

# Kexin Yan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/141136/publications.pdf>

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#	ARTICLE	IF	CITATIONS
1	Macrophage M2 Co-expression Factors Correlate With the Immune Microenvironment and Predict Outcome of Renal Clear Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 615655.	1.1	31
2	CD8+ T Cell Co-Expressed Genes Correlate With Clinical Phenotype and Microenvironments of Urothelial Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 553399.	1.3	26
3	9-Gene Signature Correlated With CD8+ T Cell Infiltration Activated by IFN- $\gamma$ : A Biomarker of Immune Checkpoint Therapy Response in Melanoma. <i>Frontiers in Immunology</i> , 2021, 12, 622563.	2.2	26
4	Identification of core genes associated with prostate cancer progression and outcome via bioinformatics analysis in multiple databases. <i>PeerJ</i> , 2020, 8, e8786.	0.9	20
5	M2 Macrophage Co-Expression Factors Correlate With Immune Phenotype and Predict Prognosis of Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 609334.	1.3	19
6	Three-gene risk model in papillary renal cell carcinoma: a robust likelihood-based survival analysis. <i>Aging</i> , 2020, 12, 21854-21873.	1.4	19
7	Identification of a Robust Five-Gene Risk Model in Prostate Cancer: A Robust Likelihood-Based Survival Analysis. <i>International Journal of Genomics</i> , 2020, 2020, 1-23.	0.8	15
8	Coexpressed Genes That Promote the Infiltration of M2 Macrophages in Melanoma Can Evaluate the Prognosis and Immunotherapy Outcome. <i>Journal of Immunology Research</i> , 2021, 2021, 1-15.	0.9	15
9	Genome instability-related long non-coding RNA in clear renal cell carcinoma determined using computational biology. <i>BMC Cancer</i> , 2021, 21, 727.	1.1	12
10	Gene Instability-Related lncRNA Prognostic Model of Melanoma Patients via Machine Learning Strategy. <i>Journal of Oncology</i> , 2021, 2021, 1-22.	0.6	8