Jiaheng Xie

List of Publications by Year
in descending order

25 papers	349 citations	932766 10 h-index	940134 16 g-index
27 all docs	27 docs citations	27 times ranked	61 citing authors

#	Article	IF	Citations
1	ADM-assisted prepectoral breast reconstruction is not associated with high complication rate as before: a Meta-analysis. Journal of Plastic Surgery and Hand Surgery, 2023, 57, 7-15.	0.4	10
2	Construction and validation of the diagnostic model of keloid based on weighted gene co-expression network analysis (WGCNA) and differential expression analysis. Journal of Plastic Surgery and Hand Surgery, 2022, , 1-9.	0.4	6
3	A novel signature based on autophagy-related lncRNA for prognostic prediction and candidate drugs for lung adenocarcinoma. Translational Cancer Research, 2022, 11, 14-28.	0.4	14
4	A novel regulatory mechanism network mediated by lncRNA TUG1 that induces the impairment of spiral artery remodeling in preeclampsia. Molecular Therapy, 2022, 30, 1692-1705.	3.7	18
5	A Necroptosis-Related Prognostic Model of Uveal Melanoma Was Constructed by Single-Cell Sequencing Analysis and Weighted Co-Expression Network Analysis Based on Public Databases. Frontiers in Immunology, 2022, 13, 847624.	2.2	34
6	Pan-cancer analysis revealed the significance of the GTPBP family in cancer. Aging, 2022, 14, 2558-2573.	1.4	2
7	Transcriptome Analysis of Solute Carrier-Associated Genes in Hepatocellular Carcinoma: Friend or Foe?. Frontiers in Genetics, 2022, 13, 856393.	1.1	3
8	Integrative analysis of TRPV family to prognosis and immune infiltration in renal clear cell carcinoma. Channels, 2022, 16, 84-96.	1.5	5
9	An immune subtype-related prognostic signature of hepatocellular carcinoma based on single-cell sequencing analysis. Aging, 2022, 14, 3276-3292.	1.4	34
10	Single-Cell Sequencing Analysis Based on Public Databases for Constructing a Metastasis-Related Prognostic Model for Gastric Cancer. Applied Bionics and Biomechanics, 2022, 2022, 1-19.	0.5	5
11	Head and Neck Squamous Cell Carcinoma: NT5E Could Be a Prognostic Biomarker. Applied Bionics and Biomechanics, 2022, 2022, 1-14.	0.5	1
12	Solute carrier transporter superfamily member SLC16A1 is a potential prognostic biomarker and associated with immune infiltration in skin cutaneous melanoma. Channels, 2021, 15, 483-495.	1.5	19
13	Pan-cancer analysis and single-cell analysis revealed the role of ABCC5 transporter in hepatocellular carcinoma. Channels, 2021, 15, 541-554.	1.5	9
14	Database mining analysis revealed the role of the putative H^+/sugar transporter solute carrier family 45 in skin cutaneous melanoma. Channels, 2021, 15, 496-506.	1.5	18
15	A pan-cancer analysis revealed the role of the SLC16 family in cancer. Channels, 2021, 15, 528-540.	1.5	18
16	A Novel Pyroptosis-Related lncRNA Signature for Predicting the Prognosis of Skin Cutaneous Melanoma. International Journal of General Medicine, 2021, Volume 14, 6517-6527.	0.8	46
17	Identification of ABCC5 Among ATP-Binding Cassette Transporter Family as a New Biomarker for Hepatocellular Carcinoma Based on Bioinformatics Analysis. International Journal of General Medicine, 2021, Volume 14, 7235-7246.	0.8	34
18	Clinical Value for Diagnosis and Prognosis of Signal Sequence Receptor 1 (SSR1) and Its Potential Mechanism in Hepatocellular Carcinoma: A Comprehensive Study Based on High-Throughput Data Analysis. International Journal of General Medicine, 2021, Volume 14, 7435-7451.	0.8	3

#	Article	IF	Citations
19	ANXA1 (Annexin A1) regulated by MYC (MYC proto-oncogene) promotes the growth of papillary thyroid carcinoma. Bioengineered, 2021, 12, 9251-9265.	1.4	10
20	Prognostic Value of SLC16A3(MCT4) in Lung Adenocarcinoma and Its Clinical Significance. International Journal of General Medicine, 2021, Volume 14, 8413-8425.	0.8	14
21	Construction and Validation of a Novel Pyroptosis-Related Gene Signature to Predict the Prognosis of Uveal Melanoma. Frontiers in Cell and Developmental Biology, 2021, 9, 761350.	1.8	19
22	Transcriptomic Alterations Induced By Vemurafenib after Treatment of Melanoma: A Comprehensive Bioinformatics Analysis. , 2021, 83, .		0
23	Single-Cell Sequencing Analysis and Weighted Co-Expression Network Analysis Based on Public Databases Identified That TNC Is a Novel Biomarker for Keloid. Frontiers in Immunology, 2021, 12, 783907.	2.2	23
24	Integrated Analysis of Genomic and Transcriptomic Profiles Identified the Role of GTP Binding Protein-4 (GTPBP4) in Breast Cancer. Frontiers in Pharmacology, 0, 13, .	1.6	3
25	Response: Commentary: Single-Cell Sequencing Analysis and Weighted CoExpression Network Analysis Based on Public Databases Identified That TNC Is a Novel Biomarker for Keloid. Frontiers in Immunology, 0, 13, .	2.2	1