

# Jinhui Liu

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/9644369/jinhui-liu-publications-by-citations.pdf>

**Version:** 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57  
papers

497  
citations

13  
h-index

19  
g-index

63  
ext. papers

855  
ext. citations

5.4  
avg, IF

4.33  
L-index

#	Paper	IF	Citations
57	Tumor-suppressor role of miR-139-5p in endometrial cancer. <i>Cancer Cell International</i> , <b>2018</b> , 18, 51	6.4	49
56	Eleven genes associated with progression and prognosis of endometrial cancer (EC) identified by comprehensive bioinformatics analysis. <i>Cancer Cell International</i> , <b>2019</b> , 19, 136	6.4	30
55	MicroRNA-665 suppresses the growth and migration of ovarian cancer cells by targeting HOXA10. <i>Molecular Medicine Reports</i> , <b>2018</b> , 18, 2661-2668	2.9	29
54	Long noncoding RNA NBAT-1 suppresses tumorigenesis and predicts favorable prognosis in ovarian cancer. <i>OncoTargets and Therapy</i> , <b>2017</b> , 10, 1993-2002	4.4	26
53	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> , <b>2019</b> , 234, 21260-21273	7	25
52	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> , <b>2019</b> , 2019, 7376034	3	23
51	Identification of Potential Biomarkers in Association With Progression and Prognosis in Epithelial Ovarian Cancer by Integrated Bioinformatics Analysis. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1031	4.5	22
50	Identification of a prognostic signature of epithelial ovarian cancer based on tumor immune microenvironment exploration. <i>Genomics</i> , <b>2020</b> , 112, 4827-4841	4.3	20
49	Exploration of a novel prognostic risk signatures and immune checkpoint molecules in endometrial carcinoma microenvironment. <i>Genomics</i> , <b>2020</b> , 112, 3117-3134	4.3	18
48	Nine glycolysis-related gene signature predicting the survival of patients with endometrial adenocarcinoma. <i>Cancer Cell International</i> , <b>2020</b> , 20, 183	6.4	15
47	Identification of Potential Biomarkers for Thyroid Cancer Using Bioinformatics Strategy: A Study Based on GEO Datasets. <i>BioMed Research International</i> , <b>2020</b> , 2020, 9710421	3	15
46	Identification of aberrantly methylated differentially expressed genes and associated pathways in endometrial cancer using integrated bioinformatic analysis. <i>Cancer Medicine</i> , <b>2020</b> , 9, 3522-3536	4.8	14
45	Construction of an immune-related gene signature for prediction of prognosis in patients with cervical cancer. <i>International Immunopharmacology</i> , <b>2020</b> , 88, 106882	5.8	13
44	A prognostic signature based on immune-related genes for cervical squamous cell carcinoma and endocervical adenocarcinoma. <i>International Immunopharmacology</i> , <b>2020</b> , 88, 106884	5.8	13
43	Identification of molecular markers associated with the progression and prognosis of endometrial cancer: a bioinformatic study. <i>Cancer Cell International</i> , <b>2020</b> , 20, 59	6.4	11
42	MiR-216a accelerates proliferation and fibrogenesis via targeting PTEN and SMAD7 in human cardiac fibroblasts. <i>Cardiovascular Diagnosis and Therapy</i> , <b>2019</b> , 9, 535-544	2.6	11
41	Identification of Key Genes in Association with Progression and Prognosis in Cervical Squamous Cell Carcinoma. <i>DNA and Cell Biology</i> , <b>2020</b> , 39, 848-863	3.6	10

40	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> , <b>2020</b> , 17, 3200-3213	3.7	10
39	ALKBH5-HOXA10 loop-mediated JAK2 m6A demethylation and cisplatin resistance in epithelial ovarian cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , <b>2021</b> , 40, 284	12.8	10
38	Development of an immune gene prognostic classifier for survival prediction and respond to immunocheckpoint inhibitor therapy/chemotherapy in endometrial cancer. <i>International Immunopharmacology</i> , <b>2020</b> , 86, 106735	5.8	9
37	Using mRNAsi to identify prognostic-related genes in endometrial carcinoma based on WGCNA. <i>Life Sciences</i> , <b>2020</b> , 258, 118231	6.8	9
36	Prognostic value of an autophagy-related gene expression signature for endometrial cancer patients. <i>Cancer Cell International</i> , <b>2020</b> , 20, 306	6.4	8
35	identified by comprehensive bioinformatic analysis as a hub candidate biological target in human epithelial ovarian cancer. <i>Cancer Management and Research</i> , <b>2019</b> , 11, 2379-2392	3.6	7
34	m6A RNA methylation regulators were associated with the malignancy and prognosis of ovarian cancer. <i>Bioengineered</i> , <b>2021</b> , 12, 3159-3176	5.7	7
33	Competing endogenous RNA network of endometrial carcinoma: A comprehensive analysis. <i>Journal of Cellular Biochemistry</i> , <b>2019</b> , 120, 15648-15660	4.7	6
32	Co-expression network analysis identified atypical chemokine receptor 1 (ACKR1) association with lymph node metastasis and prognosis in cervical cancer. <i>Cancer Biomarkers</i> , <b>2020</b> , 27, 213-223	3.8	6
31	Identification of crucial aberrantly methylated and differentially expressed genes related to cervical cancer using an integrated bioinformatics analysis. <i>Bioscience Reports</i> , <b>2020</b> , 40,	4.1	6
30	Establishment of a novel cell cycle-related prognostic signature predicting prognosis in patients with endometrial cancer. <i>Cancer Cell International</i> , <b>2020</b> , 20, 329	6.4	6
29	Methylation-driven genes and their prognostic value in cervical squamous cell carcinoma. <i>Annals of Translational Medicine</i> , <b>2020</b> , 8, 868	3.2	6
28	Development of a novel immune-related lncRNA signature as a prognostic classifier for endometrial carcinoma. <i>International Journal of Biological Sciences</i> , <b>2021</b> , 17, 448-459	11.2	6
27	A microRNA-Messenger RNA Regulatory Network and Its Prognostic Value in Cervical Cancer. <i>DNA and Cell Biology</i> , <b>2020</b> , 39, 1328-1346	3.6	5
26	Prognostic Risk Model and Tumor Immune Environment Modulation of m5C-Related LncRNAs in Pancreatic Ductal Adenocarcinoma.. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 800268	8.4	5
25	MiRNA based tumor mutation burden diagnostic and prognostic prediction models for endometrial cancer. <i>Bioengineered</i> , <b>2021</b> , 12, 3603-3620	5.7	5
24	Construction of a nine DNA repair-related gene prognostic classifier to predict prognosis in patients with endometrial carcinoma. <i>BMC Cancer</i> , <b>2021</b> , 21, 29	4.8	4
23	A Novel Prognostic Index Based on Alternative Splicing in Papillary Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1333	4.5	3

22	Pan-Cancer Analysis Revealed as a New Biomarker for Prognosis and Immunotherapy.. <i>Journal of Oncology</i> , <b>2022</b> , 2022, 3477148	4.5	3
21	Construction of an Immune Cell Infiltration Score to Evaluate the Prognosis and Therapeutic Efficacy of Ovarian Cancer Patients. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 751594	8.4	3
20	Comprehensive of N1-Methyladenosine Modifications Patterns and Immunological Characteristics in Ovarian Cancer. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 746647	8.4	3
19	A model based on tumor-infiltrating immune cells for predicting the relapse rates of patients with testicular germ cell tumors. <i>International Immunopharmacology</i> , <b>2020</b> , 86, 106710	5.8	3
18	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> , <b>2022</b> , 2022, 8028825	4.5	2
17	Development of an Oxidative Phosphorylation-Related and Immune Microenvironment Prognostic Signature in Uterine Corpus Endometrial Carcinoma.. <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 753004	5.7	2
16	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> , <b>2021</b> , 9, 735013	5.7	2
15	Prognostic and Immunological Role of mRNA ac4C Regulator NAT10 in Pan-Cancer: New Territory[For Cancer Research?. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 630417	5.3	2
14	Identification of methylation-driven genes prognosis signature and immune microenvironment in uterus corpus endometrial cancer. <i>Cancer Cell International</i> , <b>2021</b> , 21, 365	6.4	2
13	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> , <b>2021</b> , 12, 788431	8.4	2
12	Pyroptosis-related lncRNAs are potential biomarkers for predicting prognoses and immune responses in patients with UCEC.. <i>Molecular Therapy - Nucleic Acids</i> , <b>2022</b> , 27, 1036-1055	10.7	1
11	CSMD3 is Associated with Tumor Mutation Burden and Immune Infiltration in Ovarian Cancer Patients. <i>International Journal of General Medicine</i> , <b>2021</b> , 14, 7647-7657	2.3	1
10	Development of epithelial-mesenchymal transition-related lncRNA signature for predicting survival and immune microenvironment in pancreatic cancerwithexperiment validation. <i>Bioengineered</i> , <b>2021</b> , 12, 10553-10567	5.7	1
9	Construction of miRNA-mRNA Regulatory Network and Prognostic Signature in Endometrial Cancer. <i>OncoTargets and Therapy</i> , <b>2021</b> , 14, 2363-2378	4.4	1
8	Low Expression of RILPL2 Predicts Poor Prognosis and Correlates With Immune Infiltration in Endometrial Carcinoma. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 670893	5.6	1
7	SNX10 and PTGDS are associated with the progression and prognosis of cervical squamous cell carcinoma. <i>BMC Cancer</i> , <b>2021</b> , 21, 694	4.8	1
6	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> , <b>2021</b> , 9, 671736	5.7	1
5	A novel prognostic model based on immunogenomics for clear cell renal cell carcinoma. <i>International Immunopharmacology</i> , <b>2021</b> , 90, 107119	5.8	1

4	CXCL2-mediated ATR/CHK1 signaling pathway and platinum resistance in epithelial ovarian cancer. <i>Journal of Ovarian Research</i> , <b>2021</b> , 14, 115	5.5	1
3	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> , <b>2022</b> , 10, 753957	5.7	1
2	Establishing a Prognostic Signature Based on Epithelial-Mesenchymal Transition-Related Genes for Endometrial Cancer Patients.. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 805883	8.4	0
1	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> , <b>2021</b> , 13, 11771-11785	3	