Zheng Guo

List of Publications by Year
in descending order

135 papers	3,889 citations	159585 30 h-index	149698 56 g-index
148 all docs	148 docs citations	148 times ranked	4461 citing authors

#	Article	IF	Citations
1	Identification of the origin of brain metastases based on the relative methylation orderings of CpG sites. Epigenetics, 2021, 16, 908-916.	2.7	7
2	Prostate cancer early diagnosis: circulating microRNA pairs potentially beyond single microRNAs upon 1231 serum samples. Briefings in Bioinformatics, 2021, 22, .	6.5	23
3	A qualitative classification signature for post-surgery 5-fluorouracil-based adjuvant chemoradiotherapy in gastric cancer. Radiotherapy and Oncology, 2021, 155, 65-72.	0.6	3
4	Identification of Genes Universally Differentially Expressed in Gastric Cancer. BioMed Research International, 2021, 2021, 1-9.	1.9	6
5	Two novel qualitative transcriptional signatures robustly applicable to non‐research‐oriented colorectal cancer samples with low‐quality RNA. Journal of Cellular and Molecular Medicine, 2021, 25, 3622-3633.	3.6	5
6	A qualitative transcriptional signature for determining the grade of colorectal adenocarcinoma. Cancer Gene Therapy, 2020, 27, 680-690.	4.6	6
7	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
8	Transcriptomic analysis on the effects of melatonin in gastrointestinal carcinomas. BMC Gastroenterology, 2020, 20, 233.	2.0	7
9	A Five-Gene-Pair-Based Prognostic Signature for Predicting the Relapse Risk of Early Stage ER+ Breast Cancer. Frontiers in Genetics, 2020, 11, 566928.	2.3	2
10	The Effects of Age, Cigarette Smoking, Sex, and Race on the Qualitative Characteristics of Lung Transcriptome. BioMed Research International, 2020, 2020, 1-7.	1.9	1
11	Biased Influences of Low Tumor Purity on Mutation Detection in Cancer. Frontiers in Molecular Biosciences, 2020, 7, 533196.	3.5	9
12	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
13	Identification of population-level differentially expressed genes in one-phenotype data. Bioinformatics, 2020, 36, 4283-4290.	4.1	7
14	Qualitative Ras pathway signature for cetuximab therapy reveals resistant mechanism in colorectal cancer. FEBS Journal, 2020, 287, 5236-5248.	4.7	6
15	A qualitative transcriptional prognostic signature for patients with stage I-II pancreatic ductal adenocarcinoma. Translational Research, 2020, 219, 30-44.	5.0	4
16	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
17	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
18	A Qualitative Transcriptional Signature for Predicting Extreme Resistance of ER-Negative Breast Cancer to Paclitaxel, Doxorubicin, and Cyclophosphamide Neoadjuvant Chemotherapy. Frontiers in Molecular Biosciences, 2020, 7, 34.	3.5	5

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19	A Qualitative Transcriptional Signature for the Risk Assessment of Precancerous Colorectal Lesions. Frontiers in Genetics, 2020, 11, 573787.	2.3	5
20	Qualitative transcriptional signature for predicting pathological response of colorectal cancer to FOLFOX therapy. Cancer Science, 2020, 111, 253-265.	3.9	6
21	A qualitative transcriptional signature for predicting the biochemical recurrence risk of prostate cancer patients after radical prostatectomy. Prostate, 2020, 80, 376-387.	2.3	4
22	Transcriptional signatures for coupled predictions of stage II and III colorectal cancer metastasis and fluorouracilâ€based adjuvant chemotherapy benefit. FASEB Journal, 2019, 33, 151-162.	0.5	29
23	Genetic Interaction-Based Biomarkers Identification for Drug Resistance and Sensitivity in Cancer Cells. Molecular Therapy - Nucleic Acids, 2019, 17, 688-700.	5.1	15
24	A Qualitative Transcriptional Signature for Predicting Recurrence Risk of Stage Iâ€"III Bladder Cancer Patients After Surgical Resection. Frontiers in Oncology, 2019, 9, 629.	2.8	4
25	Identifying primary site of lung-limited Cancer of unknown primary based on relative gene expression orderings. BMC Cancer, 2019, 19, 67.	2.6	10
26	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
27	A qualitative transcriptional signature for the early diagnosis of colorectal cancer. Cancer Science, 2019, 110, 3225-3234.	3.9	21
28	A qualitative transcriptional signature for predicting microsatellite instability status of right-sided Colon Cancer. BMC Genomics, 2019, 20, 769.	2.8	5
29	A robust qualitative transcriptional signature for the correct pathological diagnosis of gastric cancer. Journal of Translational Medicine, 2019, 17, 63.	4.4	15
30	Qualitative transcriptional signatures for evaluating the maturity degree of pluripotent stem cell-derived cardiomyocytes. Stem Cell Research and Therapy, 2019, 10, 113.	5.5	17
31	Identification and characterization of genes with absolute mRNA abundances changes in tumor cells with varied transcriptome sizes. BMC Genomics, 2019, 20, 134.	2.8	4
32	Identification of Common and Subtype-Specific Mutated Sub-Pathways for a Cancer. Frontiers in Genetics, 2019, 10, 1228.	2.3	6
33	A qualitative transcriptional signature for the histological reclassification of lung squamous cell carcinomas and adenocarcinomas. BMC Genomics, 2019, 20, 881.	2.8	9
34	Identification of genes with universally upregulated or downregulated expressions in colorectal cancer. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 880-889.	2.8	16
35	Systematic review regulatory principles of non-coding RNAs in cardiovascular diseases. Briefings in Bioinformatics, 2019, 20, 66-76.	6.5	18
36	Link synthetic lethality to drug sensitivity of cancer cells. Briefings in Bioinformatics, 2019, 20, 1295-1307.	6.5	13

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37	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
38	A landscape of synthetic viable interactions in cancer. Briefings in Bioinformatics, 2018, 19, bbw142.	6.5	9
39	A qualitative signature for early diagnosis of hepatocellular carcinoma based on relative expression orderings. Liver International, 2018, 38, 1812-1819.	3.9	33
40	A qualitative signature for predicting pathological response to neoadjuvant chemoradiation in locally advanced rectal cancers. Radiotherapy and Oncology, 2018, 129, 149-153.	0.6	20
41	A qualitative transcriptional signature to reclassify estrogen receptor status of breast cancer patients. Breast Cancer Research and Treatment, 2018, 170, 271-277.	2.5	8
42	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
43	A simple way to detect disease-associated cellular molecular alterations from mixed-cell blood samples. Briefings in Bioinformatics, 2018, 19, 613-621.	6.5	6
44	Quantitative or qualitative transcriptional diagnostic signatures? A case study for colorectal cancer. BMC Genomics, 2018, 19, 99.	2.8	36
45	Shared liver-like transcriptional characteristics in liver metastases and corresponding primary colorectal tumors. Journal of Cancer, 2018, 9, 1500-1505.	2.5	7
46	Identifying differentially expressed genes from cross-site integrated data based on relative expression orderings. International Journal of Biological Sciences, 2018, 14, 892-900.	6.4	37
47	Individualized analysis reveals CpG sites with methylation aberrations in almost all lung adenocarcinoma tissues. Journal of Translational Medicine, 2017, 15, 26.	4.4	28
48	Evaluating hepatocellular carcinoma cell lines for tumour samples using within-sample relative expression orderings of genes. Liver International, 2017, 37, 1688-1696.	3.9	21
49	Identifying disease-associated pathways in one-phenotype data based on reversal gene expression orderings. Scientific Reports, 2017, 7, 1348.	3.3	6
50	EMT-Regulome: a database for EMT-related regulatory interactions, motifs and network. Cell Death and Disease, 2017, 8, e2872-e2872.	6.3	21
51	Differential expression analysis at the individual level reveals a lncRNA prognostic signature for lung adenocarcinoma. Molecular Cancer, 2017, 16, 98.	19.2	101
52	Conserved intergenic sequences revealed by CTAG-profiling in Salmonella: thermodynamic modeling for function prediction. Scientific Reports, 2017, 7, 43565.	3.3	7
53	Identification of molecular alterations in leukocytes from gene expression profiles of peripheral whole blood of Alzheimer's disease. Scientific Reports, 2017, 7, 14027.	3.3	17
54	Differential degeneration of the ACTAGT sequence among Salmonella: a reflection of distinct nucleotide amelioration patterns during bacterial divergence. Scientific Reports, 2017, 7, 10985.	3.3	3

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55	Adropin deficiency worsens HFD-induced metabolic defects. Cell Death and Disease, 2017, 8, e3008-e3008.	6.3	42
56	An individualized gene expression signature for prediction of lung adenocarcinoma metastases. Molecular Oncology, 2017, 11, 1630-1645.	4.6	28
57	Identification of driver copy number alterations in diverse cancer types and application in drug repositioning. Molecular Oncology, 2017, 11, 1459-1474.	4.6	15
58	Robust transcriptional signatures for low-input RNA samples based on relative expression orderings. BMC Genomics, 2017, 18, 913.	2.8	45
59	Statistically controlled identification of differentially expressed genes in one-to-one cell line comparisons of the CMAP database for drug repositioning. Journal of Translational Medicine, 2017, 15, 198.	4.4	14
60	Circumvent the uncertainty in the applications of transcriptional signatures to tumor tissues sampled from different tumor sites. Oncotarget, 2017, 8, 30265-30275.	1.8	72
61	Robust transcriptional tumor signatures applicable to both formalin-fixed paraffin-embedded and fresh-frozen samples. Oncotarget, 2017, 8, 6652-6662.	1.8	84
62	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
63	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
64	Identification of ubiquinol cytochrome *c* reductase hinge (UQCRH) as a potential diagnostic biomarker for lung adenocarcinoma. Open Biology, 2016, 6, 150256.	3.6	21
65	Discriminating cancer-related and cancer-unrelated chemoradiation-response genes for locally advanced rectal cancers. Scientific Reports, 2016, 6, 36935.	3.3	5
66	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
67	Identifying Reproducible Molecular Biomarkers for Gastric Cancer Metastasis with the Aid of Recurrence Information. Scientific Reports, 2016, 6, 24869.	3.3	38
68	Identifying reproducible cancer-associated highly expressed genes with important functional significances using multiple datasets. Scientific Reports, 2016, 6, 36227.	3.3	2
69	Autophagyâ€related prognostic signature for breast cancer. Molecular Carcinogenesis, 2016, 55, 292-299.	2.7	68
70	Individualized identification of disease-associated pathways with disrupted coordination of gene expression. Briefings in Bioinformatics, 2016, 17, 78-87.	6.5	24
71	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
72	Differential expression analysis for individual cancer samples based on robust within-sample relative gene expression orderings across multiple profiling platforms. Oncotarget, 2016, 7, 68909-68920.	1.8	63

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73	An individualized prognostic signature for gastric cancer patients treated with 5-Fluorouracil-based chemotherapy and distinct multi-omics characteristics of prognostic groups. Oncotarget, 2016, 7, 8743-8755.	1.8	36
74	Common DNA methylation alterations of Alzheimer's disease and aging in peripheral whole blood. Oncotarget, 2016, 7, 19089-19098.	1.8	25
75	An individualized prognostic signature and multi-omics distinction for early stage hepatocellular carcinoma patients with surgical resection. Oncotarget, 2016, 7, 24097-24110.	1.8	37
76	The influence of cancer tissue sampling on the identification of cancer characteristics. Scientific Reports, 2015, 5, 15474.	3.3	33
77	The BRCA1/2-directed miRNA signature predicts a good prognosis in ovarian cancer patients with wild-type BRCA1/2. Oncotarget, 2015, 6, 2397-2406.	1.8	36
78	Identification of reproducible drug-resistance-related dysregulated genes in small-scale cancer cell line experiments. Scientific Reports, 2015, 5, 11895.	3.3	11
79	Identification of lncRNA-associated competing triplets reveals global patterns and prognostic markers for cancer. Nucleic Acids Research, 2015, 43, 3478-3489.	14.5	219
80	Application of the rank-based method to DNA methylation for cancer diagnosis. Gene, 2015, 555, 203-207.	2.2	10
81	Individual-level analysis of differential expression of genes and pathways for personalized medicine. Bioinformatics, 2015, 31, 62-68.	4.1	185
82	Identifying clinically relevant drug resistance genes in drug-induced resistant cancer cell lines and post- chemotherapy tissues. Oncotarget, 2015, 6, 41216-41227.	1.8	24
83	Tamoxifen therapy benefit predictive signature coupled with prognostic signature of post-operative recurrent risk for early stage ER+ breast cancer. Oncotarget, 2015, 6, 44593-44608.	1.8	39
84	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
85	Effects and Mechanism of Bufei Yishen Formula in a Rat Chronic Obstructive Pulmonary Disease Model. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-10.	1.2	9
86	Separate enrichment analysis of pathways for up- and downregulated genes. Journal of the Royal Society Interface, 2014, 11, 20130950.	3.4	159
87	Reversal DNA methylation patterns for cancer diagnosis. , 2014, , .		2
88	Deciphering global signal features of high-throughput array data from cancers. Molecular BioSystems, 2014, 10, 1549-1556.	2.9	7
89	Similar Source of Differential Blood mRNAs in Lung Cancer and Pulmonary Inflammatory Diseases: Calls for Improved Strategy for Identifying Cancer-Specific Biomarkers. PLoS ONE, 2014, 9, e108104.	2.5	2
90	Walking the interactome to identify human miRNA-disease associations through the functional link between miRNA targets and disease genes. BMC Systems Biology, 2013, 7, 101.	3.0	227

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91	Rank-based predictors for response and prognosis of neoadjuvant taxane-anthracycline-based chemotherapy in breast cancer. Breast Cancer Research and Treatment, 2013, 139, 361-369.	2.5	16
92	A relative ordering-based predictor for tamoxifen-treated estrogen receptor-positive breast cancer patients: multi-laboratory cohort validation. Breast Cancer Research and Treatment, 2013, 142, 505-514.	2.5	17
93	Network analysis of genomic alteration profiles reveals co-altered functional modules and driver genes for glioblastoma. Molecular BioSystems, 2013, 9, 467.	2.9	18
94	Extracting a few functionally reproducible biomarkers to build robust subnetwork-based classifiers for the diagnosis of cancer. Gene, 2013, 526, 232-238.	2.2	17
95	An Integrated Approach to Uncover Driver Genes in Breast Cancer Methylation Genomes. PLoS ONE, 2013, 8, e61214.	2.5	11
96	Genes Dysregulated to Different Extent or Oppositely in Estrogen Receptor-Positive and Estrogen Receptor-Negative Breast Cancers. PLoS ONE, 2013, 8, e70017.	2.5	10
97	Functional Comparison between Genes Dysregulated in Ulcerative Colitis and Colorectal Carcinoma. PLoS ONE, 2013, 8, e71989.	2.5	6
98	Evaluating FDR and stratified FDR control approaches for high-throughput biological studies. , 2012, , .		1
99	GO-function: deriving biologically relevant functions from statistically significant functions. Briefings in Bioinformatics, 2012, 13, 216-227.	6.5	71
100	Extensive up-regulation of gene expression in cancer: the normalised use of microarray data. Molecular BioSystems, 2012, 8, 818.	2.9	27
101	Comparison of different normalization assumptions for analyses of DNA methylation data from the cancer genome. Gene, 2012, 506, 36-42.	2.2	14
102	Revealing weak differential gene expressions and their reproducible functions associated with breast cancer metastasis. Computational Biology and Chemistry, 2012, 39, 1-5.	2.3	8
103	Reproducibility and Concordance of Differential DNA Methylation and Gene Expression in Cancer. PLoS ONE, 2012, 7, e29686.	2.5	20
104	Distinct Functional Patterns of Gene Promoter Hypomethylation and Hypermethylation in Cancer Genomes. PLoS ONE, 2012, 7, e44822.	2.5	25
105	Finding co-mutated genes and candidate cancer genes in cancer genomes by stratified false discovery rate control. Molecular BioSystems, 2011, 7, 1158.	2.9	9
106	Reproducible Cancer Biomarker Discovery in SELDI-TOF MS Using Different Pre-Processing Algorithms. PLoS ONE, 2011, 6, e26294.	2.5	9
107	Functional modules with disease discrimination abilities for various cancers. Science China Life Sciences, 2011, 54, 189-193.	4.9	3
108	Analysis of pathway mutation profiles highlights collaboration between cancer-associated superpathways. Human Mutation, 2011, 32, 1028-1035.	2.5	15

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109	Extensive increase of microarray signals in cancers calls for novel normalization assumptions. Computational Biology and Chemistry, 2011, 35, 126-130.	2.3	25
110	Systematic analysis and prediction of longevity genes in Caenorhabditis elegans. Mechanisms of Ageing and Development, 2010, 131, 700-709.	4.6	25
111	Revealing and avoiding bias in semantic similarity scores for protein pairs. BMC Bioinformatics, 2010, 11, 290.	2.6	38
112	Extracting consistent knowledge from highly inconsistent cancer gene data sources. BMC Bioinformatics, 2010, 11, 76.	2.6	46
113	Multi-level reproducibility of signature hubs in human interactome for breast cancer metastasis. BMC Systems Biology, 2010, 4, 151.	3.0	30
114	Systematic Interpretation of Comutated Genes in Large-Scale Cancer Mutation Profiles. Molecular Cancer Therapeutics, 2010, 9, 2186-2195.	4.1	12
115	Viewing cancer genes from co-evolving gene modules. Bioinformatics, 2010, 26, 919-924.	4.1	3
116	Evaluating reproducibility of differential expression discoveries in microarray studies by considering correlated molecular changes. Bioinformatics, 2009, 25, 1662-1668.	4.1	100
117	Finding disease-specific coordinated functions by multi-function genes: Insight into the coordination mechanisms in diseases. Genomics, 2009, 94, 94-100.	2.9	17
118	Identifying cancer genes from cancer mutation profiles by cancer functions. Science in China Series C: Life Sciences, 2008, 51, 569-574.	1.3	1
119	Gaining confidence in biological interpretation of the microarray data: the functional consistence of the significant GO categories. Bioinformatics, 2008, 24, 265-271.	4.1	49
120	Apparently low reproducibility of true differential expression discoveries in microarray studies. Bioinformatics, 2008, 24, 2057-2063.	4.1	110
121	Edge-based scoring and searching method for identifying condition-responsive protein protein interaction sub-network. Bioinformatics, 2007, 23, 2121-2128.	4.1	139
122	Globally predicting protein functions based on co-expressed protein–protein interaction networks and ontology taxonomy similarities. Gene, 2007, 391, 113-119.	2.2	26
123	GO-2D: identifying 2-dimensional cellular-localized functional modules in Gene Ontology. BMC Genomics, 2007, 8, 30.	2.8	15
124	Widely predicting specific protein functions based on protein-protein interaction data and gene expression profile. Science in China Series C: Life Sciences, 2007, 50, 125-134.	1.3	10
125	Finding finer functions for partially characterized proteins by protein-protein interaction networks. Science Bulletin, 2007, 52, 3363-3370.	1.7	1
126	Peeling Off the Hidden Genetic Heterogeneities of Cancers Based on Disease-Relevant Functional Modules. Molecular Medicine, 2006, 12, 25-33.	4.4	11

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127	Identifying disease feature genes based on cellular localized gene functional modules and regulation networks. Science Bulletin, 2006, 51, 1848-1856.	1.7	3
128	Effects of replacing the unreliable cDNA microarray measurements on the disease classification based on gene expression profiles and functional modules. Bioinformatics, 2006, 22, 2883-2889.	4.1	36
129	Towards precise classification of cancers based on robust gene functional expression profiles. BMC Bioinformatics, 2005, 6, 58.	2.6	146
130	Broadly predicting specific gene functions with expression similarity and taxonomy similarity. Gene, 2005, 352, 75-81.	2.2	115
131	A robust hybrid between genetic algorithm and support vector machine for extracting an optimal feature gene subset. Genomics, 2005, 85, 16-23.	2.9	112
132	Learnability-based further prediction of gene functions in Gene Ontology. Genomics, 2004, 84, 922-928.	2.9	21
133	An ensemble method for gene discovery based on DNA mi-croarray data. Science in China Series C: Life Sciences, 2004, 47, 396.	1.3	6
134	Multivariate sib-pair linkage analysis of longitudinal phenotypes by three step-wise analysis approaches. BMC Genetics, 2003, 4, S68.	2.7	6
135	Locating the Genes Underlying a Simulated Complex Disease by Discriminant Analysis. Genetic Epidemiology, 2001, 21, S516-S521.	1.3	10