Lishuang Qi

List of Publications by Year
in descending order

33 papers	809 citations	840776 11 h-index	526287 27 g-index
37 all docs	37 docs citations	37 times ranked	1055 citing authors

#	ARTICLE	IF	CITATIONS
1	Individual-level analysis of differential expression of genes and pathways for personalized medicine. Bioinformatics, 2015, 31, 62-68.	4.1	185
2	Critical limitations of prognostic signatures based on risk scores summarized from gene expression levels: a case study for resected stage I non-small-cell lung cancer. Briefings in Bioinformatics, 2016, 17, 233-242.	6.5	126
3	Differential expression analysis at the individual level reveals a lncRNA prognostic signature for lung adenocarcinoma. Molecular Cancer, 2017, 16, 98.	19.2	101
4	Autophagy‐related prognostic signature for breast cancer. Molecular Carcinogenesis, 2016, 55, 292-299.	2.7	68
5	An individualised signature for predicting response with concordant survival benefit for lung adenocarcinoma patients receiving platinum-based chemotherapy. British Journal of Cancer, 2016, 115, 1513-1519.	6.4	34
6	The influence of cancer tissue sampling on the identification of cancer characteristics. Scientific Reports, 2015, 5, 15474.	3.3	33
7	An individualized gene expression signature for prediction of lung adenocarcinoma metastases. Molecular Oncology, 2017, 11, 1630-1645.	4.6	28
8	A rank-based transcriptional signature for predicting relapse risk of stage II colorectal cancer identified with proper data sources. Oncotarget, 2016, 7, 19060-19071.	1.8	27
9	A rank-based algorithm of differential expression analysis for small cell line data with statistical control. Briefings in Bioinformatics, 2019, 20, 482-491.	6.5	23
10	An absolute human stemness index associated with oncogenic dedifferentiation. Briefings in Bioinformatics, 2021, 22, 2151-2160.	6.5	22
11	Identifying metabolic reprogramming phenotypes with glycolysis-lipid metabolism discoordination and intercellular communication for lung adenocarcinoma metastasis. Communications Biology, 2022, 5, 198.	4.4	20
12	Identification of driver copy number alterations in diverse cancer types and application in drug repositioning. Molecular Oncology, 2017, 11, 1459-1474.	4.6	15
13	Genetic Interaction-Based Biomarkers Identification for Drug Resistance and Sensitivity in Cancer Cells. Molecular Therapy - Nucleic Acids, 2019, 17, 688-700.	5.1	15
14	Individualized analysis of differentially expressed miRNAs with application to the identification of miRNAs deregulated commonly in lung cancer tissues. Briefings in Bioinformatics, 2018, 19, 793-802.	6.5	11
15	Identifying primary site of lung-limited Cancer of unknown primary based on relative gene expression orderings. BMC Cancer, 2019, 19, 67.	2.6	10
16	A landscape of synthetic viable interactions in cancer. Briefings in Bioinformatics, 2018, 19, bbw142.	6.5	9
17	A qualitative transcriptional signature for the histological reclassification of lung squamous cell carcinomas and adenocarcinomas. BMC Genomics, 2019, 20, 881.	2.8	9
18	RNA-binding motif protein 10 represses tumor progression through the Wnt/β- catenin pathway in lung adenocarcinoma. International Journal of Biological Sciences, 2022, 18, 124-139.	6.4	9

#	Article	IF	Citations
19	Deconvolution of the Gene Expression Profiles of Valuable Banked Blood Specimens for Studying the Prognostic Values of Altered Peripheral Immune Cell Proportions in Cancer Patients. PLoS ONE, 2014, 9, e100934.	2.5	7
20	Reference genome and annotation updates lead to contradictory prognostic predictions in gene expression signatures: a case study of resected stage I lung adenocarcinoma. Briefings in Bioinformatics, 2021, 22, .	6.5	7
21	A qualitative transcriptional signature for determining the grade of colorectal adenocarcinoma. Cancer Gene Therapy, 2020, 27, 680-690.	4.6	6
22	Identification of Genes Universally Differentially Expressed in Gastric Cancer. BioMed Research International, 2021, 2021, 1-9.	1.9	6
23	Identifying CpG sites with different differential methylation frequencies in colorectal cancer tissues based on individualized differential methylation analysis. Oncotarget, 2017, 8, 47356-47364.	1.8	6
24	A qualitative transcriptional signature for predicting microsatellite instability status of right-sided Colon Cancer. BMC Genomics, 2019, 20, 769.	2.8	5
25	An Exon Signature to Estimate the Tumor Mutational Burden of Right-sided Colon Cancer Patients. Journal of Cancer, 2020, 11, 883-892.	2.5	5
26	An individualized transcriptional signature to predict the epithelial-mesenchymal transition based on relative expression ordering. Aging, 2020, 12, 13172-13186.	3.1	5
27	Identification of a small mutation panel of coding sequences to predict the efficacy of immunotherapy for lung adenocarcinoma. Journal of Translational Medicine, 2020, 18, 25.	4.4	4
28	Revealing biomarkers associated with PARP inhibitors based on genetic interactions in cancer genome. Computational and Structural Biotechnology Journal, 2021, 19, 4435-4446.	4.1	4
29	A Qualitative Transcriptional Signature for Predicting Recurrence Risk for High-Grade Serous Ovarian Cancer Patients Treated With Platinum-Taxane Adjuvant Chemotherapy. Frontiers in Oncology, 2019, 9, 1094.	2.8	3
30	A Qualitative Transcriptional Signature for Predicting Prognosis and Response to Bevacizumab in Metastatic Colorectal Cancer. Molecular Cancer Therapeutics, 2020, 19, 1497-1505.	4.1	3
31	Identifying 18F-FDG PET-metabolic radiomic signature for lung adenocarcinoma prognosis via the leveraging of prognostic transcriptomic module. Quantitative Imaging in Medicine and Surgery, 2022, 12, 1893-1908.	2.0	2
32	A qualitative transcriptional signature of recurrence risk for stages II–III gastric cancer patients after surgical resection. Journal of Gastroenterology and Hepatology (Australia), 2021, 36, 2501-2512.	2.8	1
33	A Qualitative Transcriptional Signature for Predicting CpG Island Methylator Phenotype Status of the Right-Sided Colon Cancer. Frontiers in Genetics, 2020, 11, 971.	2.3	0