

# Qiang-Hu Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

68  
papers

5,229  
citations

186265

28  
h-index

123424

61  
g-index

80  
all docs

80  
docs citations

80  
times ranked

10887  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of blood glucose level and prognosis of inpatients with coexistent diabetes and COVID-19. <i>Endocrine</i> , 2022, 75, 1-9.	2.3	8
2	Î²2-Microglobulin Maintains Glioblastoma Stem Cells and Induces M2-like Polarization of Tumor-Associated Macrophages. <i>Cancer Research</i> , 2022, 82, 3321-3334.	0.9	31
3	Therapy-Induced Transdifferentiation Promotes Glioma Growth Independent of EGFR Signaling. <i>Cancer Research</i> , 2021, 81, 1528-1539.	0.9	5
4	Implications of liver injury in risk-stratification and management of patients with COVID-19. <i>Hepatology International</i> , 2021, 15, 202-212.	4.2	15
5	Implications of cardiac markers in risk-stratification and management for COVID-19 patients. <i>Critical Care</i> , 2021, 25, 158.	5.8	16
6	High Expression of ACE2 and TMPRSS2 at the Resection Margin Makes Lung Cancer Survivors Susceptible to SARS-CoV-2 With Unfavorable Prognosis. <i>Frontiers in Oncology</i> , 2021, 11, 644575.	2.8	16
7	A predictive paradigm for COVID-19 prognosis based on the longitudinal measure of biomarkers. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	9
8	Pericytes augment glioblastoma cell resistance to temozolomide through CCL5-CCR5 paracrine signaling. <i>Cell Research</i> , 2021, 31, 1072-1087.	12.0	65
9	Sex-based clinical and immunological differences in COVID-19. <i>BMC Infectious Diseases</i> , 2021, 21, 647.	2.9	33
10	Comparative Characterization and Risk Stratification of Asymptomatic and Presymptomatic Patients With COVID-19. <i>Frontiers in Immunology</i> , 2021, 12, 700449.	4.8	2
11	Laboratory Testing Implications of Risk-Stratification and Management of COVID-19 Patients. <i>Frontiers in Medicine</i> , 2021, 8, 699706.	2.6	3
12	Chitinase-3-like 1 protein complexes modulate macrophage-mediated immune suppression in glioblastoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	49
13	A comparative genomics analysis of lung adenocarcinoma for Chinese population by using panel of recurrent mutations. <i>Journal of Biomedical Research</i> , 2021, 35, 11.	1.6	0
14	The androgen receptor expression and association with patient's survival in different cancers. <i>Genomics</i> , 2020, 112, 1926-1940.	2.9	34
15	Dynamic changes in anti-SARS-CoV-2 antibodies during SARS-CoV-2 infection and recovery from COVID-19. <i>Nature Communications</i> , 2020, 11, 6044.	12.8	196
16	Transcriptional regulatory networks of tumor-associated macrophages that drive malignancy in mesenchymal glioblastoma. <i>Genome Biology</i> , 2020, 21, 216.	8.8	73
17	Implications of SARS-CoV-2 infection for patients with rheumatic disease. <i>Annals of the Rheumatic Diseases</i> , 2020, , annrheumdis-2020-218050.	0.9	5
18	Improved clinical symptoms and mortality among patients with severe or critical COVID-19 after convalescent plasma transfusion. <i>Blood</i> , 2020, 136, 755-759.	1.4	125

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19	Genomic and Phenotypic Characterization of a Broad Panel of Patient-Derived Xenografts Reflects the Diversity of Glioblastoma. <i>Clinical Cancer Research</i> , 2020, 26, 1094-1104.	7.0	124
20	Interferon- $\beta$ enhances survival and modulates transcriptional profiles and the immune response in melanoma patients treated with dendritic cell vaccines. <i>Biomedicine and Pharmacotherapy</i> , 2020, 125, 109966.	5.6	8
21	Mature myelin maintenance requires Oki to coactivate PPAR $\alpha$ -RXR $\alpha$ -mediated lipid metabolism. <i>Journal of Clinical Investigation</i> , 2020, 130, 2220-2236.	8.2	50
22	The Role of Fibrinogen-Like Protein 2 on Immunosuppression and Malignant Progression in Glioma. <i>Journal of the National Cancer Institute</i> , 2019, 111, 292-300.	6.3	32
23	A PET Radiomics Model to Predict Refractory Mediastinal Hodgkin Lymphoma. <i>Scientific Reports</i> , 2019, 9, 1322.	3.3	62
24	Gene array analysis of PD-1H overexpressing monocytes reveals a pro-inflammatory profile. <i>Heliyon</i> , 2018, 4, e00545.	3.2	9
25	Large Scale Identification of Variant Proteins in Glioma Stem Cells. <i>ACS Chemical Neuroscience</i> , 2018, 9, 73-79.	3.5	12
26	TumorFusions: an integrative resource for cancer-associated transcript fusions. <i>Nucleic Acids Research</i> , 2018, 46, D1144-D1149.	14.5	179
27	EGFR heterogeneity and implications for therapeutic intervention in glioblastoma. <i>Neuro-Oncology</i> , 2018, 20, 743-752.	1.2	210
28	TMIC-14. AUTO-/PARACRINE SIGNALING OF PI3K/AKT/YKL-40 IN MESENCHYMAL GLIOBLASTOMA PROGRESSION. <i>Neuro-Oncology</i> , 2018, 20, vi258-vi259.	1.2	0
29	DRES-03. EGFR-TARGETED THERAPY-INDUCED RESISTANCE MECHANISM IN MALIGNANT GLIOMAS. <i>Neuro-Oncology</i> , 2018, 20, vi75-vi76.	1.2	0
30	miRNA Mediated Noise Making of 3'UTR Mutations in Cancer. <i>Genes</i> , 2018, 9, 545.	2.4	12
31	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054.	12.8	68
32	Systematic analysis of telomere length and somatic alterations in 31 cancer types. <i>Nature Genetics</i> , 2017, 49, 349-357.	21.4	476
33	PAF promotes stemness and radioresistance of glioma stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9086-E9095.	7.1	40
34	Tumor Evolution of Glioma-Intrinsic Gene Expression Subtypes Associates with Immunological Changes in the Microenvironment. <i>Cancer Cell</i> , 2017, 32, 42-56.e6.	16.8	1,282
35	ClioVis data portal for visualization and analysis of brain tumor expression datasets. <i>Neuro-Oncology</i> , 2017, 19, 139-141.	1.2	622
36	Oki deficiency maintains stemness of glioma stem cells in suboptimal environment by downregulating endolysosomal degradation. <i>Nature Genetics</i> , 2017, 49, 75-86.	21.4	74

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37	DRES-04. DEVELOPMENT OF A CRISPR-CAS9D10A TARGETABLE, HIGH-COMPLEXITY, SINGLE-CELL BARCODING APPROACH FOR ISOLATION OF TREATMENT RESISTANT SUBCLONES FROM HETEROGENOUS MALIGNANT GLIOMAS. <i>Neuro-Oncology</i> , 2017, 19, vi64-vi64.	1.2	0
38	GENE-36. ACCURATE DETECTION OF TERT PROMOTER MUTATION IN GLIOMAS USING INFINIUM DNA METHYLATION ARRAYS IDENTIFIES NOVEL EPIGENETIC ASSOCIATION. <i>Neuro-Oncology</i> , 2017, 19, vi100-vi100.	1.2	0
39	An Integrating Approach for Genome-Wide Screening of MicroRNA Polymorphisms Mediated Drug Response Alterations. <i>International Journal of Genomics</i> , 2017, 2017, 1-7.	1.6	5
40	A relative increase in circulating platelets following chemoradiation predicts for poor survival of patients with glioblastoma. <i>Oncotarget</i> , 2017, 8, 90488-90495.	1.8	13
41	Inferring Alcoholism SNPs and Regulatory Chemical Compounds Based on Ensemble Bayesian Network. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 107-115.	1.1	4
42	Epigenetic Activation of WNT5A Drives Glioblastoma Stem Cell Differentiation and Invasive Growth. <i>Cell</i> , 2016, 167, 1281-1295.e18.	28.9	207
43	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. <i>Nature Communications</i> , 2016, 7, 10499.	12.8	124
44	Suppression of RAF/MEK or PI3K synergizes cytotoxicity of receptor tyrosine kinase inhibitors in glioma tumor-initiating cells. <i>Journal of Translational Medicine</i> , 2016, 14, 46.	4.4	31
45	EPIG-05RADIORESISTANCE OF PODOPLANIN-EXPRESSING GLIOMA STEM CELLS IS ASSOCIATED WITH EZH2-DRIVEN POLYCOMB REPRESSIVE COMPLEX ACTIVITY. <i>Neuro-Oncology</i> , 2015, 17, v87.1-v87.	1.2	0
46	GENO-36GLIOMA SPHERE-FORMING CELLS REVEAL INTRINSIC GLOBAL HYPERMETHYLATION ASSOCIATED WITH GBM RADIATION RESISTANCE. <i>Neuro-Oncology</i> , 2015, 17, v99.5-v100.	1.2	0
47	Gamma knife stereotactic radiosurgery in the treatment of brainstem metastases: The MD Anderson experience. <i>Neuro-Oncology Practice</i> , 2015, 2, 40-47.	1.6	9
48	Mesenchymal Stem Cells Isolated From Human Gliomas Increase Proliferation and Maintain Stemness of Glioma Stem Cells Through the IL-6/gp130/STAT3 Pathway. <i>Stem Cells</i> , 2015, 33, 2400-2415.	3.2	163
49	Systematic Identification of Single Amino Acid Variants in Glioma Stem-Cell-Derived Chromosome 19 Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 778-786.	3.7	22
50	Integration Strategy Is a Key Step in Network-Based Analysis and Dramatically Affects Network Topological Properties and Inferring Outcomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	1.9	5
51	PRADA: pipeline for RNA sequencing data analysis. <i>Bioinformatics</i> , 2014, 30, 2224-2226.	4.1	147
52	Integrated Chromosome 19 Transcriptomic and Proteomic Data Sets Derived from Glioma Cancer Stem-Cell Lines. <i>Journal of Proteome Research</i> , 2014, 13, 191-199.	3.7	27
53	Prioritising risk pathways of complex human diseases based on functional profiling. <i>European Journal of Human Genetics</i> , 2013, 21, 666-672.	2.8	1
54	Inferring Potential microRNA-microRNA Associations Based on Targeting Propensity and Connectivity in the Context of Protein Interaction Network. <i>PLoS ONE</i> , 2013, 8, e69719.	2.5	22

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55	mirTarPri: Improved Prioritization of MicroRNA Targets through Incorporation of Functional Genomics Data. PLoS ONE, 2013, 8, e53685.	2.5	14
56	A novel method to quantify gene set functional association based on gene ontology. Journal of the Royal Society Interface, 2012, 9, 1063-1072.	3.4	43
57	Community of protein complexes impacts disease association. European Journal of Human Genetics, 2012, 20, 1162-1167.	2.8	25
58	Association study of ACE and eNOS single nucleotide polymorphisms with Henoch-Schönlein purpura nephritis. Molecular Medicine Reports, 2012, 6, 1171-1177.	2.4	7
59	Screening for cancer associated MiRNAs through co-gene, co-function and co-pathway analysis. Computers in Biology and Medicine, 2012, 42, 624-630.	7.0	2
60	Prioritizing Cancer Therapeutic Small Molecules by Integrating Multiple OMICS Datasets. OMICS A Journal of Integrative Biology, 2012, 16, 552-559.	2.0	9
61	The Implications of Relationships between Human Diseases and Metabolic Subpathways. PLoS ONE, 2011, 6, e21131.	2.5	48
62	Genome-wide analysis of clustering patterns and flanking characteristics for plant microRNA genes. FEBS Journal, 2011, 278, 929-940.	4.7	19
63	Systematic analysis of human microRNA divergence based on evolutionary emergence. FEBS Letters, 2011, 585, 240-248.	2.8	15
64	MicroRNA regulation constrains the organization of target genes on mammalian chromosomes. FEBS Letters, 2011, 585, 1897-1904.	2.8	5
65	Functional Homogeneity in microRNA Target Heterogeneity—a New Sight into Human microRNomics. OMICS A Journal of Integrative Biology, 2011, 15, 25-35.	2.0	10
66	Prioritizing human cancer microRNAs based on genes' functional consistency between microRNA and cancer. Nucleic Acids Research, 2011, 39, e153-e153.	14.5	60
67	SubpathwayMiner: a software package for flexible identification of pathways. Nucleic Acids Research, 2009, 37, e131-e131.	14.5	195
68	In silico detection and characteristics of novel microRNA genes in the Equus caballus genome using an integrated ab initio and comparative genomic approach. Genomics, 2009, 94, 125-131.	2.9	52