

# Kexin Yan

## List of Publications by Citations

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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.

10  
papers

36  
citations

4  
h-index

5  
g-index

11  
ext. papers

88  
ext. citations

4.7  
avg, IF

2.43  
L-index

#	Paper	IF	Citations
10	Identification of core genes associated with prostate cancer progression and outcome via bioinformatics analysis in multiple databases. <i>PeerJ</i> , <b>2020</b> , 8, e8786	3.1	7
9	Identification of a Robust Five-Gene Risk Model in Prostate Cancer: A Robust Likelihood-Based Survival Analysis. <i>International Journal of Genomics</i> , <b>2020</b> , 2020, 1097602	2.5	5
8	Three-gene risk model in papillary renal cell carcinoma: a robust likelihood-based survival analysis. <i>Aging</i> , <b>2020</b> , 12, 21854-21873	5.6	5
7	Macrophage M2 Co-expression Factors Correlate With the Immune Microenvironment and Predict Outcome of Renal Clear Cell Carcinoma. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 615655	4.5	5
6	CD8+ T Cell Co-Expressed Genes Correlate With Clinical Phenotype and Microenvironments of Urothelial Cancer. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 553399	5.3	4
5	Coexpressed Genes That Promote the Infiltration of M2 Macrophages in Melanoma Can Evaluate the Prognosis and Immunotherapy Outcome. <i>Journal of Immunology Research</i> , <b>2021</b> , 2021, 6664791	4.5	4
4	Gene Instability-Related lncRNA Prognostic Model of Melanoma Patients via Machine Learning Strategy. <i>Journal of Oncology</i> , <b>2021</b> , 2021, 5582920	4.5	2
3	9-Gene Signature Correlated With CD8 T Cell Infiltration Activated by IFN- $\gamma$ Biomarker of Immune Checkpoint Therapy Response in Melanoma. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 622563	8.4	2
2	M2 Macrophage Co-Expression Factors Correlate With Immune Phenotype and Predict Prognosis of Bladder Cancer. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 609334	5.3	1
1	Genome instability-related long non-coding RNA in clear renal cell carcinoma determined using computational biology. <i>BMC Cancer</i> , <b>2021</b> , 21, 727	4.8	1