

# Jinhui Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

1,134  
citations

430442

18  
h-index

525886

27  
g-index

63  
all docs

63  
docs citations

63  
times ranked

956  
citing authors

#	ARTICLE	IF	CITATIONS
1	ALKBH5-HOXA10 loop-mediated JAK2 m6A demethylation and cisplatin resistance in epithelial ovarian cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 284.	3.5	66
2	Eleven genes associated with progression and prognosis of endometrial cancer (EC) identified by comprehensive bioinformatics analysis. <i>Cancer Cell International</i> , 2019, 19, 136.	1.8	61
3	Tumor-suppressor role of miR-139-5p in endometrial cancer. <i>Cancer Cell International</i> , 2018, 18, 51.	1.8	58
4	Identification of Potential Biomarkers and Survival Analysis for Head and Neck Squamous Cell Carcinoma Using Bioinformatics Strategy: A Study Based on TCGA and GEO Datasets. <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	44
5	Identification of a prognostic signature of epithelial ovarian cancer based on tumor immune microenvironment exploration. <i>Genomics</i> , 2020, 112, 4827-4841.	1.3	41
6	Pyroptosis-related lncRNAs are potential biomarkers for predicting prognoses and immune responses in patients with UCEC. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 1036-1055.	2.3	41
7	Prognostic Risk Model and Tumor Immune Environment Modulation of m5C-Related LncRNAs in Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 800268.	2.2	40
8	Identification of EPHX2 and RMI2 as two novel key genes in cervical squamous cell carcinoma by an integrated bioinformatic analysis. <i>Journal of Cellular Physiology</i> , 2019, 234, 21260-21273.	2.0	36
9	Exploration of a novel prognostic risk signatures and immune checkpoint molecules in endometrial carcinoma microenvironment. <i>Genomics</i> , 2020, 112, 3117-3134.	1.3	35
10	Comprehensive of N1-Methyladenosine Modifications Patterns and Immunological Characteristics in Ovarian Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 746647.	2.2	35
11	MicroRNA-665 suppresses the growth and migration of ovarian cancer cells by targeting HOXA10. <i>Molecular Medicine Reports</i> , 2018, 18, 2661-2668.	1.1	33
12	Identification of Potential Biomarkers for Thyroid Cancer Using Bioinformatics Strategy: A Study Based on GEO Datasets. <i>BioMed Research International</i> , 2020, 2020, 1-21.	0.9	33
13	Long noncoding RNA NBAT-1 suppresses tumorigenesis and predicts favorable prognosis in ovarian cancer. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 1993-2002.	1.0	30
14	Identification of Potential Biomarkers in Association With Progression and Prognosis in Epithelial Ovarian Cancer by Integrated Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 1031.	1.1	29
15	Construction of an immune-related gene signature for prediction of prognosis in patients with cervical cancer. <i>International Immunopharmacology</i> , 2020, 88, 106882.	1.7	29
16	Nine glycolysis-related gene signature predicting the survival of patients with endometrial adenocarcinoma. <i>Cancer Cell International</i> , 2020, 20, 183.	1.8	28
17	Identification of aberrantly methylated differentially expressed genes and associated pathways in endometrial cancer using integrated bioinformatic analysis. <i>Cancer Medicine</i> , 2020, 9, 3522-3536.	1.3	28
18	Development of a novel immune-related lncRNA signature as a prognostic classifier for endometrial carcinoma. <i>International Journal of Biological Sciences</i> , 2021, 17, 448-459.	2.6	26

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19	Prognostic and Immunological Role of mRNA ac4C Regulator NAT10 in Pan-Cancer: New Territory for Cancer Research?. <i>Frontiers in Oncology</i> , 2021, 11, 630417.	1.3	26
20	Establishment of a novel cell cycle-related prognostic signature predicting prognosis in patients with endometrial cancer. <i>Cancer Cell International</i> , 2020, 20, 329.	1.8	25
21	m6A RNA methylation regulators were associated with the malignancy and prognosis of ovarian cancer. <i>Bioengineered</i> , 2021, 12, 3159-3176.	1.4	23
22	Multi-omics analysis of tumor mutational burden combined with prognostic assessment in epithelial ovarian cancer based on TCGA database. <i>International Journal of Medical Sciences</i> , 2020, 17, 3200-3213.	1.1	18
23	A prognostic signature based on immune-related genes for cervical squamous cell carcinoma and endocervical adenocarcinoma. <i>International Immunopharmacology</i> , 2020, 88, 106884.	1.7	18
24	Development of an immune gene prognostic classifier for survival prediction and respond to immunotherapy/chemotherapy in endometrial cancer. <i>International Immunopharmacology</i> , 2020, 86, 106735.	1.7	16
25	Identification of molecular markers associated with the progression and prognosis of endometrial cancer: a bioinformatic study. <i>Cancer Cell International</i> , 2020, 20, 59.	1.8	16
26	CSMD3 is Associated with Tumor Mutation Burden and Immune Infiltration in Ovarian Cancer Patients. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7647-7657.	0.8	16
27	MiR-216a accelerates proliferation and fibrogenesis via targeting PTEN and SMAD7 in human cardiac fibroblasts. <i>Cardiovascular Diagnosis and Therapy</i> , 2019, 9, 535-544.	0.7	15
28	Using mRNAsi to identify prognostic-related genes in endometrial carcinoma based on WGCNA. <i>Life Sciences</i> , 2020, 258, 118231.	2.0	15
29	Identification of Key Genes in Association with Progression and Prognosis in Cervical Squamous Cell Carcinoma. <i>DNA and Cell Biology</i> , 2020, 39, 848-863.	0.9	14
30	Construction of an Immune Cell Infiltration Score to Evaluate the Prognosis and Therapeutic Efficacy of Ovarian Cancer Patients. <i>Frontiers in Immunology</i> , 2021, 12, 751594.	2.2	13
31	Prognostic value of an autophagy-related gene expression signature for endometrial cancer patients. <i>Cancer Cell International</i> , 2020, 20, 306.	1.8	12
32	Methylation-driven genes and their prognostic value in cervical squamous cell carcinoma. <i>Annals of Translational Medicine</i> , 2020, 8, 868-868.	0.7	12
33	MiRNA based tumor mutation burden diagnostic and prognostic prediction models for endometrial cancer. <i>Bioengineered</i> , 2021, 12, 3603-3620.	1.4	12
34	Development of epithelial-mesenchymal transition-related lncRNA signature for predicting survival and immune microenvironment in pancreatic cancer with experiment validation. <i>Bioengineered</i> , 2021, 12, 10553-10567.	1.4	12
35	Development and Clinical Validation of Novel 8-Gene Prognostic Signature Associated With the Proportion of Regulatory T Cells by Weighted Gene Co-Expression Network Analysis in Uterine Corpus Endometrial Carcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 788431.	2.2	12
36	Competing endogenous RNA network of endometrial carcinoma: A comprehensive analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15648-15660.	1.2	11

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37	A microRNAâ€‘Messenger RNA Regulatory Network and Its Prognostic Value in Cervical Cancer. <i>DNA and Cell Biology</i> , 2020, 39, 1328-1346.	0.9	11
38	Co-expression network analysis identified atypical chemokine receptor 1 (ACKR1) association with lymph node metastasis and prognosis in cervical cancer. <i>Cancer Biomarkers</i> , 2020, 27, 213-223.	0.8	11
39	Identification of methylation-driven genes prognosis signature and immune microenvironment in uterus corpus endometrial cancer. <i>Cancer Cell International</i> , 2021, 21, 365.	1.8	11
40	Development of an Oxidative Phosphorylation-Related and Immune Microenvironment Prognostic Signature in Uterine Corpus Endometrial Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 753004.	1.8	11
41	Establishing a Prognostic Signature Based on Epithelialâ€‘Mesenchymal Transition-Related Genes for Endometrial Cancer Patients. <i>Frontiers in Immunology</i> , 2021, 12, 805883.	2.2	11
42	Comprehensive Analysis of the Prognostic Signature of Mutation-Derived Genome Instability-Related lncRNAs for Patients With Endometrial Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 753957.	1.8	11
43	SNX10 and PTGDS are associated with the progression and prognosis of cervical squamous cell carcinoma. <i>BMC Cancer</i> , 2021, 21, 694.	1.1	10
44	Identification of the Prognostic Signature Associated With Tumor Immune Microenvironment of Uterine Corpus Endometrial Carcinoma Based on Ferroptosis-Related Genes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 735013.	1.8	10
45	Identification of crucial aberrantly methylated and differentially expressed genes related to cervical cancer using an integrated bioinformatics analysis. <i>Bioscience Reports</i> , 2020, 40, .	1.1	9
46	&lt;p&gt;&lt;em&gt;ITLN1&lt;/em&gt; identified by comprehensive bioinformatic analysis as a hub candidate biological target in human epithelial ovarian cancer&lt;/p&gt;. <i>Cancer Management and Research</i> , 2019, Volume 11, 2379-2392.	0.9	8
47	Construction of a nine DNA repair-related gene prognostic classifier to predict prognosis in patients with endometrial carcinoma. <i>BMC Cancer</i> , 2021, 21, 29.	1.1	7
48	Construction of miRNA-mRNA Regulatory Network and Prognostic Signature in Endometrial Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 2363-2378.	1.0	7
49	Pan-Cancer Analysis Revealed SRSF9 as a New Biomarker for Prognosis and Immunotherapy. <i>Journal of Oncology</i> , 2022, 2022, 1-21.	0.6	7
50	Identification of a Novel Immune Landscape Signature for Predicting Prognosis and Response of Endometrial Carcinoma to Immunotherapy and Chemotherapy. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671736.	1.8	6
51	CXCL2-mediated ATR/CHK1 signaling pathway and platinum resistance in epithelial ovarian cancer. <i>Journal of Ovarian Research</i> , 2021, 14, 115.	1.3	6
52	Crosstalk of Redox-Related Subtypes, Establishment of a Prognostic Model and Immune Responses in Endometrial Carcinoma. <i>Cancers</i> , 2022, 14, 3383.	1.7	5
53	A model based on tumor-infiltrating immune cells for predicting the relapse rates of patients with testicular germ cell tumors. <i>International Immunopharmacology</i> , 2020, 86, 106710.	1.7	3
54	A Novel Prognostic Index Based on Alternative Splicing in Papillary Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2020, 10, 1333.	1.1	3

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55	Low Expression of RILPL2 Predicts Poor Prognosis and Correlates With Immune Infiltration in Endometrial Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 670893.	1.6	3
56	A novel prognostic model based on immunogenomics for clear cell renal cell carcinoma. <i>International Immunopharmacology</i> , 2021, 90, 107119.	1.7	2
57	Comprehensive Analysis of a Novel Lipid Metabolism-Related Gene Signature for Predicting the Prognosis and Immune Landscape in Uterine Corpus Endometrial Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-22.	0.6	2
58	Comprehensive study of a novel immune-related lncRNA for prognosis and drug treatment of cervical squamous cell carcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2021, 13, 11771-11785.	0.0	0