in cancer. Life Sciences, 2021, 282, 119848.	4.3	8
61	Identification of genomic features associated with immunotherapy response in gastrointestinal cancers. World Journal of Gastrointestinal Oncology, 2019, 11, 270-280.	2.0	8
62	DEPTH2: an mRNA-based algorithm to evaluate intratumor heterogeneity without reference to normal controls. Journal of Translational Medicine, 2022, 20, 150.	4.4	8
63	CANCER CLASSIFICATION USING SINGLE GENES. , 2009, , .		7
64	Subtyping of head and neck squamous cell cancers based on immune signatures. International Immunopharmacology, 2021, 99, 108007.	3.8	7
65	Identification of Breast Cancer Immune Subtypes by Analyzing Bulk Tumor and Single Cell Transcriptomes. Frontiers in Cell and Developmental Biology, 2021, 9, 781848.	3.7	7
66	Identification of Marker Genes for Cancer Based on Microarrays Using a Computational Biology Approach. Current Bioinformatics, 2014, 9, 140-146.	1.5	6
67	Discovery of molecular associations among aging, stem cells, and cancer based on gene expression profiling. Chinese Journal of Cancer, 2013, 32, 155-161.	4.9	6
68	Classification of lung adenocarcinoma based on stemness scores in bulk and single cell transcriptomes. Computational and Structural Biotechnology Journal, 2022, 20, 1691-1701.	4.1	6
69	Retrospective prediction of the epidemic trend of COVID‐19 in Wuhan at four phases. Journal of Medical Virology, 2021, 93, 2493-2498.	5.0	5
70	Angiotensin-converting enzyme 2 connects COVID-19 with cancer and cancer immunotherapy. World Journal of Gastrointestinal Oncology, 2021, 13, 157-160.	2.0	5
71	Identification of COVID-19 subtypes based on immunogenomic profiling. International Immunopharmacology, 2021, 96, 107615.	3.8	5
72	Pan-Cancer Analysis Reveals That E1A Binding Protein p300 Mutations Increase Genome Instability and Antitumor Immunity. Frontiers in Cell and Developmental Biology, 2021, 9, 729927.	3.7	5

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73	The spliceosome pathway activity correlates with reduced anti-tumor immunity and immunotherapy response, and unfavorable clinical outcomes in pan-cancer. Computational and Structural Biotechnology Journal, 2021, 19, 5428-5442.	4.1	5
74	Subtyping of Human Papillomavirus-Positive Cervical Cancers Based on the Expression Profiles of 50 Genes. Frontiers in Immunology, 2022, 13, 801639.	4.8	5
75	Classification of gastric cancers based on immunogenomic profiling. Translational Oncology, 2021, 14, 100888.	3.7	4
76	Identification of Breast Cancer Subtypes Based on Gene Expression Profiles in Breast Cancer Stroma. Clinical Breast Cancer, 2022, 22, 521-537.	2.4	4
77	Microarray Analysis of Ageing-related Signatures and Their Expression in Tumors Based on a Computational Biology Approach. Genomics, Proteomics and Bioinformatics, 2012, 10, 136-141.	6.9	3
78	MYTH: An algorithm to score intratumour heterogeneity based on alterations of DNA methylation profiles. Clinical and Translational Medicine, 2021, 11, e611.	4.0	3
79	Subtyping of sarcomas based on pathway enrichment scores in bulk and single cell transcriptomes. Journal of Translational Medicine, 2022, 20, 48.	4.4	3
80	Multi-OMICs data analysis identifies molecular features correlating with tumor immunity in colon cancer. Cancer Biomarkers, 2022, 33, 261-271.	1.7	3
81	Computational Analysis of Transcriptional Circuitries in Human Embryonic Stem Cells Reveals Multiple and Independent Networks. BioMed Research International, 2014, 2014, 1-10.	1.9	2
82	Predicting the development trend of the second wave of COVID‐19 in five European countries. Journal of Medical Virology, 2021, 93, 5896-5907.	5.0	2
83	An Exploration of Mutation Status of Cancer Genes in Breast Cancers. Journal of Next Generation Sequencing & Applications, 2014, 01, .	0.3	2
84	Inducing decision rules: a granular computing approach. , 0, , .		1
85	Discovering Distinct Functional Modules of Specific Cancer Types Using Protein-Protein Interaction Networks. BioMed Research International, 2015, 2015, 1-10.	1.9	1
86	Computational Identification of Tumor Suppressor Genes Based on Gene Expression Profiles in Normal and Cancerous Gastrointestinal Tissues. Journal of Oncology, 2020, 2020, 1-12.	1.3	1
87	Adenoma to carcinoma: A portrait of molecular and immunological profiles of colorectal sporadic tumors. International Immunopharmacology, 2021, 100, 108168.	3.8	1
88	Comparisons of the immunological landscape between COVID-19, influenza, and respiratory syncytial virus patients by clustering analysis. Computational and Structural Biotechnology Journal, 2021, 19, 2347-2355.	4.1	1
89	Comparisons of the immunological landscape of COVID-19 patients based on sex and disease severity by multi-omics analysis. Chemico-Biological Interactions, 2022, 352, 109777.	4.0	1
90	Identification of prostate cancer subtypes based on immune signature scores in bulk and single-cell transcriptomes. , 2022, 39, .		1

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91	Explore Genomic Profiles for Triple-Negative Breast Cancer to Discover Drug Targets. , 2019, , 423-440.		0
92	Investigation of the factors potentially responsible for the significant different prevalence of COVID-19 between African-Africans and African-Americans. AIMS Allergy and Immunology, 2021, 5, 184-191.	0.5	0
93	Determination of Glutamate and GABA Released by Mouse Embryonic Stem Cells Using HILIC-ESI-MS/MS. Natural Products Journal, 2020, 10, 122-129.	0.3	0
94	A Generalized Decision Logic Language for Information Tables. , 2007, , 16-21.		0
95	Dissection of Immune Profiles in Microsatellite Stable and Low Microsatellite Instability Colon Adenocarcinoma by Multiomics Data Analysis. Journal of Oncology, 2022, 2022, 1-20.	1.3	0
96	A Meta Analysis of Pancreatic Microarray Datasets Yields New Targets as Cancer Genes and Biomarkers. , 2014, 9, e93046.		0