Lishuang Qi

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3828128/publications.pdf

Version: 2024-02-01

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

#	Article	IF	CITATIONS
1	RNA-binding motif protein 10 represses tumor progression through the Wnt \hat{l}^2 - catenin pathway in lung adenocarcinoma. International Journal of Biological Sciences, 2022, 18, 124-139.	6.4	9
2	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
3	Identifying metabolic reprogramming phenotypes with glycolysis-lipid metabolism discoordination and intercellular communication for lung adenocarcinoma metastasis. Communications Biology, 2022, 5, 198.	4.4	20
4	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
5	An absolute human stemness index associated with oncogenic dedifferentiation. Briefings in Bioinformatics, 2021, 22, 2151-2160.	6.5	22
6	Identification of Genes Universally Differentially Expressed in Gastric Cancer. BioMed Research International, 2021, 2021, 1-9.	1.9	6
7	A qualitative transcriptional signature of recurrence risk for stages Il–III gastric cancer patients after surgical resection. Journal of Gastroenterology and Hepatology (Australia), 2021, 36, 2501-2512.	2.8	1
8	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
9	A qualitative transcriptional signature for determining the grade of colorectal adenocarcinoma. Cancer Gene Therapy, 2020, 27, 680-690.	4.6	6
10	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
11	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
12	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
13	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
14	An individualized transcriptional signature to predict the epithelial-mesenchymal transition based on relative expression ordering. Aging, 2020, 12, 13172-13186.	3.1	5
15	Genetic Interaction-Based Biomarkers Identification for Drug Resistance and Sensitivity in Cancer Cells. Molecular Therapy - Nucleic Acids, 2019, 17, 688-700.	5.1	15
16	Identifying primary site of lung-limited Cancer of unknown primary based on relative gene expression orderings. BMC Cancer, 2019, 19, 67.	2.6	10
17	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
18	A qualitative transcriptional signature for predicting microsatellite instability status of right-sided Colon Cancer. BMC Genomics, 2019, 20, 769.	2.8	5

#	Article	IF	CITATIONS
19	A qualitative transcriptional signature for the histological reclassification of lung squamous cell carcinomas and adenocarcinomas. BMC Genomics, 2019, 20, 881.	2.8	9
20	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
21	A landscape of synthetic viable interactions in cancer. Briefings in Bioinformatics, 2018, 19, bbw142.	6.5	9
22	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
23	Differential expression analysis at the individual level reveals a lncRNA prognostic signature for lung adenocarcinoma. Molecular Cancer, 2017, 16, 98.	19.2	101
24	An individualized gene expression signature for prediction of lung adenocarcinoma metastases. Molecular Oncology, 2017, 11, 1630-1645.	4.6	28
25	Identification of driver copy number alterations in diverse cancer types and application in drug repositioning. Molecular Oncology, 2017, 11, 1459-1474.	4.6	15
26	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
27	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
28	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
29	Autophagyâ€related prognostic signature for breast cancer. Molecular Carcinogenesis, 2016, 55, 292-299.	2.7	68
30	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
31	The influence of cancer tissue sampling on the identification of cancer characteristics. Scientific Reports, 2015, 5, 15474.	3.3	33
32	Individual-level analysis of differential expression of genes and pathways for personalized medicine. Bioinformatics, 2015, 31, 62-68.	4.1	185
33	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