

Jinhui Liu

List of Publications by Year in Descending Order

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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	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	10.7	1
56	Pan-Cancer Analysis Revealed as a New Biomarker for Prognosis and Immunotherapy.. <i>Journal of Oncology</i> , 2022 , 2022, 3477148	4.5	3
55	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, 8028825	4.5	2
54	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	5.7	1
53	Establishing a Prognostic Signature Based on Epithelial-Mesenchymal Transition-Related Genes for Endometrial Cancer Patients.. <i>Frontiers in Immunology</i> , 2021 , 12, 805883	8.4	0
52	Prognostic Risk Model and Tumor Immune Environment Modulation of m5C-Related lncRNAs in Pancreatic Ductal Adenocarcinoma.. <i>Frontiers in Immunology</i> , 2021 , 12, 800268	8.4	5
51	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	8.4	3
50	CSMD3 is Associated with Tumor Mutation Burden and Immune Infiltration in Ovarian Cancer Patients. <i>International Journal of General Medicine</i> , 2021 , 14, 7647-7657	2.3	1
49	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	5.7	2
48	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	5.7	1
47	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	5.7	2
46	Comprehensive of N1-Methyladenosine Modifications Patterns and Immunological Characteristics in Ovarian Cancer. <i>Frontiers in Immunology</i> , 2021 , 12, 746647	8.4	3
45	Construction of miRNA-mRNA Regulatory Network and Prognostic Signature in Endometrial Cancer. <i>OncoTargets and Therapy</i> , 2021 , 14, 2363-2378	4.4	1
44	Low Expression of RILPL2 Predicts Poor Prognosis and Correlates With Immune Infiltration in Endometrial Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 670893	5.6	1
43	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	5.3	2
42	SNX10 and PTGDS are associated with the progression and prognosis of cervical squamous cell carcinoma. <i>BMC Cancer</i> , 2021 , 21, 694	4.8	1
41	Identification of methylation-driven genes prognosis signature and immune microenvironment in uterus corpus endometrial cancer. <i>Cancer Cell International</i> , 2021 , 21, 365	6.4	2

40	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	5.7	1
39	A novel prognostic model based on immunogenomics for clear cell renal cell carcinoma. <i>International Immunopharmacology</i> , 2021 , 90, 107119	5.8	1
38	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	11.2	6
37	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	4.8	4
36	m6A RNA methylation regulators were associated with the malignancy and prognosis of ovarian cancer. <i>Bioengineered</i> , 2021 , 12, 3159-3176	5.7	7
35	CXCL2-mediated ATR/CHK1 signaling pathway and platinum resistance in epithelial ovarian cancer. <i>Journal of Ovarian Research</i> , 2021 , 14, 115	5.5	1
34	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	12.8	10
33	MiRNA based tumor mutation burden diagnostic and prognostic prediction models for endometrial cancer. <i>Bioengineered</i> , 2021 , 12, 3603-3620	5.7	5
32	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	3	
31	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	8.4	2
30	Nine glycolysis-related gene signature predicting the survival of patients with endometrial adenocarcinoma. <i>Cancer Cell International</i> , 2020 , 20, 183	6.4	15
29	Exploration of a novel prognostic risk signatures and immune checkpoint molecules in endometrial carcinoma microenvironment. <i>Genomics</i> , 2020 , 112, 3117-3134	4.3	18
28	A microRNA-Messenger RNA Regulatory Network and Its Prognostic Value in Cervical Cancer. <i>DNA and Cell Biology</i> , 2020 , 39, 1328-1346	3.6	5
27	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	3.6	10
26	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	4.8	14
25	Development of an immune gene prognostic classifier for survival prediction and respond to immuncheckpoint inhibitor therapy/chemotherapy in endometrial cancer. <i>International Immunopharmacology</i> , 2020 , 86, 106735	5.8	9
24	Identification of molecular markers associated with the progression and prognosis of endometrial cancer: a bioinformatic study. <i>Cancer Cell International</i> , 2020 , 20, 59	6.4	11
23	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	3.8	6

22	Identification of crucial aberrantly methylated and differentially expressed genes related to cervical cancer using an integrated bioinformatics analysis. <i>Bioscience Reports</i> , 2020 , 40,	4.1	6
21	Construction of an immune-related gene signature for prediction of prognosis in patients with cervical cancer. <i>International Immunopharmacology</i> , 2020 , 88, 106882	5.8	13
20	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	5.8	3
19	Prognostic value of an autophagy-related gene expression signature for endometrial cancer patients. <i>Cancer Cell International</i> , 2020 , 20, 306	6.4	8
18	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	3.7	10
17	Establishment of a novel cell cycle-related prognostic signature predicting prognosis in patients with endometrial cancer. <i>Cancer Cell International</i> , 2020 , 20, 329	6.4	6
16	Using mRNasi to identify prognostic-related genes in endometrial carcinoma based on WGCNA. <i>Life Sciences</i> , 2020 , 258, 118231	6.8	9
15	Methylation-driven genes and their prognostic value in cervical squamous cell carcinoma. <i>Annals of Translational Medicine</i> , 2020 , 8, 868	3.2	6
14	A prognostic signature based on immune-related genes for cervical squamous cell carcinoma and endocervical adenocarcinoma. <i>International Immunopharmacology</i> , 2020 , 88, 106884	5.8	13
13	Identification of a prognostic signature of epithelial ovarian cancer based on tumor immune microenvironment exploration. <i>Genomics</i> , 2020 , 112, 4827-4841	4.3	20
12	Identification of Potential Biomarkers for Thyroid Cancer Using Bioinformatics Strategy: A Study Based on GEO Datasets. <i>BioMed Research International</i> , 2020 , 2020, 9710421	3	15
11	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	4.5	22
10	Eleven genes associated with progression and prognosis of endometrial cancer (EC) identified by comprehensive bioinformatics analysis. <i>Cancer Cell International</i> , 2019 , 19, 136	6.4	30
9	Competing endogenous RNA network of endometrial carcinoma: A comprehensive analysis. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 15648-15660	4.7	6
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	7	25
7	identified by comprehensive bioinformatic analysis as a hub candidate biological target in human epithelial ovarian cancer. <i>Cancer Management and Research</i> , 2019 , 11, 2379-2392	3.6	7
6	A Novel Prognostic Index Based on Alternative Splicing in Papillary Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2019 , 10, 1333	4.5	3
5	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, 7376034	3	23

4	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	2.6	11
3	Tumor-suppressor role of miR-139-5p in endometrial cancer. <i>Cancer Cell International</i> , 2018 , 18, 51	6.4	49
2	MicroRNA-665 suppresses the growth and migration of ovarian cancer cells by targeting HOXA10. <i>Molecular Medicine Reports</i> , 2018 , 18, 2661-2668	2.9	29
1	Long noncoding RNA NBAT-1 suppresses tumorigenesis and predicts favorable prognosis in ovarian cancer. <i>OncoTargets and Therapy</i> , 2017 , 10, 1993-2002	4.4	26