

# Qingzhou Guan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1312894/publications.pdf>

Version: 2024-02-01

41  
papers

765  
citations

567281

15  
h-index

552781

26  
g-index

45  
all docs

45  
docs citations

45  
times ranked

674  
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust transcriptional tumor signatures applicable to both formalin-fixed paraffin-embedded and fresh-frozen samples. <i>Oncotarget</i> , 2017, 8, 6652-6662.	1.8	84
2	Differential expression analysis for individual cancer samples based on robust within-sample relative gene expression orderings across multiple profiling platforms. <i>Oncotarget</i> , 2016, 7, 68909-68920.	1.8	63
3	Robust transcriptional signatures for low-input RNA samples based on relative expression orderings. <i>BMC Genomics</i> , 2017, 18, 913.	2.8	45
4	Tamoxifen therapy benefit predictive signature coupled with prognostic signature of post-operative recurrent risk for early stage ER+ breast cancer. <i>Oncotarget</i> , 2015, 6, 44593-44608.	1.8	39
5	Identifying Reproducible Molecular Biomarkers for Gastric Cancer Metastasis with the Aid of Recurrence Information. <i>Scientific Reports</i> , 2016, 6, 24869.	3.3	38
6	Identifying differentially expressed genes from cross-site integrated data based on relative expression orderings. <i>International Journal of Biological Sciences</i> , 2018, 14, 892-900.	6.4	37
7	An individualized prognostic signature and multi-omics distinction for early stage hepatocellular carcinoma patients with surgical resection. <i>Oncotarget</i> , 2016, 7, 24097-24110.	1.8	37
8	Quantitative or qualitative transcriptional diagnostic signatures? A case study for colorectal cancer. <i>BMC Genomics</i> , 2018, 19, 99.	2.8	36
9	An individualized prognostic signature for gastric cancer patients treated with 5-Fluorouracil-based chemotherapy and distinct multi-omics characteristics of prognostic groups. <i>Oncotarget</i> , 2016, 7, 8743-8755.	1.8	36
10	A qualitative signature for early diagnosis of hepatocellular carcinoma based on relative expression orderings. <i>Liver International</i> , 2018, 38, 1812-1819.	3.9	33
11	Individualized analysis reveals CpG sites with methylation aberrations in almost all lung adenocarcinoma tissues. <i>Journal of Translational Medicine</i> , 2017, 15, 26.	4.4	28
12	Identifying clinically relevant drug resistance genes in drug-induced resistant cancer cell lines and post- chemotherapy tissues. <i>Oncotarget</i> , 2015, 6, 41216-41227.	1.8	24
13	A rank-based algorithm of differential expression analysis for small cell line data with statistical control. <i>Briefings in Bioinformatics</i> , 2019, 20, 482-491.	6.5	23
14	Evaluating hepatocellular carcinoma cell lines for tumour samples using within-sample relative expression orderings of genes. <i>Liver International</i> , 2017, 37, 1688-1696.	3.9	21
15	A qualitative transcriptional signature for the early diagnosis of colorectal cancer. <i>Cancer Science</i> , 2019, 110, 3225-3234.	3.9	21
16	A qualitative signature for predicting pathological response to neoadjuvant chemoradiation in locally advanced rectal cancers. <i>Radiotherapy and Oncology</i> , 2018, 129, 149-153.	0.6	20
17	Multi-omics landscapes of colorectal cancer subtypes discriminated by an individualized prognostic signature for 5-fluorouracil-based chemotherapy. <i>Oncogenesis</i> , 2016, 5, e242-e242.	4.9	17
18	Identification of genes with universally upregulated or downregulated expressions in colorectal cancer. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019, 34, 880-889.	2.8	16

#	ARTICLE	IF	CITATIONS
19	A robust qualitative transcriptional signature for the correct pathological diagnosis of gastric cancer. <i>Journal of Translational Medicine</i> , 2019, 17, 63.	4.4	15
20	Statistically controlled identification of differentially expressed genes in one-to-one cell line comparisons of the CMAP database for drug repositioning. <i>Journal of Translational Medicine</i> , 2017, 15, 198.	4.4	14
21	Identification of reproducible drug-resistance-related dysregulated genes in small-scale cancer cell line experiments. <i>Scientific Reports</i> , 2015, 5, 11895.	3.3	11
22	Individualized analysis of differentially expressed miRNAs with application to the identification of miRNAs deregulated commonly in lung cancer tissues. <i>Briefings in Bioinformatics</i> , 2018, 19, 793-802.	6.5	11
23	Biased Influences of Low Tumor Purity on Mutation Detection in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 533196.	3.5	9
24	The Anti-Inflammatory Effect of a Combination of Five Compounds From Five Chinese Herbal Medicines Used in the Treatment of COPD. <i>Frontiers in Pharmacology</i> , 2021, 12, 709702.	3.5	8
25	Identification of Potential Key Genes in the Pathogenesis of Chronic Obstructive Pulmonary Disease Through Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 754569.	2.3	8
26	Identification of population-level differentially expressed genes in one-phenotype data. <i>Bioinformatics</i> , 2020, 36, 4283-4290.	4.1	7
27	Identifying disease-associated pathways in one-phenotype data based on reversal gene expression orderings. <i>Scientific Reports</i> , 2017, 7, 1348.	3.3	6
28	Identification of Common and Subtype-Specific Mutated Sub-Pathways for a Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 1228.	2.3	6
29	Identification of Genes Universally Differentially Expressed in Gastric Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-9.	1.9	6
30	Qualitative transcriptional signature for predicting pathological response of colorectal cancer to FOLFOX therapy. <i>Cancer Science</i> , 2020, 111, 253-265.	3.9	6
31	Identifying CpG sites with different differential methylation frequencies in colorectal cancer tissues based on individualized differential methylation analysis. <i>Oncotarget</i> , 2017, 8, 47356-47364.	1.8	6
32	Discriminating cancer-related and cancer-unrelated chemoradiation-response genes for locally advanced rectal cancers. <i>Scientific Reports</i> , 2016, 6, 36935.	3.3	5
33	A Qualitative Transcriptional Signature for Predicting Extreme Resistance of ER-Negative Breast Cancer to Paclitaxel, Doxorubicin, and Cyclophosphamide Neoadjuvant Chemotherapy. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 34.	3.5	5
34	A Qualitative Transcriptional Signature for the Risk Assessment of Precancerous Colorectal Lesions. <i>Frontiers in Genetics</i> , 2020, 11, 573787.	2.3	5
35	A Qualitative Transcriptional Signature for Predicting Recurrence Risk of Stage Iâ€“III Bladder Cancer Patients After Surgical Resection. <i>Frontiers in Oncology</i> , 2019, 9, 629.	2.8	4
36	Identification and characterization of genes with absolute mRNA abundances changes in tumor cells with varied transcriptome sizes. <i>BMC Genomics</i> , 2019, 20, 134.	2.8	4

#	ARTICLE	IF	CITATIONS
37	Identification of Tamoxifen-Resistant Breast Cancer Cell Lines and Drug Response Signature. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 564005.	3.5	4
38	Qualitative diagnostic signature for pancreatic ductal adenocarcinoma based on the within-sample relative expression orderings. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021, 36, 1714-1720.	2.8	4
39	TGF- $\beta$ -induced CCR8 promoted macrophage transdifferentiation into myofibroblast-like cells. <i>Experimental Lung Research</i> , 2022, , 1-14.	1.2	2
40	The Effects of Age, Cigarette Smoking, Sex, and Race on the Qualitative Characteristics of Lung Transcriptome. <i>BioMed Research International</i> , 2020, 2020, 1-7.	1.9	1
41	Population Change of Myeloid and Lymphoid Cells Contributes to the Blood-Based Protein Biomarkers. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0