

TCGAbiolinks: an R/Bioconductor package for integrati

Nucleic Acids Research

44, e71-e71

DOI: [10.1093/nar/gkv1507](https://doi.org/10.1093/nar/gkv1507)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Integrating genetics and epigenetics in breast cancer: biological insights, experimental, computational methods and therapeutic potential. <i>BMC Systems Biology</i> , 2015, 9, 62.	3.0	40
2	The Mutational Landscape of the Oncogenic MZF1 SCAN Domain in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 78.	1.6	34
3	MicroRNAs as Biomarkers for Diagnosis, Prognosis and Theranostics in Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2016, 17, 421.	1.8	117
4	TCGA Expedition: A Data Acquisition and Management System for TCGA Data. <i>PLoS ONE</i> , 2016, 11, e0165395.	1.1	62
5	How interacting pathways are regulated by miRNAs in breast cancer subtypes. <i>BMC Bioinformatics</i> , 2016, 17, 348.	1.2	20
6	HOX genes: potential candidates for the progression of laryngeal squamous cell carcinoma. <i>Tumor Biology</i> , 2016, 37, 15087-15096.	0.8	24
7	scan_tcga tools for integrated epigenomic and transcriptomic analysis of tumor subgroups. <i>Epigenomics</i> , 2016, 8, 1315-1330.	1.0	13
8	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw051.	3.2	57
9	<i>MIR7</i> 3HG, a MYC-dependent modulator of cell proliferation, inhibits autophagy by a regulatory loop involving <i>AMBRA1</i> . <i>Autophagy</i> , 2017, 13, 554-566.	4.3	38
10	Identification of genetic determinants of breast cancer immune phenotypes by integrative genome-scale analysis. <i>Oncolmmunology</i> , 2017, 6, e1253654.	2.1	146
11	Chromosome 20q Amplification Defines a Subtype of Microsatellite Stable, Left-Sided Colon Cancers with Wild-type RAS/RAF and Better Overall Survival. <i>Molecular Cancer Research</i> , 2017, 15, 708-713.	1.5	24
12	Leptin induction following irradiation is a conserved feature in mammalian epithelial cells and tissues. <i>International Journal of Radiation Biology</i> , 2017, 93, 947-957.	1.0	4
13	DeepBlueR: large-scale epigenomic analysis in R. <i>Bioinformatics</i> , 2017, 33, 2063-2064.	1.8	8
14	Prediction of genome-wide DNA methylation in repetitive elements. <i>Nucleic Acids Research</i> , 2017, 45, 8697-8711.	6.5	106
15	Dynamic Organization of lncRNA and Circular RNA Regulators Collectively Controlled Cardiac Differentiation in Humans. <i>EBioMedicine</i> , 2017, 24, 137-146.	2.7	73
16	Loss of Myosin Vb in colorectal cancer is a strong prognostic factor for disease recurrence. <i>British Journal of Cancer</i> , 2017, 117, 1689-1701.	2.9	58
17	Cardamonin inhibits colonic neoplasia through modulation of MicroRNA expression. <i>Scientific Reports</i> , 2017, 7, 13945.	1.6	37
18	Human primary liver cancer-derived organoid cultures for disease modeling and drug screening. <i>Nature Medicine</i> , 2017, 23, 1424-1435.	15.2	905

#	ARTICLE	IF	CITATIONS
19	Developing Cancer Informatics Applications and Tools Using the NCI Genomic Data Commons API. <i>Cancer Research</i> , 2017, 77, e15-e18.	0.4	32
20	Identification of Long Noncoding RNAs Deregulated in Papillary Thyroid Cancer and Correlated with BRAFV600E Mutation by Bioinformatics Integrative Analysis. <i>Scientific Reports</i> , 2017, 7, 1662.	1.6	27
21	Transcriptome-wide analysis of natural antisense transcripts shows their potential role in breast cancer. <i>Scientific Reports</i> , 2017, 7, 17452.	1.6	39
22	Comparing the genomes of cutaneous melanoma tumors to commercially available cell lines. <i>Oncotarget</i> , 2017, 8, 114877-114893.	0.8	10
23	Redundancy analysis allows improved detection of methylation changes in large genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 553.	1.2	8
24	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 274.	1.8	50
25	Immune landscape of papillary thyroid cancer and immunotherapeutic implications. <i>Endocrine-Related Cancer</i> , 2018, 25, 523-531.	1.6	74
26	<i>gDCRNATools</i> : an R/Bioconductor package for integrative analysis of lncRNA, miRNA and mRNA data in GDC. <i>Bioinformatics</i> , 2018, 34, 2515-2517.	1.8	195
27	Profiling of 179 miRNA Expression in Blood Plasma of Lung Cancer Patients and Cancer-Free Individuals. <i>Scientific Reports</i> , 2018, 8, 6348.	1.6	35
28	A Catalogue of Putative <i>cis</i> -Regulatory Interactions Between Long Non-coding RNAs and Proximal Coding Genes Based on Correlative Analysis Across Diverse Human Tumors. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2019-2025.	0.8	3
29	Specific blockade of CD73 alters the exhausted phenotype of T cells in head and neck squamous cell carcinoma. <i>International Journal of Cancer</i> , 2018, 143, 1494-1504.	2.3	31
30	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. <i>Cell</i> , 2018, 173, 649-664.e20.	13.5	238
31	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
32	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
33	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
34	Differential expression and prognostic value of long non-coding RNA in HPV-negative head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2018, 40, 1555-1564.	0.9	28
35	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. <i>Cell Reports</i> , 2018, 23, 637-651.	2.9	137
36	Cooperative targeting of melanoma heterogeneity with an AXL antibody-drug conjugate and BRAF/MEK inhibitors. <i>Nature Medicine</i> , 2018, 24, 203-212.	15.2	178

#	ARTICLE	IF	CITATIONS
37	TCGA-assembler 2: software pipeline for retrieval and processing of TCGA/CPTAC data. <i>Bioinformatics</i> , 2018, 34, 1615-1617.	1.8	182
38	Immune Cell Production of Interleukin 17 Induces Stem Cell Features of Pancreatic Intraepithelial Neoplasia Cells. <i>Gastroenterology</i> , 2018, 155, 210-223.e3.	0.6	114
39	Personalised drug repositioning for Clear Cell Renal Cell Carcinoma using gene expression. <i>Scientific Reports</i> , 2018, 8, 5250.	1.6	14
40	Alpha-oxoglutarate inhibits the proliferation of immortalized normal bladder epithelial cells via an epigenetic switch involving ARID1A. <i>Scientific Reports</i> , 2018, 8, 4505.	1.6	13
41	PLK1 has tumor-suppressive potential in APC-truncated colon cancer cells. <i>Nature Communications</i> , 2018, 9, 1106.	5.8	47
42	Interleukin 8 mediates bcl-2-induced enhancement of human melanoma cell dissemination and angiogenesis in a zebrafish xenograft model. <i>International Journal of Cancer</i> , 2018, 142, 584-596.	2.3	51
43	Modeling phenotypes of malignant gliomas. <i>Cancer Science</i> , 2018, 109, 6-14.	1.7	15
44	Exploiting Radiation-Induced Signaling to Increase the Susceptibility of Resistant Cancer Cells to Targeted Drugs: AKT and mTOR Inhibitors as an Example. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 355-367.	1.9	27
45	Bayesian variable selection for parametric survival model with applications to cancer omics data. <i>Human Genomics</i> , 2018, 12, 49.	1.4	11
46	Integrative epigenetic taxonomy of primary prostate cancer. <i>Nature Communications</i> , 2018, 9, 4900.	5.8	107
47	Epigenetic profiling for the molecular classification of metastatic brain tumors. <i>Nature Communications</i> , 2018, 9, 4627.	5.8	79
48	microRNA 193a-5p Regulates Levels of Nucleolar- and Spindle-Associated Protein 1 to Suppress Hepatocarcinogenesis. <i>Gastroenterology</i> , 2018, 155, 1951-1966.e26.	0.6	86
49	Tissue-Specific Down-Regulation of the Long Non-Coding RNAs PCAT18 and LINC01133 in Gastric Cancer Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3881.	1.8	37
50	Metabolic control of PPAR activity by aldehyde dehydrogenase regulates invasive cell behavior and predicts survival in hepatocellular and renal clear cell carcinoma. <i>BMC Cancer</i> , 2018, 18, 1180.	1.1	22
51	MSIpred: a python package for tumor microsatellite instability classification from tumor mutation annotation data using a support vector machine. <i>Scientific Reports</i> , 2018, 8, 17546.	1.6	41
52	MUC16 mutations improve patients' prognosis by enhancing the infiltration and antitumor immunity of cytotoxic T lymphocytes in the endometrial cancer microenvironment. <i>Oncolmmunology</i> , 2018, 7, e1487914.	2.1	27
53	Warburg Effect Metabolism Drives Neoplasia in a Drosophila Genetic Model of Epithelial Cancer. <i>Current Biology</i> , 2018, 28, 3220-3228.e6.	1.8	33
54	DNA Methylation Predicts the Response of Triple-Negative Breast Cancers to All-Trans Retinoic Acid. <i>Cancers</i> , 2018, 10, 397.	1.7	22

#	ARTICLE	IF	CITATIONS
55	Transcriptomic and functional network features of lung squamous cell carcinoma through integrative analysis of GEO and TCGA data. <i>Scientific Reports</i> , 2018, 8, 15834.	1.6	91
56	mRNA circularization by METTL3â€eIF3h enhances translation and promotes oncogenesis. <i>Nature</i> , 2018, 561, 556-560.	13.7	498
57	BCNTB bioinformatics: the next evolutionary step in the bioinformatics of breast cancer tissue banking. <i>Nucleic Acids Research</i> , 2018, 46, D1055-D1061.	6.5	4
58	Cytolytic Activity Score to Assess Anticancer Immunity in Colorectal Cancer. <i>Annals of Surgical Oncology</i> , 2018, 25, 2323-2331.	0.7	107
59	A radiosensitivity gene signature and PD-L1 predict the clinical outcomes of patients with lower grade glioma in TCGA. <i>Radiotherapy and Oncology</i> , 2018, 128, 245-253.	0.3	38
60	A <sc>HIF</sc> â€“ <sc>LIMD</sc> 1 negative feedback mechanism mitigates the proâ€tumorogenic effects of hypoxia. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	17
61	Characterization of Alternative Splicing Events in HPV-Negative Head and Neck Squamous Cell Carcinoma Identifies an Oncogenic DOCK5 Variant. <i>Clinical Cancer Research</i> , 2018, 24, 5123-5132.	3.2	36
62	PDGF family function and prognostic value in tumor biology. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 984-990.	1.0	45
63	In silico identification of drug target pathways in breast cancer subtypes using pathway cross-talk inhibition. <i>Journal of Translational Medicine</i> , 2018, 16, 154.	1.8	24
64	Tree-based machine learning algorithms identified minimal set of miRNA biomarkers for breast cancer diagnosis and molecular subtyping. <i>Gene</i> , 2018, 677, 111-118.	1.0	36
65	Analysis of the Cancer Genome Atlas Data Reveals Novel Putative ncRNAs Targets in Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	16
66	Integration of multiple networks and pathways identifies cancer driver genes in pan-cancer analysis. <i>BMC Genomics</i> , 2018, 19, 25.	1.2	46
67	USP10 suppresses tumor progression by inhibiting mTOR activation in hepatocellular carcinoma. <i>Cancer Letters</i> , 2018, 436, 139-148.	3.2	49
68	In-Silico Integration Approach to Identify a Key miRNA Regulating a Gene Network in Aggressive Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 910.	1.8	11
69	Cancerin: A computational pipeline to infer cancer-associated ceRNA interaction networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006318.	1.5	39
70	Genetic and Epigenetic Features of Rapidly Progressing IDH-Mutant Astrocytomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2018, 77, 542-548.	0.9	34
71	Systematic identification of non-coding pharmacogenomic landscape in cancer. <i>Nature Communications</i> , 2018, 9, 3192.	5.8	73
72	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , 2018, 361, 594-599.	6.0	511

#	ARTICLE	IF	CITATIONS
73	Ultrahigh thermal conductivity confirmed in boron arsenide. <i>Science</i> , 2018, 361, 549-550.	6.0	42
74	Using Supervised Learning Methods for Gene Selection in RNA-Seq Case-Control Studies. <i>Frontiers in Genetics</i> , 2018, 9, 297.	1.1	36
75	TCIApathfinder: An R Client for the Cancer Imaging Archive REST API. <i>Cancer Research</i> , 2018, 78, 4424-4426.	0.4	10
76	Cell-of-Origin DNA Methylation Signatures Are Maintained during Colorectal Carcinogenesis. <i>Cell Reports</i> , 2018, 23, 3407-3418.	2.9	66
77	MiRNA-181d Expression Significantly Affects Treatment Responses to Carmustine Wafer Implantation. <i>Neurosurgery</i> , 2019, 85, 147-155.	0.6	10
78	DCARS: differential correlation across ranked samples. <i>Bioinformatics</i> , 2019, 35, 823-829.	1.8	7
79	Co-expression Network Analysis Identified Key Proteins in Association With Hepatic Metastatic Colorectal Cancer. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1900017.	0.8	16
80	A STAT3-based gene signature stratifies glioma patients for targeted therapy. <i>Nature Communications</i> , 2019, 10, 3601.	5.8	67
81	Data Normalisation using Differential Evolution and Aggregated Logistic Functions. , 2019, , .		2
82	A cross-cancer metastasis signature in the microRNA-mRNA axis of paired tissue samples. <i>Molecular Biology Reports</i> , 2019, 46, 5919-5930.	1.0	7
83	miRNA profile obtained by next-generation sequencing in metastatic breast cancer patients is able to predict the response to systemic treatments. <i>International Journal of Molecular Medicine</i> , 2019, 44, 1267-1280.	1.8	16
84	The impact of DNA methylation on the cancer proteome. <i>PLoS Computational Biology</i> , 2019, 15, e1007245.	1.5	9
85	Distinct signatures of lung cancer types: aberrant mucin O-glycosylation and compromised immune response. <i>BMC Cancer</i> , 2019, 19, 824.	1.1	34
86	Decision tree-based classifiers for lung cancer diagnosis and subtyping using TCGA miRNA expression data. <i>Oncology Letters</i> , 2019, 18, 2125-2131.	0.8	27
87	DUX4 Suppresses MHC Class I to Promote Cancer Immune Evasion and Resistance to Checkpoint Blockade. <i>Developmental Cell</i> , 2019, 50, 658-671.e7.	3.1	76
88	Comprehensive Gene Expression Analysis in NMIBC Using RNA-seq Reveals New Therapy Strategies. <i>Frontiers in Oncology</i> , 2019, 9, 523.	1.3	11
89	Augmenting Immunotherapy Impact by Lowering Tumor TNF Cytotoxicity Threshold. <i>Cell</i> , 2019, 178, 585-599.e15.	13.5	162
90	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	2.9	103

#	ARTICLE	IF	CITATIONS
91	Clinicopathological Features of Triple-Negative Breast Cancer Epigenetic Subtypes. <i>Annals of Surgical Oncology</i> , 2019, 26, 3344-3353.	0.7	15
92	Survival Analysis of Multi-Omics Data Identifies Potential Prognostic Markers of Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Genetics</i> , 2019, 10, 624.	1.1	64
93	Circulating miRNAs in Untreated Breast Cancer: An Exploratory Multimodality Morpho-Functional Study. <i>Cancers</i> , 2019, 11, 876.	1.7	36
94	Integrating proteomics and transcriptomics for the identification of potential targets in early colorectal cancer. <i>International Journal of Oncology</i> , 2019, 55, 439-450.	1.4	15
95	Integrated analysis identifying new lncRNA markers revealed in ceRNA network for tumor recurrence in papillary thyroid carcinoma and build of nomogram. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19673-19683.	1.2	23
96	Integrative Network Analysis Reveals a MicroRNA-Based Signature for Prognosis Prediction of Epithelial Ovarian Cancer. <i>BioMed Research International</i> , 2019, 2019, 1-8.	0.9	9
97	Gene relevance based on multiple evidences in complex networks. <i>Bioinformatics</i> , 2020, 36, 865-871.	1.8	6
98	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , 2019, 20, 745.	1.2	40
99	Multi-task learning based survival analysis for multi-source block-wise missing data. <i>Neurocomputing</i> , 2019, 364, 95-107.	3.5	10
100	Targeting of copper-trafficking chaperones causes gene-specific systemic pathology in <i>Drosophila melanogaster</i> : prospective expansion of mutational landscapes that regulate tumor resistance to cisplatin. <i>Biology Open</i> , 2019, 8, .	0.6	6
101	DriverDBv3: a multi-omics database for cancer driver gene research. <i>Nucleic Acids Research</i> , 2020, 48, D863-D870.	6.5	104
102	Assessing reliability of intra-tumor heterogeneity estimates from single sample whole exome sequencing data. <i>PLoS ONE</i> , 2019, 14, e0224143.	1.1	16
103	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
104	Comprehensive Genomic Review of TCGA Head and Neck Squamous Cell Carcinomas (HNSCC). <i>Journal of Clinical Medicine</i> , 2019, 8, 1896.	1.0	49
105	Heat-Shock Protein 90 Controls the Expression of Cell-Cycle Genes by Stabilizing Metazoan-Specific Host-Cell Factor HCFC1. <i>Cell Reports</i> , 2019, 29, 1645-1659.e9.	2.9	22
106	TIMP-1-Mediated Chemoresistance via Induction of IL-6 in NSCLC. <i>Cancers</i> , 2019, 11, 1184.	1.7	13
107	HTR1D, TIMP1, SERPINE1, MMP3 and CNR2 affect the survival of patients with colon adenocarcinoma. <i>Oncology Letters</i> , 2019, 18, 2448-2454.	0.8	20
108	Gastric Normal Adjacent Mucosa Versus Healthy and Cancer Tissues: Distinctive Transcriptomic Profiles and Biological Features. <i>Cancers</i> , 2019, 11, 1248.	1.7	34

#	ARTICLE	IF	CITATIONS
109	The transcribed pseudogene RPSAP52 enhances the oncofetal HMGA2-IGF2BP2-RAS axis through LIN28B-dependent and independent let-7 inhibition. <i>Nature Communications</i> , 2019, 10, 3979.	5.8	51
110	A large cohort study identifying a novel prognosis prediction model for lung adenocarcinoma through machine learning strategies. <i>BMC Cancer</i> , 2019, 19, 886.	1.1	54
111	Development and validation of a CIMP-associated prognostic model for hepatocellular carcinoma. <i>EBioMedicine</i> , 2019, 47, 128-141.	2.7	54
112	miRNA-26a expression influences the therapy response to carmustine wafer implantation in patients with glioblastoma multiforme. <i>Acta Neurochirurgica</i> , 2019, 161, 2299-2309.	0.9	7
113	IFN-gamma-induced PD-L1 expression in melanoma depends on p53 expression. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 397.	3.5	111
114	Differential effect of GLUT1 overexpression on survival and tumor immune microenvironment of human papilloma virus type 16-positive and -negative cervical cancer. <i>Scientific Reports</i> , 2019, 9, 13301.	1.6	18
115	Automatic discovery of 100-miRNA signature for cancer classification using ensemble feature selection. <i>BMC Bioinformatics</i> , 2019, 20, 480.	1.2	54
116	Expression of FGF8, FGF18, and FGFR4 in Gastroesophageal Adenocarcinomas. <i>Cells</i> , 2019, 8, 1092.	1.8	13
117	Identification of β -catenin target genes in colorectal cancer by interrogating gene fitness screening data. <i>Oncology Letters</i> , 2019, 18, 3769-3777.	0.8	5
118	Identification of key modules and prognostic markers in adrenocortical carcinoma by weighted gene co-expression network analysis. <i>Oncology Letters</i> , 2019, 18, 3673-3681.	0.8	11
119	GEF-H1 Signaling upon Microtubule Destabilization Is Required for Dendritic Cell Activation and Specific Anti-tumor Responses. <i>Cell Reports</i> , 2019, 28, 3367-3380.e8.	2.9	37
120	SFTA1P, LINC00968, GATA6-AS1, TBX5-AS1, and FEZF1-AS1 are crucial long non-coding RNAs associated with the prognosis of lung squamous cell carcinoma. <i>Oncology Letters</i> , 2019, 18, 3985-3993.	0.8	20
121	An increased cell cycle gene network determines MEK and Akt inhibitor double resistance in triple-negative breast cancer. <i>Scientific Reports</i> , 2019, 9, 13308.	1.6	15
122	Cancer-Specific Thresholds Adjust for Whole Exome Sequencing-Based Tumor Mutational Burden Distribution. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	1.5	21
123	Low mutation and neoantigen burden and fewer effector tumor infiltrating lymphocytes correlate with breast cancer metastasization to lymph nodes. <i>Scientific Reports</i> , 2019, 9, 253.	1.6	18
124	The molecular landscape of histone lysine methyltransferases and demethylases in non-small cell lung cancer. <i>International Journal of Medical Sciences</i> , 2019, 16, 922-930.	1.1	9
125	Development of a predictive model for stromal content in prostate cancer samples to improve signature performance. <i>Journal of Pathology</i> , 2019, 249, 411-424.	2.1	3
126	Locally advanced rectal cancer transcriptomic-based secretome analysis reveals novel biomarkers useful to identify patients according to neoadjuvant chemoradiotherapy response. <i>Scientific Reports</i> , 2019, 9, 8702.	1.6	14

#	ARTICLE	IF	CITATIONS
127	A Pre-operative Nomogram for Prediction of Lymph Node Metastasis in Bladder Urothelial Carcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 488.	1.3	11
128	Methylation and transcription patterns are distinct in IDH mutant gliomas compared to other IDH mutant cancers. <i>Scientific Reports</i> , 2019, 9, 8946.	1.6	44
129	MiRNA expression patterns are associated with tumor mutational burden in lung adenocarcinoma. <i>Oncolmmunology</i> , 2019, 8, e1629260.	2.1	24
130	ResMarkerDB: a database of biomarkers of response to antibody therapy in breast and colorectal cancer. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	10
131	Correlation between renin-angiotensin system (RAS) related genes, type 2 diabetes, and cancer: Insights from metanalysis of transcriptomics data. <i>Molecular and Cellular Endocrinology</i> , 2019, 493, 110455.	1.6	6
132	Serine/Arginine-Rich Splicing Factor 3 Modulates the Alternative Splicing of Cytoplasmic Polyadenylation Element Binding Protein 2. <i>Molecular Cancer Research</i> , 2019, 17, 1920-1930.	1.5	8
133	Total copy number variation as a prognostic factor in adult astrocytoma subtypes. <i>Acta Neuropathologica Communications</i> , 2019, 7, 92.	2.4	48
134	miRNAs and Long-term Breast Cancer Survival: Evidence from the WHEL Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1525-1533.	1.1	14
135	Identification of differentially expressed genes between triple and non-triple-negative breast cancer using bioinformatics analysis. <i>Breast Cancer</i> , 2019, 26, 784-791.	1.3	16
136	Identifying and targeting cancer-specific metabolism with network-based drug target prediction. <i>EBioMedicine</i> , 2019, 43, 98-106.	2.7	53
137	Metabolic reprogramming and Notch activity distinguish between non-small cell lung cancer subtypes. <i>British Journal of Cancer</i> , 2019, 121, 51-64.	2.9	33
138	Kremen1-induced cell death is regulated by homo- and heterodimerization. <i>Cell Death Discovery</i> , 2019, 5, 91.	2.0	16
139	Analysis of Genes Involved in Ulcerative Colitis Activity and Tumorigenesis Through Systematic Mining of Gene Co-expression Networks. <i>Frontiers in Physiology</i> , 2019, 10, 662.	1.3	29
140	Extracting predictors for lung adenocarcinoma based on Granger causality test and stepwise character selection. <i>BMC Bioinformatics</i> , 2019, 20, 197.	1.2	4
141	An essential role for GLUT5-mediated fructose utilization in exacerbating the malignancy of clear cell renal cell carcinoma. <i>Cell Biology and Toxicology</i> , 2019, 35, 471-483.	2.4	18
142	The combination of neoantigen quality and T lymphocyte infiltrates identifies glioblastomas with the longest survival. <i>Communications Biology</i> , 2019, 2, 135.	2.0	49
143	A novel CRISPR-engineered prostate cancer cell line defines the AR-V transcriptome and identifies PARP inhibitor sensitivities. <i>Nucleic Acids Research</i> , 2019, 47, 5634-5647.	6.5	41
144	Construction and Analysis of miRNA Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, 1970, 121-167.	0.4	0

#	ARTICLE	IF	CITATIONS
145	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
146	Genes CEP55, FOXD3, FOXF2, GNAO1, GRIA4, and KCNA5 as potential diagnostic biomarkers in colorectal cancer. <i>BMC Medical Genomics</i> , 2019, 12, 54.	0.7	39
147	Cancer stemness, intratumoral heterogeneity, and immune response across cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9020-9029.	3.3	372
148	Stabilization of E2-EPF UCP protein is implicated in hepatitis B virus-associated hepatocellular carcinoma progression. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 2647-2662.	2.4	6
149	Discovery of therapeutic agents for prostate cancer using genome-scale metabolic modeling and drug repositioning. <i>EBioMedicine</i> , 2019, 42, 386-396.	2.7	69
150	G protein $\hat{\pm}q$ exerts expression level-dependent distinct signaling paradigms. <i>Cellular Signalling</i> , 2019, 58, 34-43.	1.7	11
151	A Systematic Investigation of the Malignant Functions and Diagnostic Potential of the Cancer Secretome. <i>Cell Reports</i> , 2019, 26, 2622-2635.e5.	2.9	57
152	Effective breast cancer combination therapy targeting BACH1 and mitochondrial metabolism. <i>Nature</i> , 2019, 568, 254-258.	13.7	233
153	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. <i>PLoS Computational Biology</i> , 2019, 15, e1006701.	1.5	319
154	A gene signature associated with prognosis and immune processes in head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2019, 41, 2581-2590.	0.9	13
155	Tumor Microenvironment Characterization in Gastric Cancer Identifies Prognostic and Immunotherapeutically Relevant Gene Signatures. <i>Cancer Immunology Research</i> , 2019, 7, 737-750.	1.6	691
156	Drug Repositioning Strategies to Explore New Candidates Treating Prostate Cancer. , 2019, , 801-826.		2
157	isma: an R package for the integrative analysis of mutations detected by multiple pipelines. <i>BMC Bioinformatics</i> , 2019, 20, 107.	1.2	5
158	KRAS-IRF2 Axis Drives Immune Suppression and Immune Therapy Resistance in Colorectal Cancer. <i>Cancer Cell</i> , 2019, 35, 559-572.e7.	7.7	353
159	Separation of breast cancer and organ microenvironment transcriptomes in metastases. <i>Breast Cancer Research</i> , 2019, 21, 36.	2.2	36
160	HERC3-Mediated SMAD7 Ubiquitination Degradation Promotes Autophagy-Induced EMT and Chemoresistance in Glioblastoma. <i>Clinical Cancer Research</i> , 2019, 25, 3602-3616.	3.2	81
161	Clinical and research applications of a brain tumor tissue bank in the age of precision medicine. <i>Personalized Medicine</i> , 2019, 16, 145-156.	0.8	4
162	NOJAH: NOt Just Another Heatmap for genome-wide cluster analysis. <i>PLoS ONE</i> , 2019, 14, e0204542.	1.1	9

#	ARTICLE	IF	CITATIONS
163	Identification of Prognostic Alternative Splicing Signature in Breast Carcinoma. <i>Frontiers in Genetics</i> , 2019, 10, 278.	1.1	49
164	Glucocorticoid receptor expression is associated with inferior overall survival independent of BRCA mutation status in ovarian cancer. <i>International Journal of Gynecological Cancer</i> , 2019, 29, 357-364.	1.2	15
165	DNA Damage Signaling-Induced Cancer Cell Reprogramming as a Driver of Tumor Relapse. <i>Molecular Cell</i> , 2019, 74, 651-663.e8.	4.5	20
166	Long Noncoding RNA ASB16-AS1 Promotes Proliferation, Migration, and Invasion in Glioma Cells. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	31
167	The impact of estimated tumour purity on gene expression-based drug repositioning of Clear Cell Renal Cell Carcinoma samples. <i>Scientific Reports</i> , 2019, 9, 2495.	1.6	7
168	Radiogenomic Analysis of F-18-Fluorodeoxyglucose Positron Emission Tomography and Gene Expression Data Elucidates the Epidemiological Complexity of Colorectal Cancer Landscape. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 177-185.	1.9	51
169	Prediction of the Outcome for Patients with Glioblastoma with lncRNA Expression Profiles. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	5
170	Lightweight Convolutional Neural Network for Breast Cancer Classification Using RNA-Seq Gene Expression Data. <i>IEEE Access</i> , 2019, 7, 185338-185348.	2.6	42
171	MicroRNA-155 coordinates the immunological landscape within murine melanoma and correlates with immunity in human cancers. <i>JCI Insight</i> , 2019, 4, .	2.3	31
172	<p>Emerging Roles Of hsa-circ-0046600 Targeting The miR-640/HIF-1± Signalling Pathway In The Progression Of HCC</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 9291-9302.	1.0	33
173	Common polymorphic inversions at 17q21.31 and 8p23.1 associate with cancer prognosis. <i>Human Genomics</i> , 2019, 13, 57.	1.4	4
174	APOBEC3-Mediated RNA Editing in Breast Cancer is Associated with Heightened Immune Activity and Improved Survival. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5621.	1.8	46
175	DeePathology: Deep Multi-Task Learning for Inferring Molecular Pathology from Cancer Transcriptome. <i>Scientific Reports</i> , 2019, 9, 16526.	1.6	32
176	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. <i>Genome Biology</i> , 2019, 20, 236.	3.8	53
177	Identification of a Five-Gene Signature and Establishment of a Prognostic Nomogram to Predict Progression-Free Interval of Papillary Thyroid Carcinoma. <i>Frontiers in Endocrinology</i> , 2019, 10, 790.	1.5	28
178	Impact of HFE variants and sex in lung cancer. <i>PLoS ONE</i> , 2019, 14, e0226821.	1.1	0
179	FIREVAT: finding reliable variants without artifacts in human cancer samples using etiologically relevant mutational signatures. <i>Genome Medicine</i> , 2019, 11, 81.	3.6	8
180	Characterization of genetic subclonal evolution in pancreatic cancer mouse models. <i>Nature Communications</i> , 2019, 10, 5435.	5.8	14

#	ARTICLE	IF	CITATIONS
181	In Silico Approach for the Definition of radiomiRNomic Signatures for Breast Cancer Differential Diagnosis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5825.	1.8	16
182	POLE mutations improve the prognosis of endometrial cancer via regulating cellular metabolism through AMF/AMFR signal transduction. <i>BMC Medical Genetics</i> , 2019, 20, 202.	2.1	21
183	An Integrated Pan-Cancer Analysis and Structure-Based Virtual Screening of GPR15. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6226.	1.8	15
184	Computational modeling demonstrates that glioblastoma cells can survive spatial environmental challenges through exploratory adaptation. <i>Nature Communications</i> , 2019, 10, 5704.	5.8	21
185	Competitive Endogenous RNA Network Construction and Comparison of Lung Squamous Cell Carcinoma in Smokers and Nonsmokers. <i>Disease Markers</i> , 2019, 2019, 1-14.	0.6	10
186	Characterization of Blood Surrogate Immune-Methylation Biomarkers for Immune Cell Infiltration in Chronic Inflammaging Disorders. <i>Frontiers in Genetics</i> , 2019, 10, 1229.	1.1	8
187	The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling. <i>Frontiers in Genetics</i> , 2019, 10, 1203.	1.1	78
188	Alterations of the interactome of Bcl-2 proteins in breast cancer at the transcriptional, mutational and structural level. <i>PLoS Computational Biology</i> , 2019, 15, e1007485.	1.5	42
189	Bioinformatic Analysis Reveals an Immune/Inflammatory-Related Risk Signature for Oral Cavity Squamous Cell Carcinoma. <i>Journal of Oncology</i> , 2019, 2019, 1-10.	0.6	5
190	Identification of LINC01615 as potential metastasis-related long noncoding RNA in hepatocellular carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 12964-12970.	2.0	16
191	Butyrate-Induced <i>In Vitro</i> Colonocyte Differentiation Network Model Identifies ITGB1, SYK, CDKN2A, CHAF1A, and LRP1 as the Prognostic Markers for Colorectal Cancer Recurrence. <i>Nutrition and Cancer</i> , 2019, 71, 257-271.	0.9	6
192	A Whole-genome CRISPR Screen Identifies a Role of MSH2 in Cisplatin-mediated Cell Death in Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2019, 75, 242-250.	0.9	57
193	Distinct Molecular Profiles and Immunotherapy Treatment Outcomes of V600E and V600K <i>BRAF</i> -Mutant Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 1272-1279.	3.2	57
194	TULP3: A potential biomarker in colorectal cancer?. <i>PLoS ONE</i> , 2019, 14, e0210762.	1.1	10
195	Circulating Tumor Cell Clustering Shapes DNA Methylation to Enable Metastasis Seeding. <i>Cell</i> , 2019, 176, 98-112.e14.	13.5	578
196	RRM2 is a potential prognostic biomarker with functional significance in glioma. <i>International Journal of Biological Sciences</i> , 2019, 15, 533-543.	2.6	46
197	Astrocytoma progression scoring system based on the WHO 2016 criteria. <i>Scientific Reports</i> , 2019, 9, 96.	1.6	14
198	Characterization of <i>inv(3)</i> cell line OCI-AML-20 with stroma-dependent CD34 expression. <i>Experimental Hematology</i> , 2019, 69, 27-36.	0.2	5

#	ARTICLE	IF	CITATIONS
199	Identification of <i>LINC01234</i> and <i>MIR210HG</i> as novel prognostic signature for colorectal adenocarcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 6769-6777.	2.0	32
200	The transcriptome profiles and methylation status revealed the potential cancer-related lncRNAs in patients with cervical cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 9756-9763.	2.0	21
201	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. <i>Bioinformatics</i> , 2019, 35, 1974-1977.	1.8	87
202	Chromatin regulatory genes served as potential therapeutic targets for patients with urothelial bladder carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 6976-6982.	2.0	7
203	The molecular landscape of glioma in patients with Neurofibromatosis 1. <i>Nature Medicine</i> , 2019, 25, 176-187.	15.2	145
204	Comprehensive Workflow for Integrative Transcriptomics Meta-Analysis. , 2019, , 1-16.		0
205	Integrated analysis of transcription factors and targets co-expression profiles reveals reduced correlation between transcription factors and target genes in cancer. <i>Functional and Integrative Genomics</i> , 2019, 19, 191-204.	1.4	6
206	MicroRNA-301a promotes pancreatic cancer invasion and metastasis through the JAK/STAT3 signaling pathway by targeting SOCS5. <i>Carcinogenesis</i> , 2020, 41, 502-514.	1.3	46
207	Pan-cancer analysis of iron metabolic landscape across the Cancer Genome Atlas. <i>Journal of Cellular Physiology</i> , 2020, 235, 1013-1024.	2.0	43
208	Using R and Bioconductor in Clinical Genomics and Transcriptomics. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 3-20.	1.2	77
209	EuRBPDB: a comprehensive resource for annotation, functional and oncological investigation of eukaryotic RNA binding proteins (RBPs). <i>Nucleic Acids Research</i> , 2020, 48, D307-D313.	6.5	58
210	Variational nonparametric discriminant analysis. <i>Computational Statistics and Data Analysis</i> , 2020, 142, 106817.	0.7	3
211	An integrative pan-cancer analysis of biological and clinical impacts underlying ubiquitin-specific-processing proteases. <i>Oncogene</i> , 2020, 39, 587-602.	2.6	11
212	Metabolic reprogramming associated with aggressiveness occurs in the G-CIMP-high molecular subtypes of IDH1mut lower grade gliomas. <i>Neuro-Oncology</i> , 2020, 22, 480-492.	0.6	31
213	DNA hypermethylation is associated with invasive phenotype of malignant melanoma. <i>Experimental Dermatology</i> , 2020, 29, 39-50.	1.4	30
214	Gene networks in cancer are biased by aneuploidies and sample impurities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194444.	0.9	3
215	Disordered chromatin packing regulates phenotypic plasticity. <i>Science Advances</i> , 2020, 6, eaax6232.	4.7	34
216	Checkpoint Genes at the Cancer Side of the Immunological Synapse in Bladder Cancer. <i>Translational Oncology</i> , 2020, 13, 193-200.	1.7	16

#	ARTICLE	IF	CITATIONS
217	Race-specific alterations in DNA methylation among middle-aged African Americans and Whites with metabolic syndrome. <i>Epigenetics</i> , 2020, 15, 462-482.	1.3	37
218	Genome-wide characterization of cytosine-specific 5-hydroxymethylation in normal breast tissue. <i>Epigenetics</i> , 2020, 15, 398-418.	1.3	11
219	Identification of Distinct Immune Subtypes in Colorectal Cancer Based on the Stromal Compartment. <i>Frontiers in Oncology</i> , 2019, 9, 1497.	1.3	38
220	Theranostic application of <i>miR-429</i> in HER2+ breast cancer. <i>Theranostics</i> , 2020, 10, 50-61.	4.6	24
221	Introducing a panel for early detection of lung adenocarcinoma by using data integration of genomics, epigenomics, transcriptomics and proteomics. <i>Experimental and Molecular Pathology</i> , 2020, 112, 104360.	0.9	17
222	Deep learning of pharmacogenomics resources: moving towards precision oncology. <i>Briefings in Bioinformatics</i> , 2020, 21, 2066-2083.	3.2	43
223	53BP1/RIF1 signaling promotes cell survival after multifractionated radiotherapy. <i>Nucleic Acids Research</i> , 2020, 48, 1314-1326.	6.5	15
224	Sparse classification with paired covariates. <i>Advances in Data Analysis and Classification</i> , 2020, 14, 571-588.	0.9	5
225	A novel RNA sequencing-based risk score model to predict papillary thyroid carcinoma recurrence. <i>Clinical and Experimental Metastasis</i> , 2020, 37, 257-267.	1.7	12
226	Identification of Periostin as a Potential Biomarker in Gliomas by Database Mining. <i>World Neurosurgery</i> , 2020, 135, e137-e163.	0.7	4
227	CaSpER identifies and visualizes CNV events by integrative analysis of single-cell or bulk RNA-sequencing data. <i>Nature Communications</i> , 2020, 11, 89.	5.8	96
228	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69.	5.8	66
229	Stable gene expression for normalisation and single-sample scoring. <i>Nucleic Acids Research</i> , 2020, 48, e113-e113.	6.5	34
230	Analysis of genomic and transcriptomic variations as prognostic signature for lung adenocarcinoma. <i>BMC Bioinformatics</i> , 2020, 21, 368.	1.2	36
231	<p>Dihydrotestosterone Induces Proliferation, Migration, and Invasion of Human Glioblastoma Cell Lines</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 8813-8823.	1.0	14
232	A Global and Integrated Analysis of CINSARC-Associated Genetic Defects. <i>Cancer Research</i> , 2020, 80, 5282-5290.	0.4	8
233	High NRF2 Levels Correlate with Poor Prognosis in Colorectal Cancer Patients and with Sensitivity to the Kinase Inhibitor AT9283 In Vitro. <i>Biomolecules</i> , 2020, 10, 1365.	1.8	22
234	Lipid metabolism gene-wide profile and survival signature of lung adenocarcinoma. <i>Lipids in Health and Disease</i> , 2020, 19, 222.	1.2	34

#	ARTICLE	IF	CITATIONS
235	Identification of Prognosis Associated microRNAs in HNSCC Subtypes Based on TCGA Dataset. <i>Medicina (Lithuania)</i> , 2020, 56, 535.	0.8	8
236	IL4I1 Is a Metabolic Immune Checkpoint that Activates the AHR and Promotes Tumor Progression. <i>Cell</i> , 2020, 182, 1252-1270.e34.	13.5	259
237	OpenGDC: Unifying, Modeling, Integrating Cancer Genomic Data and Clinical Metadata. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 6367.	1.3	12
238	Selecting suitable reference genes for qPCR normalization: a comprehensive analysis in MCF-7 breast cancer cell line. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 68.	1.0	9
239	Loss of UTX/KDM6A and the activation of FGFR3 converge to regulate differentiation gene-expression programs in bladder cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25732-25741.	3.3	26
240	Identification of ATP8B1 as a Tumor Suppressor Gene for Colorectal Cancer and Its Involvement in Phospholipid Homeostasis. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	8
241	Enhancer Reprogramming Confers Dependence on Glycolysis and IGF Signaling in KMT2D Mutant Melanoma. <i>Cell Reports</i> , 2020, 33, 108293.	2.9	39
242	The Clinical Kinase Index: A Method to Prioritize Understudied Kinases as Drug Targets for the Treatment of Cancer. <i>Cell Reports Medicine</i> , 2020, 1, 100128.	3.3	41
243	PyGNA: a unified framework for geneset network analysis. <i>BMC Bioinformatics</i> , 2020, 21, 476.	1.2	0
244	CD155 on Tumor Cells Drives Resistance to Immunotherapy by Inducing the Degradation of the Activating Receptor CD226 in CD8+ T Cells. <i>Immunity</i> , 2020, 53, 805-823.e15.	6.6	79
245	FBXO11 is a candidate tumor suppressor in the leukemic transformation of myelodysplastic syndrome. <i>Blood Cancer Journal</i> , 2020, 10, 98.	2.8	13
246	The ALPK1/TIFA/NF- κ B axis links a bacterial carcinogen to R-loop-induced replication stress. <i>Nature Communications</i> , 2020, 11, 5117.	5.8	67
247	Prediction of survival rate and effect of drugs on cancer patients with somatic mutations of genes: An AI-based approach. <i>Chemical Biology and Drug Design</i> , 2020, 96, 1005-1019.	1.5	4
248	Candidate methylation sites associated with endocrine therapy resistance in ER+/HER2- breast cancer. <i>BMC Cancer</i> , 2020, 20, 676.	1.1	8
249	Molecular Correlates of Long Survival in IDH-Wildtype Glioblastoma Cohorts. <i>Journal of Neuropathology and Experimental Neurology</i> , 2020, 79, 843-854.	0.9	32
250	Molecular gene mutation profiles, TMB and the impact of prognosis in Caucasians and east Asian patients with lung adenocarcinoma. <i>Translational Lung Cancer Research</i> , 2020, 9, 629-638.	1.3	10
251	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
252	Prognostic Biomarker TP53 Mutations for Immune Checkpoint Blockade Therapy and Its Association With Tumor Microenvironment of Lung Adenocarcinoma. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 602328.	1.6	30

#	ARTICLE	IF	CITATIONS
253	The Expression Profiles of ADME Genes in Human Cancers and Their Associations with Clinical Outcomes. <i>Cancers</i> , 2020, 12, 3369.	1.7	15
254	Integrative omics analysis reveals relationships of genes with synthetic lethal interactions through a pan-cancer analysis. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3243-3254.	1.9	4
255	Bioinformatics Analysis of Differentially Expressed Genes and miRNAs in Low-Grade Gliomas. <i>Cancer Informatics</i> , 2020, 19, 117693512096969.	0.9	4
256	Causal Discovery of Gene Regulation with Incomplete Data. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2020, 183, 1747-1775.	0.6	7
257	The Significance of Secreted Phosphoprotein 1 in Multiple Human Cancers. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 565383.	1.6	33
258	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
259	Deconvolution of cellular subsets in human tissue based on targeted DNA methylation analysis at individual CpG sites. <i>BMC Biology</i> , 2020, 18, 178.	1.7	28
260	Multi-Omics Analysis Reveals Novel Subtypes and Driver Genes in Glioblastoma. <i>Frontiers in Genetics</i> , 2020, 11, 565341.	1.1	12
261	Functional Radiogenetic Profiling Implicates ERCC6L2 in Non-homologous End Joining. <i>Cell Reports</i> , 2020, 32, 108068.	2.9	29
262	Tumor-infiltrating podoplanin ⁺ cells in gastric cancer: clinical outcomes and association with immune contexture. <i>Oncolmmunology</i> , 2020, 9, 1845038.	2.1	7
263	The landscape of long noncoding RNA-involved and tumor-specific fusions across various cancers. <i>Nucleic Acids Research</i> , 2020, 48, 12618-12631.	6.5	24
264	An Integrative Computational Approach Based on Expression Similarity Signatures to Identify Protein-Protein Interaction Networks in Female-Specific Cancers. <i>Frontiers in Genetics</i> , 2020, 11, 612521.	1.1	5
265	Major Histocompatibility Complex Genes as Therapeutic Opportunity for Immune Cold Molecular Cancer Subtypes. <i>Journal of Immunology Research</i> , 2020, 2020, 1-9.	0.9	2
266	Age and Mutations as Predictors of the Response to Immunotherapy in Head and Neck Squamous Cell Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 608969.	1.8	29
267	A pan-cancer analysis of HER2 index revealed transcriptional pattern for precise selection of HER2-targeted therapy. <i>EBioMedicine</i> , 2020, 62, 103074.	2.7	32
268	<p>>Overexpression of >GIHCG is Associated with a Poor Prognosis and Immune Infiltration in Hepatocellular Carcinoma</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 11607-11619.	1.0	11
269	Interactome analysis of gene expression profiles identifies CDC6 as a potential therapeutic target modified by miR-215-5p in hepatocellular carcinoma. <i>International Journal of Medical Sciences</i> , 2020, 17, 2926-2940.	1.1	6
270	Drug Response Associated With and Prognostic lncRNAs Mediated by DNA Methylation and Transcription Factors in Colon Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 554833.	1.1	3

#	ARTICLE	IF	CITATIONS
271	Integrative in silico and in vitro transcriptomics analysis revealed new lncRNAs related to intrinsic apoptotic genes in colorectal cancer. <i>Cancer Cell International</i> , 2020, 20, 546.	1.8	9
272	Hypermethylation of LATS2 Promoter and Its Prognostic Value in IDH-Mutated Low-Grade Gliomas. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 586581.	1.8	5
273	Screening and Identification of Potential Biomarkers in Hepatitis B Virus-Related Hepatocellular Carcinoma by Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 555537.	1.1	11
274	Identification of Mutations Related to Cisplatin-Resistance and Prognosis of Patients With Lung Adenocarcinoma. <i>Frontiers in Pharmacology</i> , 2020, 11, 572627.	1.6	9
275	Identification of synthetic chemosensitivity genes paired with BRAF for BRAF/MAPK inhibitors. <i>Scientific Reports</i> , 2020, 10, 20001.	1.6	2
276	EPHA5 mutation predicts the durable clinical benefit of immune checkpoint inhibitors in patients with lung adenocarcinoma. <i>Cancer Gene Therapy</i> , 2021, 28, 864-874.	2.2	27
277	Development and Validation of a Gene Signature for Prediction of Relapse in Stage I Testicular Germ Cell Tumors. <i>Frontiers in Oncology</i> , 2020, 10, 1147.	1.3	2
278	Systematic Evaluation of the Diagnostic and Prognostic Significance of Competitive Endogenous RNA Networks in Prostate Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 785.	1.1	3
279	Crosstalk Between the MSI Status and Tumor Microenvironment in Colorectal Cancer. <i>Frontiers in Immunology</i> , 2020, 11, 2039.	2.2	187
280	A deep learning model to predict RNA-Seq expression of tumours from whole slide images. <i>Nature Communications</i> , 2020, 11, 3877.	5.8	247
281	Label-free quantitative proteomic analysis identifies the oncogenic role of FOXA1 in BaP-transformed 16HBE cells. <i>Toxicology and Applied Pharmacology</i> , 2020, 403, 115160.	1.3	5
282	Development and validation of an oxidative phosphorylation-related gene signature in lung adenocarcinoma. <i>Epigenomics</i> , 2020, 12, 1333-1348.	1.0	10
283	Human FBXL8 Is a Novel E3 Ligase Which Promotes BRCA Metastasis by Stimulating Pro-Tumorigenic Cytokines and Inhibiting Tumor Suppressors. <i>Cancers</i> , 2020, 12, 2210.	1.7	11
284	The P72R Polymorphism in R248Q/W p53 Mutants Modifies the Mutant Effect on Epithelial to Mesenchymal Transition Phenotype and Cell Invasion via CXCL1 Expression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8025.	1.8	4
285	Characterization of the Tumor Immune Microenvironment Identifies M0 Macrophage-Enriched Cluster as a Poor Prognostic Factor in Hepatocellular Carcinoma. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 1002-1013.	1.0	29
286	Expression of NK cell receptor ligands in primary colorectal cancer tissue in relation to the phenotype of circulating NK- and NKT cells, and clinical outcome. <i>Molecular Immunology</i> , 2020, 128, 205-218.	1.0	15
287	Early Diagnosis of Pancreatic Ductal Adenocarcinoma by Combining Relative Expression Orderings With Machine-Learning Method. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 582864.	1.8	28
288	Multiomic Integration of Public Oncology Databases in Bioconductor. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 958-971.	1.0	42

#	ARTICLE	IF	CITATIONS
289	Finding disease modules for cancer and COVID-19 in gene co-expression networks with the Core&Peel method. Scientific Reports, 2020, 10, 17628.	1.6	6
290	ACKR4 restrains antitumor immunity by regulating CCL21. Journal of Experimental Medicine, 2020, 217, .	4.2	25
291	Multivariate gene expression-based survival predictor model in esophageal adenocarcinoma. Thoracic Cancer, 2020, 11, 2896-2908.	0.8	8
292	Human Endogenous Retrovirus Expression Is Associated with Head and Neck Cancer and Differential Survival. Viruses, 2020, 12, 956.	1.5	20
293	A protein interaction map identifies existing drugs targeting SARS-CoV-2. BMC Pharmacology & Toxicology, 2020, 21, 65.	1.0	18
294	Methylation of immune-regulatory cytokine genes and pancreatic cancer outcomes. Epigenomics, 2020, 12, 1273-1285.	1.0	8
295	VAV2 signaling promotes regenerative proliferation in both cutaneous and head and neck squamous cell carcinoma. Nature Communications, 2020, 11, 4788.	5.8	27
296	Development of Autophagy Signature-Based Prognostic Nomogram for Refined Glioma Survival Prognostication. BioMed Research International, 2020, 2020, 1-23.	0.9	7
297	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	13.5	126
298	Reference-free deconvolution, visualization and interpretation of complex DNA methylation data using DecompPipeline, MeDeCom and FactorViz. Nature Protocols, 2020, 15, 3240-3263.	5.5	19
299	HPV-EM: an accurate HPV detection and genotyping EM algorithm. Scientific Reports, 2020, 10, 14340.	1.6	3
300	The NK cell granule protein NKG7 regulates cytotoxic granule exocytosis and inflammation. Nature Immunology, 2020, 21, 1205-1218.	7.0	110
301	Mutant POLQ and POLZ/REV3L DNA polymerases may contribute to the favorable survival of patients with tumors with POLE mutations outside the exonuclease domain. BMC Medical Genetics, 2020, 21, 167.	2.1	2
302	Genome-Wide Analysis of the FOXA1 Transcriptional Network Identifies Novel Protein-Coding and Long Noncoding RNA Targets in Colorectal Cancer Cells. Molecular and Cellular Biology, 2020, 40, .	1.1	13
303	Infiltration by IL22-Producing T Cells Promotes Neutrophil Recruitment and Predicts Favorable Clinical Outcome in Human Colorectal Cancer. Cancer Immunology Research, 2020, 8, 1452-1462.	1.6	15
304	KIAA1522 potentiates TNF α -NF κ B signaling to antagonize platinum-based chemotherapy in lung adenocarcinoma. Journal of Experimental and Clinical Cancer Research, 2020, 39, 170.	3.5	13
305	Identification of Transcription Factor/Gene Axis in Colon Cancer Using a Methylome Approach. Frontiers in Genetics, 2020, 11, 864.	1.1	1
306	Immune expression signatures as candidate prognostic biomarkers of age and gender survival differences in cutaneous melanoma. Scientific Reports, 2020, 10, 12322.	1.6	6

#	ARTICLE	IF	CITATIONS
307	CeRNA Network Analysis Representing Characteristics of Different Tumor Environments Based on 1p/19q Codeletion in Oligodendrogliomas. <i>Cancers</i> , 2020, 12, 2543.	1.7	5
308	Negative Regulation of Serine Threonine Kinase 11 (STK11) through miR-100 in Head and Neck Cancer. <i>Genes</i> , 2020, 11, 1058.	1.0	10
309	TENET 2.0: Identification of key transcriptional regulators and enhancers in lung adenocarcinoma. <i>PLoS Genetics</i> , 2020, 16, e1009023.	1.5	20
310	ATM Mutations Benefit Bladder Cancer Patients Treated With Immune Checkpoint Inhibitors by Acting on the Tumor Immune Microenvironment. <i>Frontiers in Genetics</i> , 2020, 11, 933.	1.1	32
311	A pan-cancer assessment of alterations of the kinase domain of ULK1, an upstream regulator of autophagy. <i>Scientific Reports</i> , 2020, 10, 14874.	1.6	18
312	<p>Favorable Immune Microenvironment in Patients with EGFR and MAPK Co-Mutations</p>. <i>Lung Cancer: Targets and Therapy</i> , 2020, Volume 11, 59-71.	1.3	0
313	COCOA: coordinate covariation analysis of epigenetic heterogeneity. <i>Genome Biology</i> , 2020, 21, 240.	3.8	10
314	Prognosis of Lung Adenocarcinoma Patients With NTRK3 Mutations to Immune Checkpoint Inhibitors. <i>Frontiers in Pharmacology</i> , 2020, 11, 1213.	1.6	28
315	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2115-2125.	2.5	145
316	Decreased expression of the thyroid hormone-inactivating enzyme type 3 deiodinase is associated with lower survival rates in breast cancer. <i>Scientific Reports</i> , 2020, 10, 13914.	1.6	5
317	<i>ERINA</i> Is an Estrogen-Responsive LncRNA That Drives Breast Cancer through the E2F1/RB1 Pathway. <i>Cancer Research</i> , 2020, 80, 4399-4413.	0.4	31
318	High infiltration of B cells in tertiary lymphoid structures, TCR oligoclonality, and neoantigens are part of esophageal squamous cell carcinoma microenvironment. <i>Journal of Leukocyte Biology</i> , 2020, 108, 1307-1318.	1.5	12
319	Estradiol Induces Epithelial to Mesenchymal Transition of Human Glioblastoma Cells. <i>Cells</i> , 2020, 9, 1930.	1.8	24
320	Prognostic value of intratumoral lymphocyte-to-monocyte ratio and M0 macrophage enrichment in tumor immune microenvironment of melanoma. <i>Melanoma Management</i> , 2020, 7, MMT51.	0.1	14
321	A Topic Modeling Analysis of TCGA Breast and Lung Cancer Transcriptomic Data. <i>Cancers</i> , 2020, 12, 3799.	1.7	12
322	SETDB1 Overexpression Sets an Intertumoral Transcriptomic Divergence in Non-small Cell Lung Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 573515.	1.1	10
323	Germline Genetic Association between Stromal Interaction Molecule 1 (STIM1) and Clinical Outcomes in Breast Cancer Patients. <i>Journal of Personalized Medicine</i> , 2020, 10, 287.	1.1	2
324	An Integrative Pan-Cancer Analysis Revealing LCN2 as an Oncogenic Immune Protein in Tumor Microenvironment. <i>Frontiers in Oncology</i> , 2020, 10, 605097.	1.3	40

#	ARTICLE	IF	CITATIONS
325	Regulatory T Cells Support Breast Cancer Progression by Opposing IFN- γ -Dependent Functional Reprogramming of Myeloid Cells. <i>Cell Reports</i> , 2020, 33, 108482.	2.9	28
326	GJA1 Expression and Its Prognostic Value in Cervical Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	7
327	Intestinal region-specific Wnt signalling profiles reveal interrelation between cell identity and oncogenic pathway activity in cancer development. <i>Cancer Cell International</i> , 2020, 20, 578.	1.8	8
328	Mi-RNA-888-5p Is Involved in S-Adenosylmethionine Antitumor Effects in Laryngeal Squamous Cancer Cells. <i>Cancers</i> , 2020, 12, 3665.	1.7	9
329	An Epithelial-Mesenchymal Transition (EMT) Preoperative Nomogram for Prediction of Lymph Node Metastasis in Bladder Cancer (BLCA). <i>Disease Markers</i> , 2020, 2020, 1-17.	0.6	5
330	Identification of prognosis-associated immune genes and exploration of immune cell infiltration in colorectal cancer. <i>Biomarkers in Medicine</i> , 2020, 14, 1353-1369.	0.6	5
331	Prediction of survival and recurrence in patients with pancreatic cancer by integrating multi-omics data. <i>Scientific Reports</i> , 2020, 10, 18951.	1.6	42
332	Potential predictive value of SCN4A mutation status for immune checkpoint inhibitors in melanoma. <i>Biomedicine and Pharmacotherapy</i> , 2020, 131, 110633.	2.5	6
333	Role of specialized composition of SWI/SNF complexes in prostate cancer lineage plasticity. <i>Nature Communications</i> , 2020, 11, 5549.	5.8	76
334	Molecular characterization, biological function, tumor microenvironment association and clinical significance of m6A regulators in lung adenocarcinoma. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	100
335	TGFB2 serves as a link between epithelial-mesenchymal transition and tumor mutation burden in gastric cancer. <i>International Immunopharmacology</i> , 2020, 84, 106532.	1.7	25
336	Predicting cancer origins with a DNA methylation-based deep neural network model. <i>PLoS ONE</i> , 2020, 15, e0226461.	1.1	29
337	Reduction of Liver Metastasis Stiffness Improves Response to Bevacizumab in Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2020, 37, 800-817.e7.	7.7	179
338	DNA methylation profiling to predict overall survival risk in gastric cancer: development and validation of a nomogram to optimize clinical management. <i>Journal of Cancer</i> , 2020, 11, 4352-4365.	1.2	7
339	Gene networks and expression quantitative trait loci associated with adjuvant chemotherapy response in high-grade serous ovarian cancer. <i>BMC Cancer</i> , 2020, 20, 413.	1.1	6
340	DNF: A differential network flow method to identify rewiring drivers for gene regulatory networks. <i>Neurocomputing</i> , 2020, 410, 202-210.	3.5	9
341	A systematic review of genes affecting mitochondrial processes in cancer. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165846.	1.8	2
342	Construction and Analysis of a ceRNA Network Reveals Potential Prognostic Markers in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 418.	1.1	13

#	ARTICLE	IF	CITATIONS
343	Single-Cell Mapping of Human Brain Cancer Reveals Tumor-Specific Instruction of Tissue-Invading Leukocytes. <i>Cell</i> , 2020, 181, 1626-1642.e20.	13.5	388
344	Interrogation of the Microenvironmental Landscape in Brain Tumors Reveals Disease-Specific Alterations of Immune Cells. <i>Cell</i> , 2020, 181, 1643-1660.e17.	13.5	554
345	Hybrid Stem Cell States: Insights Into the Relationship Between Mammary Development and Breast Cancer Using Single-Cell Transcriptomics. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 288.	1.8	21
346	Clinical Multigene Panel Sequencing Identifies Distinct Mutational Association Patterns in Metastatic Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 560.	1.3	12
347	TGF β Promotes Chemoresistance of Malignant Pleural Mesothelioma. <i>Cancers</i> , 2020, 12, 1484.	1.7	2
348	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. <i>Nature Medicine</i> , 2020, 26, 1041-1043.	15.2	161
349	Age, sex, and specific gene mutations affect the effects of immune checkpoint inhibitors in colorectal cancer. <i>Pharmacological Research</i> , 2020, 159, 105028.	3.1	45
350	Construction and analysis of a lncRNA-miRNA-mRNA network based on competitive endogenous RNA reveal functional lncRNAs in oral cancer. <i>BMC Medical Genomics</i> , 2020, 13, 84.	0.7	28
351	SNPNexus: a web server for functional annotation of human genome sequence variation (2020) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42 6.5 140	6.5	140
352	Macrophage correlates with immunophenotype and predicts anti-PD-L1 response of urothelial cancer. <i>Theranostics</i> , 2020, 10, 7002-7014.	4.6	108
353	Rewired functional regulatory networks among miRNA isoforms (isomiRs) from let-7 and miR-10 gene families in cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1238-1248.	1.9	11
354	Comprehensive Characterization of the Prognosis Value of Alternative Splicing Events in Acute Myeloid Leukemia. <i>DNA and Cell Biology</i> , 2020, 39, 1243-1255.	0.9	4
355	Stromal beta-catenin activation impacts nephron progenitor differentiation in the developing kidney and may contribute to Wilms tumor. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	16
356	Classification of Cancer Types Using Graph Convolutional Neural Networks. <i>Frontiers in Physics</i> , 2020, 8, .	1.0	64
357	WNT and inflammatory signaling distinguish human Fallopian tube epithelial cell populations. <i>Scientific Reports</i> , 2020, 10, 9837.	1.6	13
358	Identification of Hub Genes Associated With Development of Head and Neck Squamous Cell Carcinoma by Integrated Bioinformatics Analysis. <i>Frontiers in Oncology</i> , 2020, 10, 681.	1.3	56
359	Analysis of Gene Signatures of Tumor Microenvironment Yields Insight Into Mechanisms of Resistance to Immunotherapy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 348.	2.0	4
360	The Landscape of Iron Metabolism-Related and Methylated Genes in the Prognosis Prediction of Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 788.	1.3	19

#	ARTICLE	IF	CITATIONS
361	Development and Validation of a 12-Gene Immune Relevant Prognostic Signature for Lung Adenocarcinoma Through Machine Learning Strategies. <i>Frontiers in Oncology</i> , 2020, 10, 835.	1.3	14
362	Multi-Omic Regulation of the PAM50 Gene Signature in Breast Cancer Molecular Subtypes. <i>Frontiers in Oncology</i> , 2020, 10, 845.	1.3	15
363	LPAR1, Correlated With Immune Infiltrates, Is a Potential Prognostic Biomarker in Prostate Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 846.	1.3	59
364	TERT Promoter Mutations and Their Impact on Gene Expression Profile in Papillary Thyroid Carcinoma. <i>Cancers</i> , 2020, 12, 1597.	1.7	13
365	Integrative analysis of DNA methylation and gene expression in papillary renal cell carcinoma. <i>Molecular Genetics and Genomics</i> , 2020, 295, 807-824.	1.0	22
366	Integrative Analysis of MicroRNA and Gene Interactions for Revealing Candidate Signatures in Prostate Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 176.	1.1	41
367	ecTMB: a robust method to estimate and classify tumor mutational burden. <i>Scientific Reports</i> , 2020, 10, 4983.	1.6	17
368	Matrix-Targeting Immunotherapy Controls Tumor Growth and Spread by Switching Macrophage Phenotype. <i>Cancer Immunology Research</i> , 2020, 8, 368-382.	1.6	42
369	Transcriptomic Analyses for Identification and Prioritization of Genes Associated With Alzheimer's Disease in Humans. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 31.	2.0	19
370	Edgetic perturbation signatures represent known and novel cancer biomarkers. <i>Scientific Reports</i> , 2020, 10, 4350.	1.6	5
371	Machine Learning Supports Long Noncoding RNAs as Expression Markers for Endometrial Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	1
372	Proteogenomics Uncovers a Vast Repertoire of Shared Tumor-Specific Antigens in Ovarian Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 544-555.	1.6	48
373	Hypoxia-Induced Adaptations of miRNomes and Proteomes in Melanoma Cells and Their Secreted Extracellular Vesicles. <i>Cancers</i> , 2020, 12, 692.	1.7	32
374	The pan-cancer landscape of netrin family reveals potential oncogenic biomarkers. <i>Scientific Reports</i> , 2020, 10, 5224.	1.6	22
375	Co-regulation of the antagonistic RepoMan:Aurora-B pair in proliferating cells. <i>Molecular Biology of the Cell</i> , 2020, 31, 419-438.	0.9	9
376	Molecular profile reveals immune-associated markers of lymphatic invasion in human colon adenocarcinoma. <i>International Immunopharmacology</i> , 2020, 83, 106402.	1.7	7
377	An atlas of human metabolism. <i>Science Signaling</i> , 2020, 13, .	1.6	223
378	Identification of immune cells and mRNA associated with prognosis of gastric cancer. <i>BMC Cancer</i> , 2020, 20, 206.	1.1	37

#	ARTICLE	IF	CITATIONS
379	m6A regulator-mediated methylation modification patterns and tumor microenvironment infiltration characterization in gastric cancer. <i>Molecular Cancer</i> , 2020, 19, 53.	7.9	704
380	Identification of supervised and sparse functional genomic pathways. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2020, 19, .	0.2	3
381	Sphere-Forming Culture for Expanding Genetically Distinct Patient-Derived Glioma Stem Cells by Cellular Growth Rate Screening. <i>Cancers</i> , 2020, 12, 549.	1.7	2
382	Genome-Scale CRISPR Screening in Human Intestinal Organoids Identifies Drivers of TGF- β Resistance. <i>Cell Stem Cell</i> , 2020, 26, 431-440.e8.	5.2	103
383	RNA processing genes characterize RNA splicing and further stratify colorectal cancer. <i>Cell Proliferation</i> , 2020, 53, e12861.	2.4	4
384	A Comprehensive Network Pharmacology-Based Strategy to Investigate Multiple Mechanisms of HeChan Tablet on Lung Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-17.	0.5	7
385	Gastric Cancer Tumor Microenvironment Characterization Reveals Stromal-Related Gene Signatures Associated With Macrophage Infiltration. <i>Frontiers in Genetics</i> , 2020, 11, 663.	1.1	31
386	Tumor Immune Microenvironment Clusters in Localized Prostate Adenocarcinoma: Prognostic Impact of Macrophage Enriched/Plasma Cell Non-Enriched Subtypes. <i>Journal of Clinical Medicine</i> , 2020, 9, 1973.	1.0	10
387	Integrated pharmaco-proteogenomics defines two subgroups in isocitrate dehydrogenase wild-type glioblastoma with prognostic and therapeutic opportunities. <i>Nature Communications</i> , 2020, 11, 3288.	5.8	44
388	Integrator restrains paraspeckles assembly by promoting isoform switching of the lncRNA <i>NEAT1</i> . <i>Science Advances</i> , 2020, 6, eaaz9072.	4.7	33
389	PRMT5 control of cGAS/STING and NLRC5 pathways defines melanoma response to antitumor immunity. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	111
390	High Expression of FAP in Colorectal Cancer Is Associated With Angiogenesis and Immunoregulation Processes. <i>Frontiers in Oncology</i> , 2020, 10, 979.	1.3	50
391	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
392	Prognostic Value of CD200R1 mRNA Expression in Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2020, 12, 1777.	1.7	9
393	Identification of miRNA Master Regulators in Breast Cancer. <i>Cells</i> , 2020, 9, 1610.	1.8	20
394	Lymphocyte cytosolic protein 1 (LCP1) is a novel TRAF3 dysregulation biomarker with potential prognostic value in multiple myeloma. <i>Genome Instability & Disease</i> , 2020, 1, 286-299.	0.5	5
395	Quantitative and qualitative impairments in dendritic cell subsets of patients with ovarian or prostate cancer. <i>European Journal of Cancer</i> , 2020, 135, 173-182.	1.3	32
396	A conditional mouse expressing an activating mutation in <i>NRF2</i> displays hyperplasia of the upper gastrointestinal tract and decreased white adipose tissue. <i>Journal of Pathology</i> , 2020, 252, 125-137.	2.1	16

#	ARTICLE	IF	CITATIONS
397	Analysis of H3K4me3 and H3K27me3 bivalent promoters in HER2+ breast cancer cell lines reveals variations depending on estrogen receptor status and significantly correlates with gene expression. BMC Medical Genomics, 2020, 13, 92.	0.7	8
398	Efficient weighted univariate clustering maps outstanding dysregulated genomic zones in human cancers. Bioinformatics, 2020, 36, 5027-5036.	1.8	24
399	Presence of a 34-gene signature is a favorable prognostic marker in squamous non-small cell lung carcinoma. Journal of Translational Medicine, 2020, 18, 271.	1.8	8
400	Biologically Aggressive Phenotype and Anti-cancer Immunity Counterbalance in Breast Cancer with High Mutation Rate. Scientific Reports, 2020, 10, 1852.	1.6	65
401	CDK4/RB/E2Fs axis as potential therapeutic target of endometrial cancer. Biomedicine and Pharmacotherapy, 2020, 125, 109870.	2.5	8
402	Impact of accumulated alterations in driver and passenger genes on response to radiation therapy. British Journal of Radiology, 2020, 93, 20190625.	1.0	0
403	Integrative Transcriptomic Analysis Reveals a Multiphasic Epithelial-Mesenchymal Spectrum in Cancer and Non-tumorigenic Cells. Frontiers in Oncology, 2019, 9, 1479.	1.3	28
404	DeepTRIAGE: interpretable and individualised biomarker scores using attention mechanism for the classification of breast cancer sub-types. BMC Medical Genomics, 2020, 13, 20.	0.7	17
405	The Impact of Normalization Approaches to Automatically Detect Radiogenomic Phenotypes Characterizing Breast Cancer Receptors Status. Cancers, 2020, 12, 518.	1.7	38
406	Classification of clear cell renal cell carcinoma based on PKM alternative splicing. Heliyon, 2020, 6, e03440.	1.4	9
407	MetaOmGraph: a workbench for interactive exploratory data analysis of large expression datasets. Nucleic Acids Research, 2020, 48, e23-e23.	6.5	19
408	Pan-cancer characterization of immune-related lncRNAs identifies potential oncogenic biomarkers. Nature Communications, 2020, 11, 1000.	5.8	293
409	Variability in estimated gene expression among commonly used RNA-seq pipelines. Scientific Reports, 2020, 10, 2734.	1.6	43
410	The pan-cancer landscape of prognostic germline variants in 10,582 patients. Genome Medicine, 2020, 12, 15.	3.6	22
411	The Role of mPR ¹ and mPR ² in Human Glioblastoma Cells: Expression, Hormonal Regulation, and Possible Clinical Outcome. Hormones and Cancer, 2020, 11, 117-127.	4.9	13
412	System-Based Differential Gene Network Analysis for Characterizing a Sample-Specific Subnetwork. Biomolecules, 2020, 10, 306.	1.8	9
413	Cancer prognosis with shallow tumor RNA sequencing. Nature Medicine, 2020, 26, 188-192.	15.2	33
414	p53 functional states are associated with distinct aldehyde dehydrogenase transcriptomic signatures. Scientific Reports, 2020, 10, 1097.	1.6	5

#	ARTICLE	IF	CITATIONS
415	An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates. <i>Cancer Cell</i> , 2020, 37, 21-36.e13.	7.7	253
416	Profiles of prognostic alternative splicing signature in hepatocellular carcinoma. <i>Cancer Medicine</i> , 2020, 9, 2171-2180.	1.3	19
417	Discovery of novel akt1 inhibitor induces autophagy associated death in hepatocellular carcinoma cells. <i>European Journal of Medicinal Chemistry</i> , 2020, 189, 112076.	2.6	20
418	Development and validation of an immune prognostic classifier for clear cell renal cell carcinoma. <i>Cancer Biomarkers</i> , 2020, 27, 265-275.	0.8	7
419	Identification of three m6A-related mRNAs signature and risk score for the prognostication of hepatocellular carcinoma. <i>Cancer Medicine</i> , 2020, 9, 1877-1889.	1.3	60
420	Frequent KRAS mutations in oncocytic papillary renal neoplasm with inverted nuclei. <i>Histopathology</i> , 2020, 76, 1070-1083.	1.6	32
421	Poor clinical outcome in metastatic melanoma is associated with a microRNA-modulated immunosuppressive tumor microenvironment. <i>Journal of Translational Medicine</i> , 2020, 18, 56.	1.8	28
422	A Network-Based Approach for Identification of Subtype-Specific Master Regulators in Pancreatic Ductal Adenocarcinoma. <i>Genes</i> , 2020, 11, 155.	1.0	8
423	AR/ER Ratio Correlates with Expression of Proliferation Markers and with Distinct Subset of Breast Tumors. <i>Cells</i> , 2020, 9, 1064.	1.8	21
424	Molecular description of ANGPT2 associated colorectal carcinoma. <i>International Journal of Cancer</i> , 2020, 147, 2007-2018.	2.3	15
425	Identification of cancer stem cell-related biomarkers in lung adenocarcinoma by stemness index and weighted correlation network analysis. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 1463-1472.	1.2	26
426	KMT2D Deficiency Impairs Super-Enhancers to Confer a Glycolytic Vulnerability in Lung Cancer. <i>Cancer Cell</i> , 2020, 37, 599-617.e7.	7.7	137
427	Integration of multiple key molecules in lung adenocarcinoma identifies prognostic and immunotherapeutic relevant gene signatures. <i>International Immunopharmacology</i> , 2020, 83, 106477.	1.7	19
428	Differences in gene-expression profiles in breast cancer between African and European-ancestry women. <i>Carcinogenesis</i> , 2020, 41, 887-893.	1.3	8
429	Early Diagnosis of Hepatocellular Carcinoma Using Machine Learning Method. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 254.	2.0	74
430	Immunoscore Predicts Survival in Early-Stage Lung Adenocarcinoma Patients. <i>Frontiers in Oncology</i> , 2020, 10, 691.	1.3	17
431	Analysis of the Circadian Regulation of Cancer Hallmarks by a Cross-Platform Study of Colorectal Cancer Time-Series Data Reveals an Association with Genes Involved in Huntington's Disease. <i>Cancers</i> , 2020, 12, 963.	1.7	15
432	STAT3 independent analysis reveals PDK4 as independent predictor of recurrence in prostate cancer. <i>Molecular Systems Biology</i> , 2020, 16, e9247.	3.2	38

#	ARTICLE	IF	CITATIONS
433	Transcription Factor Profiling to Predict Recurrence-Free Survival in Breast Cancer: Development and Validation of a Nomogram to Optimize Clinical Management. <i>Frontiers in Genetics</i> , 2020, 11, 333.	1.1	8
434	Canonical BMP Signaling Executes Epithelial-Mesenchymal Transition Downstream of SNAIL1. <i>Cancers</i> , 2020, 12, 1019.	1.7	17
435	Integrating Genomic Data with Transcriptomic Data for Improved Survival Prediction for Adult Diffuse Glioma. <i>Journal of Cancer</i> , 2020, 11, 3794-3802.	1.2	5
436	Comprehensive Analysis of the Tumor Microenvironment in Cutaneous Melanoma associated with Immune Infiltration. <i>Journal of Cancer</i> , 2020, 11, 3858-3870.	1.2	22
437	Network-based prioritization of cancer genes by integrative ranks from multi-omics data. <i>Computers in Biology and Medicine</i> , 2020, 119, 103692.	3.9	16
438	Molecular profiling of driver events in metastatic uveal melanoma. <i>Nature Communications</i> , 2020, 11, 1894.	5.8	108
439	Viral status, immune microenvironment and immunological response to checkpoint inhibitors in hepatocellular carcinoma. , 2020, 8, e000394.		39
440	Topological Tumor Graphs: A Graph-Based Spatial Model to Infer Stromal Recruitment for Immunosuppression in Melanoma Histology. <i>Cancer Research</i> , 2020, 80, 1199-1209.	0.4	43
441	Right and left-sided colon cancers - specificity of molecular mechanisms in tumorigenesis and progression. <i>BMC Cancer</i> , 2020, 20, 317.	1.1	51
442	Induced Tumor Heterogeneity Reveals Factors Informing Radiation and Immunotherapy Combinations. <i>Clinical Cancer Research</i> , 2020, 26, 2972-2985.	3.2	9
443	Convolutional neural network models for cancer type prediction based on gene expression. <i>BMC Medical Genomics</i> , 2020, 13, 44.	0.7	103
444	In Silico Discovery of Candidate Drugs against Covid-19. <i>Viruses</i> , 2020, 12, 404.	1.5	156
445	Integrin $\alpha 3 \beta 1$ on Tumor Keratinocytes Is Essential to Maintain Tumor Growth and Promotes a Tumor-Supportive Keratinocyte Secretome. <i>Journal of Investigative Dermatology</i> , 2021, 141, 142-151.e6.	0.3	7
446	Normal tissue content impact on the GBM molecular classification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
447	ZFH3 mutation as a protective biomarker for immune checkpoint blockade in non-small cell lung cancer. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 137-151.	2.0	69
448	Irinotecan and vandetanib create synergies for treatment of pancreatic cancer patients with concomitant TP53 and KRAS mutations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	19
449	Prognostic nomogram based on immune scores for laryngeal squamous cell cancer. <i>European Archives of Oto-Rhino-Laryngology</i> , 2021, 278, 141-148.	0.8	3
450	Protein anabolism is key to long-term survival in high-grade serous ovarian cancer. <i>Translational Oncology</i> , 2021, 14, 100885.	1.7	6

#	ARTICLE	IF	CITATIONS
451	Immune microenvironment of the gene signature reflecting the standardised uptake value on 18F-fluorodeoxyglucose positron emission tomography/computed tomography in head and neck squamous cell carcinoma. <i>Annals of Nuclear Medicine</i> , 2021, 35, 65-75.	1.2	3
452	Proteomic Analyses Identify Differentially Expressed Proteins and Pathways Between Low-Risk and High-Risk Subtypes of Early-Stage Lung Adenocarcinoma and Their Prognostic Impacts. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100015.	2.5	10
453	Senescence Reprogramming by TIMP1 Deficiency Promotes Prostate Cancer Metastasis. <i>Cancer Cell</i> , 2021, 39, 68-82.e9.	7.7	66
455	Combined BRAF, MEK, and CDK4/6 Inhibition Depletes Intratumoral Immune-Potentiating Myeloid Populations in Melanoma. <i>Cancer Immunology Research</i> , 2021, 9, 136-146.	1.6	12
456	A balance score between immune stimulatory and suppressive microenvironments identifies mediators of tumour immunity and predicts pan-cancer survival. <i>British Journal of Cancer</i> , 2021, 124, 760-769.	2.9	13
457	FOX11 expression in chromophobe renal cell carcinoma and renal oncocytoma: a study of The Cancer Genome Atlas transcriptome-based outlier mining and immunohistochemistry. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2021, 478, 647-658.	1.4	26
458	miR-34c-3p targets CDK1 a synthetic lethality partner of KRAS in non-small cell lung cancer. <i>Cancer Gene Therapy</i> , 2021, 28, 413-426.	2.2	13
459	The effect of tissue composition on gene co-expression. <i>Briefings in Bioinformatics</i> , 2021, 22, 127-139.	3.2	25
460	Alteration in stemness causes exclusivity between Epstein-Barr virus-positivity and microsatellite instability status in gastric cancer. <i>Gastric Cancer</i> , 2021, 24, 602-610.	2.7	3
461	A multi-omics study on cutaneous and uveal melanoma. <i>International Journal of Ophthalmology</i> , 2021, 14, 32-41.	0.5	3
462	Immune signature-based risk stratification and prediction of immune checkpoint inhibitor's efficacy for lung adenocarcinoma. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 1705-1719.	2.0	96
463	Ethanol exposure drives colon location specific cell composition changes in a normal colon crypt 3D organoid model. <i>Scientific Reports</i> , 2021, 11, 432.	1.6	14
464	ARMT: An automatic RNA-seq data mining tool based on comprehensive and integrative analysis in cancer research. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4426-4434.	1.9	2
465	Defining muscle-invasive bladder cancer immunotypes by introducing tumor mutation burden, CD8+ T cells, and molecular subtypes. <i>Hereditas</i> , 2021, 158, 1.	0.5	11
466	Spliceosome-targeted therapies trigger an antiviral immune response in triple-negative breast cancer. <i>Cell</i> , 2021, 184, 384-403.e21.	13.5	94
467	DNA methylation profiling reveals new potential subtype-specific gene markers for early-stage renal cell carcinoma in Caucasian population. <i>Quantitative Biology</i> , 2022, 10, 79-93.	0.3	0
468	Stratification of lung adenocarcinoma patients for d-limonene intervention based on the expression signature genes. <i>Food and Function</i> , 2021, 12, 7214-7226.	2.1	3
469	LncTx: A network-based method to repurpose drugs acting on the survival-related lncRNAs in lung cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3990-4002.	1.9	5

#	ARTICLE	IF	CITATIONS
471	TRIP13 is identified as a prognosis biomarker for renal clear cell carcinoma and promotes renal cell carcinoma cell proliferation, migration and invasion. <i>Biocell</i> , 2021, 45, 577-588.	0.4	2
472	Identification of Four Genes as Prognosis Signatures in Lung Adenocarcinoma Microenvironment. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 15-26.	0.4	2
473	Pathway-based classification of glioblastoma uncovers a mitochondrial subtype with therapeutic vulnerabilities. <i>Nature Cancer</i> , 2021, 2, 141-156.	5.7	163
474	The elevated transcription of ADAM19 by the oncohistone H2BE76K contributes to oncogenic properties in breast cancer. <i>Journal of Biological Chemistry</i> , 2021, 296, 100374.	1.6	17
475	MetaCancer: A deep learning-based pan-cancer metastasis prediction model developed using multi-omics data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4404-4411.	1.9	19
476	Aldo Keto Reductases AKR1B1 and AKR1B10 in Cancer: Molecular Mechanisms and Signaling Networks. <i>Advances in Experimental Medicine and Biology</i> , 2021, , 65-82.	0.8	17
477	Identification of a Five-Autophagy-Related-lncRNA Signature as a Novel Prognostic Biomarker for Hepatocellular Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 611626.	1.6	32
478	Systems pharmacology dissection of Epimedium targeting tumor microenvironment to enhance cytotoxic T lymphocyte responses in lung cancer. <i>Aging</i> , 2021, 13, 2912-2940.	1.4	11
479	Integrative Bioinformatics Analysis Identified Hub Genes in Association with Development of Lung Adenocarcinoma. <i>Advances in Clinical Medicine</i> , 2021, 11, 2970-2977.	0.0	0
480	Comprehensive Characterization of Immunological Profiles and Clinical Significance in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 574778.	1.3	4
481	Association of variably methylated tumour DNA regions with overall survival for invasive lobular breast cancer. <i>Clinical Epigenetics</i> , 2021, 13, 11.	1.8	12
482	Unsupervised subtyping and methylation landscape of pancreatic ductal adenocarcinoma. <i>Heliyon</i> , 2021, 7, e06000.	1.4	11
483	Anti-PD-1 in Combination With Trametinib Suppresses Tumor Growth and Improves Survival of Intrahepatic Cholangiocarcinoma in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 1166-1178.	2.3	15
484	PPP2R2B downregulation is associated with immune evasion and predicts poor clinical outcomes in triple-negative breast cancer. <i>Cancer Cell International</i> , 2021, 21, 13.	1.8	17
485	A novel three-long noncoding RNA risk score system for the prognostic prediction of triple-negative breast cancer. <i>Biomarkers in Medicine</i> , 2021, 15, 43-55.	0.6	4
486	Adaptor Protein ShcD/SHC4 Interacts with Tie2 Receptor to Synergistically Promote Glioma Cell Invasion. <i>Molecular Cancer Research</i> , 2021, 19, 757-770.	1.5	6
487	Discovery of Functional Alternatively Spliced PKM Transcripts in Human Cancers. <i>Cancers</i> , 2021, 13, 348.	1.7	8
488	Identification of hsa_circ_0002024 as a prognostic competing endogenous RNA (ceRNA) through the hsa_miR_129-5p/Anti-Silencing Function 1B Histone Chaperone (ASF1B) axis in renal cell carcinoma. <i>Bioengineered</i> , 2021, 12, 6579-6593.	1.4	8

#	ARTICLE	IF	CITATIONS
489	Novel insights into clear cell renal cell carcinoma prognosis by comprehensive characterization of aberrant alternative splicing signature: a study based on large-scale sequencing data. <i>Bioengineered</i> , 2021, 12, 1091-1110.	1.4	3
490	DIMEimmune: Robust estimation of infiltrating lymphocytes in CNS tumors from DNA methylation profiles. <i>OncImmunity</i> , 2021, 10, 1932365.	2.1	17
491	Genome-wide CRISPR/Cas9 knockout screening uncovers a novel inflammatory pathway critical for resistance to arginine-deprivation therapy. <i>Theranostics</i> , 2021, 11, 3624-3641.	4.6	11
492	Concurrent depletion of Vps37 proteins evokes ESCRT-I destabilization and profound cellular stress responses. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	12
493	High Expression of RhoBTB3 Predicts Favorable Chemotherapy Outcomes in non-M3 Acute Myeloid Leukemia. <i>Journal of Cancer</i> , 2021, 12, 4229-4239.	1.2	3
494	A Machine Learning Approach to Differentiate Two Specific Breast Cancer Subtypes Using Androgen Receptor Pathway Genes. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382110279.	0.8	5
495	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	2
497	A universal molecular prognostic score for gastrointestinal tumors. <i>Npj Genomic Medicine</i> , 2021, 6, 6.	1.7	6
498	The HIF-1 α antisense long non-coding RNA drives a positive feedback loop of HIF-1 α mediated transactivation and glycolysis. <i>Nature Communications</i> , 2021, 12, 1341.	5.8	91
500	m ⁶ A modification patterns and tumor immune landscape in clear cell renal carcinoma. , 2021, 9, e001646.		42
501	Developing Tumor Radiosensitivity Signatures Using LncRNAs. <i>Radiation Research</i> , 2021, 195, 324-333.	0.7	10
502	Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. <i>Nature Communications</i> , 2021, 12, 734.	5.8	26
503	circ ⁰⁰⁰⁰²¹² promotes cell proliferation of colorectal cancer by sponging miR ⁴⁹¹ and modulating FOXP4 expression. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	10
504	Computational Techniques and Tools for Omics Data Analysis: State-of-the-Art, Challenges, and Future Directions. <i>Archives of Computational Methods in Engineering</i> , 2021, 28, 4595-4631.	6.0	33
505	Identification of Potential Driver Genes Based on Multi-Genomic Data in Cervical Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 598304.	1.1	15
507	Long Non-Coding RNA Landscape in Prostate Cancer Molecular Subtypes: A Feature Selection Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2227.	1.8	2
508	Type 2 Innate Lymphoid Cells Protect against Colorectal Cancer Progression and Predict Improved Patient Survival. <i>Cancers</i> , 2021, 13, 559.	1.7	31
509	Patient-Specific Network for Personalized Breast Cancer Therapy with Multi-Omics Data. <i>Entropy</i> , 2021, 23, 225.	1.1	5

#	ARTICLE	IF	CITATIONS
510	Comprehensive Analysis of the Immune and Prognostic Implication of COL6A6 in Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 633420.	1.3	6
511	Eukaryotic Translation Initiation Factor 4A1: A Potential Novel Target in Neuroblastoma. <i>Cells</i> , 2021, 10, 301.	1.8	10
512	Genetic alterations associated with 18F-fluorodeoxyglucose positron emission tomography/computed tomography in head and neck squamous cell carcinoma. <i>Translational Oncology</i> , 2021, 14, 100988.	1.7	4
513	Facilitating Drug Discovery in Breast Cancer by Virtually Screening Patients Using In Vitro Drug Response Modeling. <i>Cancers</i> , 2021, 13, 885.	1.7	6
514	A Histone Acetylation Modulator Gene Signature for Classification and Prognosis of Breast Cancer. <i>Current Oncology</i> , 2021, 28, 928-939.	0.9	5
516	Effect of the p53 P72R Polymorphism on Mutant TP53 Allele Selection in Human Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1246-1257.	3.0	16
517	Effects of the Novel PFKFB3 Inhibitor KAN0438757 on Colorectal Cancer Cells and Its Systemic Toxicity Evaluation In Vivo. <i>Cancers</i> , 2021, 13, 1011.	1.7	22
518	Comprehensive Profiling of Genomic and Transcriptomic Differences between Risk Groups of Lung Adenocarcinoma and Lung Squamous Cell Carcinoma. <i>Journal of Personalized Medicine</i> , 2021, 11, 154.	1.1	23
520	Exploring the mechanism of aidi injection for lung cancer by network pharmacology approach and molecular docking validation. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
521	Prediction of Lymph-Node Metastasis in Cancers Using Differentially Expressed mRNA and Non-coding RNA Signatures. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 605977.	1.8	5
522	Potential Molecular Mechanism of TNF Superfamily-Related Genes in Glioblastoma Multiforme Based on Transcriptome and Epigenome. <i>Frontiers in Neurology</i> , 2021, 12, 576382.	1.1	6
523	Inferring perturbation profiles of cancer samples. <i>Bioinformatics</i> , 2021, 37, 2441-2449.	1.8	1
524	Long Non-coding RNA Expression Patterns in Stomach Adenocarcinoma Serve as an Indicator of Tumor Mutation Burden and Are Associated With Tumor-Infiltrating Lymphocytes and Microsatellite Instability. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 618313.	1.8	6
525	Construction of the optimization prognostic model based on differentially expressed immune genes of lung adenocarcinoma. <i>BMC Cancer</i> , 2021, 21, 213.	1.1	9
526	Computational Tumor Infiltration Phenotypes Enable the Spatial and Genomic Analysis of Immune Infiltration in Colorectal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 552331.	1.3	4
527	RNA-Associated Co-expression Network Identifies Novel Biomarkers for Digestive System Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 659788.	1.1	7
528	Non-Metabolic Functions of PKM2 Contribute to Cervical Cancer Cell Proliferation Induced by the HPV16 E7 Oncoprotein. <i>Viruses</i> , 2021, 13, 433.	1.5	8
530	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	7.7	189

#	ARTICLE	IF	CITATIONS
531	Investigation of the putative role of antisense transcripts as regulators of sense transcripts by correlation analysis of sense-antisense pairs in colorectal cancers. <i>FASEB Journal</i> , 2021, 35, e21482.	0.2	3
532	Fibrinogen in the glioblastoma microenvironment contributes to the invasiveness of brain tumor-initiating cells. <i>Brain Pathology</i> , 2021, 31, e12947.	2.1	16
533	TSPAN1, TMPRSS4, SDR16C5, and CTSE as Novel Panel for Pancreatic Cancer: A Bioinformatics Analysis and Experiments Validation. <i>Frontiers in Immunology</i> , 2021, 12, 649551.	2.2	15
534	Effect of NCOR1 Mutations on Immune Microenvironment and Efficacy of Immune Checkpoint Inhibitors in Patient with Bladder Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 630773.	2.2	22
535	Molecular Characteristics, Prognostic Value, and Immune Characteristics of m6A Regulators Identified in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 629718.	1.3	9
536	The influence of lncRNAs on the prognosis of prostate cancer based on TCGA database. <i>Translational Andrology and Urology</i> , 2021, 10, 1302-1313.	0.6	5
537	ETV4 plays a role on the primary events during the adenoma-adenocarcinoma progression in colorectal cancer. <i>BMC Cancer</i> , 2021, 21, 207.	1.1	10
538	RNA splicing and aggregate gene expression differences in lung squamous cell carcinoma between patients of West African and European ancestry. <i>Lung Cancer</i> , 2021, 153, 90-98.	0.9	6
539	Triple negative aggressive phenotype controlled by miR-135b and miR-365: new theranostics candidates. <i>Scientific Reports</i> , 2021, 11, 6553.	1.6	9
540	SPINK7 expression changes accompanied by HER2, P53 and RB1 can be relevant in predicting oral squamous cell carcinoma at a molecular level. <i>Scientific Reports</i> , 2021, 11, 6939.	1.6	7
541	GASC1 promotes hepatocellular carcinoma progression by inhibiting the degradation of ROCK2. <i>Cell Death and Disease</i> , 2021, 12, 253.	2.7	6
543	Identification of Breast Cancer Subtype-Specific Biomarkers by Integrating Copy Number Alterations and Gene Expression Profiles. <i>Medicina (Lithuania)</i> , 2021, 57, 261.	0.8	8
544	A Detailed Catalogue of Multi-Omics Methodologies for Identification of Putative Biomarkers and Causal Molecular Networks in Translational Cancer Research. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2822.	1.8	8
548	An Information Theoretical Multilayer Network Approach to Breast Cancer Transcriptional Regulation. <i>Frontiers in Genetics</i> , 2021, 12, 617512.	1.1	6
549	RNA Modification of N6-Methyladenosine Predicts Immune Phenotypes and Therapeutic Opportunities in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 642159.	1.3	30
550	Heterogeneity of glial progenitor cells during the neurogenesis-to-gliogenesis switch in the developing human cerebral cortex. <i>Cell Reports</i> , 2021, 34, 108788.	2.9	55
552	Pan-Cancer Analysis of Human Kinome Gene Expression and Promoter DNA Methylation Identifies Dark Kinase Biomarkers in Multiple Cancers. <i>Cancers</i> , 2021, 13, 1189.	1.7	16
554	Clinical significance of CD34+CD117dim/CD34+CD117bri myeloblast-associated gene expression in t(8;21) acute myeloid leukemia. <i>Frontiers of Medicine</i> , 2021, 15, 608-620.	1.5	13

#	ARTICLE	IF	CITATIONS
555	Molecular Signatures of Chromosomal Instability Correlate With Copy Number Variation Patterns and Patient Outcome in IDH-Mutant and IDH-Wildtype Astrocytomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021, 80, 354-365.	0.9	12
556	Identification of 4 immune cells and a 5-lncRNA risk signature with prognosis for early-stage lung adenocarcinoma. <i>Journal of Translational Medicine</i> , 2021, 19, 127.	1.8	26
557	Plasma cell marker, immunoglobulin J polypeptide, predicts early disease-specific mortality in HPV+ HNSCC. , 2021, 9, e001259.		9
558	Comprehensive Analysis of Correlations in the Expression of miRNA Genes and Immune Checkpoint Genes in Bladder Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2553.	1.8	3
559	High expression of MMP28 indicates unfavorable prognosis in pancreatic cancer. <i>Medicine (United Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.4	0
560	DNA-methylation for the detection and distinction of 19 human malignancies. <i>Epigenetics</i> , 2022, 17, 191-201.	1.3	7
562	High BLM Expression Predicts Poor Clinical Outcome and Contributes to Malignant Progression in Human Cholangiocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 633899.	1.3	8
563	Model-based feature selection and clustering of RNA-seq data for unsupervised subtype discovery. <i>Annals of Applied Statistics</i> , 2021, 15, 481-508.	0.5	6
565	PRKCA Overexpression Is Frequent in Young Oral Tongue Squamous Cell Carcinoma Patients and Is Associated with Poor Prognosis. <i>Cancers</i> , 2021, 13, 2082.	1.7	8
566	An R package for divergence analysis of omics data. <i>PLoS ONE</i> , 2021, 16, e0249002.	1.1	2
567	Screening and identification of haptoglobin showing its important role in pathophysiological process of gallbladder carcinoma. <i>Gene</i> , 2021, 776, 145429.	1.0	2
569	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
570	Significance of Alpha-inhibin Expression in Pheochromocytomas and Paragangliomas. <i>American Journal of Surgical Pathology</i> , 2021, 45, 1264-1273.	2.1	19
572	Epigenomic landscape of human colorectal cancer unveils an aberrant core of pan-cancer enhancers orchestrated by YAP/TAZ. <i>Nature Communications</i> , 2021, 12, 2340.	5.8	43
573	Identifying prognostic markers for multiple myeloma through integration and analysis of MMRF-CoMMpass data. <i>Journal of Computational Science</i> , 2021, 51, 101346.	1.5	6
574	Genomic Analysis of Glioblastoma Multiforme Reveals a Key Transcription Factor Signature Relevant to Prognosis and the Immune Processes. <i>Frontiers in Oncology</i> , 2021, 11, 657531.	1.3	6
575	Machine learning-based investigation of the cancer protein secretory pathway. <i>PLoS Computational Biology</i> , 2021, 17, e1008898.	1.5	7
576	Score tests for scale effects, with application toÂgenomic analysis. <i>Statistics in Medicine</i> , 2021, 40, 3808-3822.	0.8	0

#	ARTICLE	IF	CITATIONS
577	Utility of a metabolic-associated nomogram to predict the recurrence-free survival of stage I cervical cancer. <i>Future Oncology</i> , 2021, 17, 1325-1337.	1.1	3
578	Identification of transcriptional subtypes in lung adenocarcinoma and squamous cell carcinoma through integrative analysis of microarray and RNA sequencing data. <i>Scientific Reports</i> , 2021, 11, 8709.	1.6	8
579	Integrative genome-scale analysis of immune infiltration in esophageal carcinoma. <i>International Immunopharmacology</i> , 2021, 93, 107371.	1.7	4
580	Multiregional Sequencing of IDH-WT Glioblastoma Reveals High Genetic Heterogeneity and a Dynamic Evolutionary History. <i>Cancers</i> , 2021, 13, 2044.	1.7	5
581	The Quandary of DNA-Based Treatment Assessment in De Novo Metastatic Prostate Cancer in the Era of Precision Oncology. <i>Journal of Personalized Medicine</i> , 2021, 11, 330.	1.1	1
582	Performance Comparison of Deep Learning Autoencoders for Cancer Subtype Detection Using Multi-Omics Data. <i>Cancers</i> , 2021, 13, 2013.	1.7	31
583	Molecular Characterization of Low-Grade IDH-Wildtype Astrocytomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021, 80, 431-435.	0.9	12
585	Systematic Investigation of DNA Methylation Associated With Platinum Chemotherapy Resistance Across 13 Cancer Types. <i>Frontiers in Pharmacology</i> , 2021, 12, 616529.	1.6	4
586	MMRFBiolinks: an R-package for integrating and analyzing MMRF-CoMMpass data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5
588	Prognostic significance of genome-wide DNA methylation profiles within the randomized, phase 3, EORTC CATNON trial on non-1p/19q deleted anaplastic glioma. <i>Neuro-Oncology</i> , 2021, 23, 1547-1559.	0.6	34
589	Controlling for cellular heterogeneity using single-cell deconvolution of gene expression reveals novel markers of colorectal tumors exhibiting microsatellite instability. <i>Oncotarget</i> , 2021, 12, 767-782.	0.8	5
590	AMBRA1 regulates cyclin D to guard S-phase entry and genomic integrity. <i>Nature</i> , 2021, 592, 799-803.	13.7	78
591	Screening of immunosuppressive cells from colorectal adenocarcinoma and identification of prognostic markers. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
593	An integrative analysis of the age-associated multi-omic landscape across cancers. <i>Nature Communications</i> , 2021, 12, 2345.	5.8	54
594	Epigenetic reprogramming of tumor cellâ€intrinsic STING function sculpts antigenicity and T cell recognition of melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	78
595	Cancer LncRNA Census 2 (CLC2): an enhanced resource reveals clinical features of cancer lncRNAs. <i>NAR Cancer</i> , 2021, 3, zcab013.	1.6	21
596	mi-IsoNet: systems-scale microRNA landscape reveals rampant isoform-mediated gain of target interaction diversity and signaling specificity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
598	Potential Impact of ALKBH5 and YTHDF1 on Tumor Immunity in Colon Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 670490.	1.3	20

#	ARTICLE	IF	CITATIONS
599	Identification of a methylomics-associated nomogram for predicting overall survival of stage I-II lung adenocarcinoma. <i>Scientific Reports</i> , 2021, 11, 9938.	1.6	2
600	ZBP1 not RIPK1 mediates tumor necroptosis in breast cancer. <i>Nature Communications</i> , 2021, 12, 2666.	5.8	74
601	Genes and pathways monotonically dysregulated during progression from normal through leukoplakia to gingivo-buccal oral cancer. <i>Npj Genomic Medicine</i> , 2021, 6, 32.	1.7	18
603	Locus-Specific Characterization of Human Endogenous Retrovirus Expression in Prostate, Breast, and Colon Cancers. <i>Cancer Research</i> , 2021, 81, 3449-3460.	0.4	20
604	Differentiation-related zinc finger protein 750 suppresses cell growth in esophageal squamous cell carcinoma. <i>Oncology Letters</i> , 2021, 22, 513.	0.8	2
605	Evaluation of a Three-Marker Panel for the Detection of Uveal Melanoma Metastases: A Single-Center Retrospective Analysis. <i>Cancers</i> , 2021, 13, 2464.	1.7	3
606	Multimiomics characteristics of neurogenesis-related gene are dysregulated in tumor immune microenvironment. <i>Npj Genomic Medicine</i> , 2021, 6, 37.	1.7	7
607	Long non-coding RNAs and their targets as potential biomarkers in breast cancer. <i>IET Systems Biology</i> , 2021, 15, 137-147.	0.8	3
608	DNA methylation signatures associated with prognosis of gastric cancer. <i>BMC Cancer</i> , 2021, 21, 610.	1.1	9
609	A systematic dissection of the epigenomic heterogeneity of lung adenocarcinoma reveals two different subclasses with distinct prognosis and core regulatory networks. <i>Genome Biology</i> , 2021, 22, 156.	3.8	17
612	Ferroptosis-related gene signature predicts prognosis and immunotherapy in glioma. <i>CNS Neuroscience and Therapeutics</i> , 2021, 27, 973-986.	1.9	55
613	Identification of the EMT-Related Genes Signature for Predicting Occurrence and Progression in Thyroid Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3119-3131.	1.0	5
614	Crinet: A computational tool to infer genome-wide competing endogenous RNA (ceRNA) interactions. <i>PLoS ONE</i> , 2021, 16, e0251399.	1.1	5
615	Association Between FSIP2 Mutation and an Improved Efficacy of Immune Checkpoint Inhibitors in Patients With Skin Cutaneous Melanoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 629330.	1.6	3
616	The Role of the Meiotic Component in Reproduction of B-RAF-Mutated Melanoma: A Review and Brainstorming Session. , 0, , .		2
617	Molecular Characterization and Clinical Relevance of Lysine Acetylation Regulators in Urological Cancers. <i>Frontiers in Oncology</i> , 2021, 11, 647221.	1.3	0
619	DNA Methylation Signatures and the Contribution of Age-Associated Methylomic Drift to Carcinogenesis in Early-Onset Colorectal Cancer. <i>Cancers</i> , 2021, 13, 2589.	1.7	18
620	Multi-omic profiling of lung and liver tumor microenvironments of metastatic pancreatic cancer reveals site-specific immune regulatory pathways. <i>Genome Biology</i> , 2021, 22, 154.	3.8	30

#	ARTICLE	IF	CITATIONS
622	Dickkopf-1: A Promising Target for Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 658097.	2.2	37
623	Integrated genomics and comprehensive validation reveal drivers of genomic evolution in esophageal adenocarcinoma. <i>Communications Biology</i> , 2021, 4, 617.	2.0	7
626	Identification of autophagy-related genes signature predicts chemotherapeutic and immunotherapeutic efficiency in bladder cancer (BLCA). <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 5417-5433.	1.6	11
627	Differential alternative RNA splicing and transcription events between tumors from African American and White patients in The Cancer Genome Atlas. <i>Genomics</i> , 2021, 113, 1234-1246.	1.3	10
628	Identification of KIF4A as a pan-cancer diagnostic and prognostic biomarker via bioinformatics analysis and validation in osteosarcoma cell lines. <i>PeerJ</i> , 2021, 9, e11455.	0.9	4
630	African Americans and European Americans exhibit distinct gene expression patterns across tissues and tumors associated with immunologic functions and environmental exposures. <i>Scientific Reports</i> , 2021, 11, 9905.	1.6	15
631	Fenchel duality of Cox partial likelihood with an application in survival kernel learning. <i>Artificial Intelligence in Medicine</i> , 2021, 116, 102077.	3.8	4
632	TENT4A Non-Canonical Poly(A) Polymerase Regulates DNA-Damage Tolerance via Multiple Pathways That Are Mutated in Endometrial Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6957.	1.8	9
633	Identification and Validation of Hub Genes Associated With Hepatocellular Carcinoma Via Integrated Bioinformatics Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 614531.	1.3	9
634	Differential chromatin accessibility landscape of gain-of-function mutant p53 tumours. <i>BMC Cancer</i> , 2021, 21, 669.	1.1	2
635	Genome-Wide Transcriptomic Analysis of Non-Tumorigenic Tissues Reveals Aging-Related Prognostic Markers and Drug Targets in Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 3045.	1.7	10
636	Deletion of Lats1/2 in adult kidney epithelia leads to renal cell carcinoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	12
637	Consensus molecular subtyping of colorectal cancers is influenced by goblet cell content. <i>Cancer Genetics</i> , 2021, 254-255, 34-39.	0.2	5
638	Correlations Between the Characteristics of Alternative Splicing Events, Prognosis, and the Immune Microenvironment in Breast Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 686298.	1.1	3
639	Mammary cell gene expression atlas links epithelial cell remodeling events to breast carcinogenesis. <i>Communications Biology</i> , 2021, 4, 660.	2.0	29
640	Catenin Alpha-2 Mutation Changes the Immune Microenvironment in Lung Adenocarcinoma Patients Receiving Immune Checkpoint Inhibitors. <i>Frontiers in Pharmacology</i> , 2021, 12, 645862.	1.6	7
641	DecoPath: a web application for decoding pathway enrichment analysis. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab087.	1.5	3
642	MOGONET integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification. <i>Nature Communications</i> , 2021, 12, 3445.	5.8	152

#	ARTICLE	IF	CITATIONS
643	DNA methylation regulator-mediated modification patterns and tumor microenvironment characterization in gastric cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 695-710.	2.3	25
644	Genomic and Transcriptome Analysis to Identify the Role of the mTOR Pathway in Kidney Renal Clear Cell Carcinoma and Its Potential Therapeutic Significance. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-28.	1.9	5
645	Alternative splicing perturbation landscape identifies RNA binding proteins as potential therapeutic targets in cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 792-806.	2.3	15
646	Integrated Analysis of Microarray and RNA-Seq Data for the Identification of Hub Genes and Networks Involved in the Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 663787.	1.1	13
647	Tumor Cell-Derived Exosomal miR-770 Inhibits M2 Macrophage Polarization via Targeting MAP3K1 to Inhibit the Invasion of Non-small Cell Lung Cancer Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 679658.	1.8	22
649	Immune infiltration phenotypes of prostate adenocarcinoma and their clinical implications. <i>Cancer Medicine</i> , 2021, 10, 5358-5374.	1.3	3
651	Integrative Transcriptomic Analysis Reveals Distinctive Molecular Traits and Novel Subtypes of Collecting Duct Carcinoma. <i>Cancers</i> , 2021, 13, 2903.	1.7	7
652	Comprehensive Analysis of the Immune Infiltrates and PD-L1 of m6A RNA Methylation Regulators in Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 681745.	1.8	11
653	The efficacy of anti-EGFR therapy in treating metastatic colorectal cancer differs between the middle/low rectum and the left-sided colon. <i>British Journal of Cancer</i> , 2021, 125, 816-825.	2.9	7
654	ZNRF3 and RNF43 cooperate to safeguard metabolic liver zonation and hepatocyte proliferation. <i>Cell Stem Cell</i> , 2021, 28, 1822-1837.e10.	5.2	42
655	Integrin $\alpha 7$ Inhibits Colorectal Cancer Pathogenesis via Maintaining Antitumor Immunity. <i>Cancer Immunology Research</i> , 2021, 9, 967-980.	1.6	11
656	Lung adenocarcinoma and lung squamous cell carcinoma cancer classification, biomarker identification, and gene expression analysis using overlapping feature selection methods. <i>Scientific Reports</i> , 2021, 11, 13323.	1.6	60
657	Identification of Tumor Microenvironment-Related Prognostic Biomarkers for Ovarian Serous Cancer 3-Year Mortality Using Targeted Maximum Likelihood Estimation: A TCGA Data Mining Study. <i>Frontiers in Genetics</i> , 2021, 12, 625145.	1.1	2
658	DNA Methylation Markers from Negative Surgical Margins Can Predict Recurrence of Oral Squamous Cell Carcinoma. <i>Cancers</i> , 2021, 13, 2915.	1.7	11
659	YB1 regulates miR-205/200b-ZEB1 axis by inhibiting microRNA maturation in hepatocellular carcinoma. <i>Cancer Communications</i> , 2021, 41, 576-595.	3.7	18
660	Tumors exploit FTO-mediated regulation of glycolytic metabolism to evade immune surveillance. <i>Cell Metabolism</i> , 2021, 33, 1221-1233.e11.	7.2	138
661	Association of Circadian Clock Gene Expression with Glioma Tumor Microenvironment and Patient Survival. <i>Cancers</i> , 2021, 13, 2756.	1.7	9
662	miR-361-5p as a promising qRT-PCR internal control for tumor and normal breast tissues. <i>PLoS ONE</i> , 2021, 16, e0253009.	1.1	4

#	ARTICLE	IF	CITATIONS
663	Impact of Neoantigen Expression and T-Cell Activation on Breast Cancer Survival. <i>Cancers</i> , 2021, 13, 2879.	1.7	8
664	A prognostic nomogram based on competing endogenous RNA network for clearâ€cell renal cell carcinoma. <i>Cancer Medicine</i> , 2021, 10, 5499-5512.	1.3	2
665	YAP inactivation in estrogen receptor alpha-positive hepatocellular carcinoma with less aggressive behavior. <i>Experimental and Molecular Medicine</i> , 2021, 53, 1055-1067.	3.2	6
666	HER2-Low Breast Cancer: Molecular Characteristics and Prognosis. <i>Cancers</i> , 2021, 13, 2824.	1.7	117
667	Identification of Early Diagnostic and Prognostic Biomarkers via WGCNA in Stomach Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 636461.	1.3	23
668	Adrenocortical Carcinoma Steroid Profiles: In Silico Pan-Cancer Analysis of TCGA Data Uncovers Immunotherapy Targets for Potential Improved Outcomes. <i>Frontiers in Endocrinology</i> , 2021, 12, 672319.	1.5	6
669	Transcriptome profiling by combined machine learning and statistical R analysis identifies TMEM236 as a potential novel diagnostic biomarker for colorectal cancer. <i>Scientific Reports</i> , 2021, 11, 14304.	1.6	22
670	Identification and Confirmation of the miR-30 Family as a Potential Central Player in Tobacco-Related Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 616372.	1.3	5
671	Integrated multiâ€omics profiling of highâ€grade estrogen receptorâ€positive, HER2â€negative breast cancer. <i>Molecular Oncology</i> , 2022, 16, 2413-2431.	2.1	3
672	DNA methylation association with stage progression of head and neck squamous cell carcinoma. <i>Computers in Biology and Medicine</i> , 2021, 134, 104473.	3.9	6
673	Predictive Immune-Checkpoint Blockade Classifiers Identify Tumors Responding to Inhibition of PD-1 and/or CTLA-4. <i>Clinical Cancer Research</i> , 2021, 27, 5389-5400.	3.2	3
674	Pan-Cancer Survey of Tumor Mass Dormancy and Underlying Mutational Processes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 698659.	1.8	3
675	Identification of CXCL10-Relevant Tumor Microenvironment Characterization and Clinical Outcome in Ovarian Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 678747.	1.1	5
676	Regulatory landscapes of specific miRNAs are conserved between cell lines and primary tumors. <i>F1000Research</i> , 0, 10, 633.	0.8	0
677	Ten-gene signature reveals the significance of clinical prognosis and immuno-correlation of osteosarcoma and study on novel skeleton inhibitors regarding MMP9. <i>Cancer Cell International</i> , 2021, 21, 377.	1.8	19
678	DNA Damage Repair Status Predicts Opposite Clinical Prognosis Immunotherapy and Non-Immunotherapy in Hepatocellular Carcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 676922.	2.2	15
679	Prognosis of Non-small-cell Lung Cancer Patients With Lipid Metabolism Pathway Alternations to Immunotherapy. <i>Frontiers in Genetics</i> , 2021, 12, 646362.	1.1	9
680	Exploring the Mechanism of <i>Scutellaria baicalensis</i> Georgi Efficacy against Oral Squamous Cell Carcinoma Based on Network Pharmacology and Molecular Docking Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	4

#	ARTICLE	IF	CITATIONS
682	A High Epigenetic Risk Score Shapes the Non-Inflamed Tumor Microenvironment in Breast Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 675198.	1.6	1
683	Systematic identification of novel cancer genes through analysis of deep shRNA perturbation screens. <i>Nucleic Acids Research</i> , 2021, 49, 8488-8504.	6.5	4
684	Analysis of Interleukin-1 Signaling Alterations of Colon Adenocarcinoma Identified Implications for Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 665002.	2.2	1
686	A pan-cancer transcriptomic study showing tumor specific alterations in central metabolism. <i>Scientific Reports</i> , 2021, 11, 13637.	1.6	11
687	Transcriptomic signatures of tumors undergoing T cell attack. <i>Cancer Immunology, Immunotherapy</i> , 2021, , 1.	2.0	6
688	oncoPredict: an R package for predicting <i>in vivo</i> or cancer patient drug response and biomarkers from cell line screening data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	492
689	Radiomic profiling of clear cell renal cell carcinoma reveals subtypes with distinct prognoses and molecular pathways. <i>Translational Oncology</i> , 2021, 14, 101078.	1.7	6
690	Stratification of patients with clear cell renal cell carcinoma to facilitate drug repositioning. <i>IScience</i> , 2021, 24, 102722.	1.9	8
691	Therapeutic potential of the human endogenous retroviral envelope protein HEMO: a pan-cancer analysis. <i>Molecular Oncology</i> , 2021, , .	2.1	7
692	Metabolic landscapes in sarcomas. <i>Journal of Hematology and Oncology</i> , 2021, 14, 114.	6.9	10
693	Reprogramming of bivalent chromatin states in NRAS mutant melanoma suggests PRC2 inhibition as a therapeutic strategy. <i>Cell Reports</i> , 2021, 36, 109410.	2.9	17
694	3D heterospecies spheroids of pancreatic stroma and cancer cells demonstrate key phenotypes of pancreatic ductal adenocarcinoma. <i>Translational Oncology</i> , 2021, 14, 101107.	1.7	8
695	PLEKHA8P1 Promotes Tumor Progression and Indicates Poor Prognosis of Liver Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7614.	1.8	7
696	SCISSOR _{sc} : a single-cell inferred site-specific omics resource for tumor microenvironment association study. <i>NAR Cancer</i> , 2021, 3, zcab037.	1.6	1
697	NR5A2 Is One of 12 Transcription Factors Predicting Prognosis in HNSCC and Regulates Cancer Cell Proliferation in a p53-Dependent Manner. <i>Frontiers in Oncology</i> , 2021, 11, 691318.	1.3	3
698	Transcription factor RFX7 governs a tumor suppressor network in response to p53 and stress. <i>Nucleic Acids Research</i> , 2021, 49, 7437-7456.	6.5	17
699	Development of a Novel Immune Infiltration-Related ceRNA Network and Prognostic Model for Sarcoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 652300.	1.8	2
700	Meta-Analysis of Microdissected Breast Tumors Reveals Genes Regulated in the Stroma but Hidden in Bulk Analysis. <i>Cancers</i> , 2021, 13, 3371.	1.7	9

#	ARTICLE	IF	CITATIONS
701	Plasma Metabolome Profiling Identifies Metabolic Subtypes of Pancreatic Ductal Adenocarcinoma. <i>Cells</i> , 2021, 10, 1821.	1.8	9
702	An N6-Methyladenosine-Related Gene Set Variation Score as a Prognostic Tool for Lung Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 651575.	1.8	8
704	ETV7 regulates breast cancer stem-like cell features by repressing IFN-response genes. <i>Cell Death and Disease</i> , 2021, 12, 742.	2.7	16
706	Identification of Novel RNA Binding Proteins Influencing Circular RNA Expression in Hepatocellular Carcinoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7477.	1.8	5
707	Construction of Immune-Associated Nomogram for Predicting the Recurrence Survival Risk of Stage I Cervical Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	0
708	iRGvalid: A Robust in silico Method for Optimal Reference Gene Validation. <i>Frontiers in Genetics</i> , 2021, 12, 716653.	1.1	0
709	Interpretable, Scalable, and Transferrable Functional Projection of Large-Scale Transcriptome Data Using Constrained Matrix Decomposition. <i>Frontiers in Genetics</i> , 2021, 12, 719099.	1.1	2
710	An immune-related prognostic signature for thyroid carcinoma to predict survival and response to immune checkpoint inhibitors. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 747-759.	2.0	8
712	Tumor microenvironment evaluation promotes precise checkpoint immunotherapy of advanced gastric cancer. , 2021, 9, e002467.		97
713	Prediction and interpretation of cancer survival using graph convolution neural networks. <i>Methods</i> , 2021, 192, 120-130.	1.9	29
714	Predicting and characterizing a cancer dependency map of tumors with deep learning. <i>Science Advances</i> , 2021, 7, .	4.7	29
715	iGlioSub: an integrative transcriptomic and epigenomic classifier for glioblastoma molecular subtypes. <i>BioData Mining</i> , 2021, 14, 42.	2.2	7
716	XOMiVAE: an interpretable deep learning model for cancer classification using high-dimensional omics data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	37
717	Prediction of the mechanism of miRNAs in laryngeal squamous cell carcinoma based on the miRNA-mRNA regulatory network. <i>PeerJ</i> , 2021, 9, e12075.	0.9	1
718	The Identification of the Metabolism Subtypes of Skin Cutaneous Melanoma Associated With the Tumor Microenvironment and the Immunotherapy. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 707677.	1.8	9
719	Large contribution of copy number alterations in early stage of Papillary Thyroid Carcinoma. <i>Computers in Biology and Medicine</i> , 2021, 135, 104584.	3.9	3
720	Transcriptional Reprogramming and Constitutive PD-L1 Expression in Melanoma Are Associated with Dedifferentiation and Activation of Interferon and Tumour Necrosis Factor Signalling Pathways. <i>Cancers</i> , 2021, 13, 4250.	1.7	9
721	Scoring System Based on RNA Modification Writer-Related Genes to Predict Overall Survival and Therapeutic Response in Bladder Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 724541.	2.2	3

#	ARTICLE	IF	CITATIONS
722	Integrated pan-cancer of <i>AURKA</i> expression and drug sensitivity analysis reveals increased expression of <i>AURKA</i> is responsible for drug resistance. <i>Cancer Medicine</i> , 2021, 10, 6428-6441.	1.3	15
723	Synthetic Evaluation of MicroRNA-1-3p Expression in Head and Neck Squamous Cell Carcinoma Based on Microarray Chips and MicroRNA Sequencing. <i>BioMed Research International</i> , 2021, 2021, 1-24.	0.9	2
724	Modeling the effects of EMT-immune dynamics on carcinoma disease progression. <i>Communications Biology</i> , 2021, 4, 983.	2.0	3
725	Joint Modeling of RNAseq and Radiomics Data for Glioma Molecular Characterization and Prediction. <i>Frontiers in Medicine</i> , 2021, 8, 705071.	1.2	3
726	A stacking ensemble deep learning approach to cancer type classification based on TCGA data. <i>Scientific Reports</i> , 2021, 11, 15626.	1.6	62
727	Essential amino acid metabolism-related molecular classification in triple-negative breast cancer. <i>Epigenomics</i> , 2021, 13, 1247-1268.	1.0	3
728	Transcriptomics based multi-dimensional characterization and drug screen in esophageal squamous cell carcinoma. <i>EBioMedicine</i> , 2021, 70, 103510.	2.7	22
729	The Ratio of Exhausted to Resident Infiltrating Lymphocytes Is Prognostic for Colorectal Cancer Patient Outcome. <i>Cancer Immunology Research</i> , 2021, 9, 1125-1140.	1.6	18
731	N6-Methyladenosine Writer Gene ZC3H13 Predicts Immune Phenotype and Therapeutic Opportunities in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 718644.	1.3	15
732	Relevant and Non-Redundant Feature Selection for Cancer Classification and Subtype Detection. <i>Cancers</i> , 2021, 13, 4297.	1.7	8
733	Transfer learning between preclinical models and human tumors identifies a conserved NK cell activation signature in anti-CTLA-4 responsive tumors. <i>Genome Medicine</i> , 2021, 13, 129.	3.6	17
734	RNA N6-Methyladenosine Patterns in Hepatocellular Carcinoma Reveal a Distinct Immune Infiltration Landscape and Clinical Significance. <i>Medical Science Monitor</i> , 2021, 27, e930994.	0.5	4
735	Multi-layered proteogenomic analysis unravels cancer metastasis directed by MMP-2 and focal adhesion kinase signaling. <i>Scientific Reports</i> , 2021, 11, 17130.	1.6	14
736	A merged microarray meta-dataset for transcriptionally profiling colorectal neoplasm formation and progression. <i>Scientific Data</i> , 2021, 8, 214.	2.4	4
737	Sequential inverse dysregulation of the RNA helicases DDX3X and DDX3Y facilitates MYC-driven lymphomagenesis. <i>Molecular Cell</i> , 2021, 81, 4059-4075.e11.	4.5	42
739	USP12 downregulation orchestrates a protumorigenic microenvironment and enhances lung tumour resistance to PD-1 blockade. <i>Nature Communications</i> , 2021, 12, 4852.	5.8	18
740	Human T cells engineered with a leukemia lipid-specific TCR enables donor-unrestricted recognition of CD1c-expressing leukemia. <i>Nature Communications</i> , 2021, 12, 4844.	5.8	3
741	Beta-adrenergic pathway activation enhances aggressiveness and inhibits stemness in head and neck cancer. <i>Translational Oncology</i> , 2021, 14, 101117.	1.7	9

#	ARTICLE	IF	CITATIONS
742	A systematic comparison of data- and knowledge-driven approaches to disease subtype discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
743	Transcriptional overlap links DNA hypomethylation with DNA hypermethylation at adjacent promoters in cancer. <i>Scientific Reports</i> , 2021, 11, 17346.	1.6	8
744	Potential drugs against COVID-19 revealed by gene expression profile, molecular docking and molecular dynamic simulation. <i>Future Virology</i> , 2021, 16, 527-542.	0.9	5
745	Transcriptional control of brain tumor stem cells by a carbohydrate binding protein. <i>Cell Reports</i> , 2021, 36, 109647.	2.9	18
746	A New Survival Model Based on ADAMTSs for Prognostic Prediction in Clear Cell Renal Cell Carcinoma. <i>Journal of Oncology</i> , 2021, 2021, 1-10.	0.6	3
747	Analysis of MicroRNA Expression Changes During the Course of Therapy In Rectal Cancer Patients. <i>Frontiers in Oncology</i> , 2021, 11, 702258.	1.3	11
748	Identification of Iron Metabolism-Related Genes as Prognostic Indicators for Lower-Grade Glioma. <i>Frontiers in Oncology</i> , 2021, 11, 729103.	1.3	18
750	Developmental chromatin programs determine oncogenic competence in melanoma. <i>Science</i> , 2021, 373, eabc1048.	6.0	80
752	Uncovering the Association Between m5C Regulator-Mediated Methylation Modification Patterns and Tumour Microenvironment Infiltration Characteristics in Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 727935.	1.8	15
753	A Metabolic-associated Nomogram Predicts Recurrence Survival of Thyroid Cancer. <i>Current Medical Science</i> , 2021, 41, 1004-1011.	0.7	0
754	Novel insights into the molecular mechanisms underlying risk of colorectal cancer from smoking and red/processed meat carcinogens by modeling exposure in normal colon organoids. <i>Oncotarget</i> , 2021, 12, 1863-1877.	0.8	5
755	Classification of Estrogen Receptor-Positive Breast Cancer Based on Immunogenomic Profiling and Validation at Single-Cell Resolution. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 722841.	1.8	0
756	SOCS3 is Related to Cell Proliferation in Neuronal Tissue: An Integrated Analysis of Bioinformatics and Experiments. <i>Frontiers in Genetics</i> , 2021, 12, 743786.	1.1	6
757	miRNome Profiling Reveals Shared Features in Breast Cancer Subtypes and Highlights miRNAs That Potentially Regulate MYB and EZH2 Expression. <i>Frontiers in Oncology</i> , 2021, 11, 710919.	1.3	1
758	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer. <i>Molecular Oncology</i> , 2021, 15, 3348-3362.	2.1	3
759	CdGAP promotes prostate cancer metastasis by regulating epithelial-to-mesenchymal transition, cell cycle progression, and apoptosis. <i>Communications Biology</i> , 2021, 4, 1042.	2.0	9
760	Targeting Tumorâ€™Stromal IL6/STAT3 Signaling through IL1 Receptor Inhibition in Pancreatic Cancer. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 2280-2290.	1.9	23
761	Diagnostic and Prognostic Potential of MiR-379/656 MicroRNA Cluster in Molecular Subtypes of Breast Cancer. <i>Journal of Clinical Medicine</i> , 2021, 10, 4071.	1.0	3

#	ARTICLE	IF	CITATIONS
762	Data analysis of high-throughput sequencing and microarray to identify key signatures of microribonucleic acids in glioblastoma. <i>IssledovaniĀ I Praktika V Medicine</i> , 2021, 8, 21-33.	0.1	1
763	The Landscape of Immune Cells Indicates Prognosis and Applicability of Checkpoint Therapy in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 744951.	1.3	9
764	A New Survival Model Based on Cholesterol Biosynthesis-Related Genes for Prognostic Prediction in Clear Cell Renal Cell Carcinoma. <i>BioMed Research International</i> , 2021, 2021, 1-15.	0.9	5
765	Comprehensive Analysis of HDAC Family Identifies HDAC1 as a Prognostic and Immune Infiltration Indicator and HDAC1-Related Signature for Prognosis in Glioma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 720020.	1.6	13
766	A Novel Tool for the Risk Assessment and Personalized Chemo-/Immunotherapy Response Prediction of Adenocarcinoma and Squamous Cell Carcinoma Lung Cancer. <i>International Journal of General Medicine</i> , 2021, Volume 14, 5771-5785.	0.8	2
767	Genomic Instability-Related LncRNA Signature Predicts the Prognosis and Highlights LINC01614 Is a Tumor Microenvironment-Related Oncogenic lncRNA of Papillary Thyroid Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 737867.	1.3	8
769	A synthetic lethal screen identifies HDAC4 as a potential target in MELK overexpressing cancers. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
770	A ferroptosis-associated gene signature for the prediction of prognosis and therapeutic response in luminal-type breast carcinoma. <i>Scientific Reports</i> , 2021, 11, 17610.	1.6	4
771	Bioinformatics-guided analysis uncovers TIGIT as an epigenetically regulated immunomodulator affecting immunotherapeutic sensitivity of gastric cancer. <i>Cancer Biomarkers</i> , 2022, 33, 349-358.	0.8	5
772	TNF-Alpha Pathway Alternation Predicts Survival of Immune Checkpoint Inhibitors in Non-Small Cell Lung Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 667875.	2.2	11
773	Single-cell analysis of a tumor-derived exosome signature correlates with prognosis and immunotherapy response. <i>Journal of Translational Medicine</i> , 2021, 19, 381.	1.8	14
774	Damage-Net: A program for DNA repair meta-analysis identifies a network of novel repair genes that facilitate cancer evolution. <i>DNA Repair</i> , 2021, 105, 103158.	1.3	3
775	Characterization of Modification Patterns, Biological Function, Clinical Implication, and Immune Microenvironment Association of m6A Regulators in Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 702072.	1.1	5
776	The expressed mutational landscape of microsatellite stable colorectal cancers. <i>Genome Medicine</i> , 2021, 13, 142.	3.6	4
777	Aberrant DNA Methylation-Mediated FOXF2 Dysregulation Is a Prognostic Risk Factor for Gastric Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 645470.	1.6	5
779	Development of a Toll-Like Receptor-Based Gene Signature That Can Predict Prognosis, Tumor Microenvironment, and Chemotherapy Response for Hepatocellular Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 729789.	1.6	6
780	Identification of colorectal cancer associated biomarkers: an integrated analysis of miRNA expression. <i>Aging</i> , 2021, 13, 21991-22029.	1.4	15
781	Clinicopathological, gene expression and genetic features of stage I lung adenocarcinoma with necrosis. <i>Lung Cancer</i> , 2021, 159, 74-83.	0.9	5

#	ARTICLE	IF	CITATIONS
782	Characterization of hypoxia response patterns identified prognosis and immunotherapy response in bladder cancer. <i>Molecular Therapy - Oncolytics</i> , 2021, 22, 277-293.	2.0	19
783	Effect of mesenchymal-epithelial transition amplification on immune microenvironment and efficacy of immune checkpoint inhibitors in patients with non-small cell lung cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1475-1475.	0.7	3
785	The Effect of Smoking on the Immune Microenvironment and Immunogenicity and Its Relationship With the Prognosis of Immune Checkpoint Inhibitors in Non-small Cell Lung Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 745859.	1.8	14
786	Multiomix: a cloud-based platform to infer cancer genomic and epigenomic events associated with gene expression modulation. <i>Bioinformatics</i> , 2022, 38, 866-868.	1.8	1
787	In Silico Methods for the Identification of Diagnostic and Favorable Prognostic Markers in Acute Myeloid Leukemia. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9601.	1.8	8
788	Therapeutic Effects of Inhibition of Sphingosine-1-Phosphate Signaling in HIF-2 α Inhibitor-Resistant Clear Cell Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 4801.	1.7	6
789	Characterization of gastric cancer stem-like molecular features, immune and pharmacogenomic landscapes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	11
790	Upregulation of the APOBEC3 Family Is Associated with a Poor Prognosis and Influences Treatment Response to Raf Inhibitors in Low Grade Glioma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10390.	1.8	4
792	A molecular taxonomy of tumors independent of tissue-of-origin. <i>IScience</i> , 2021, 24, 103084.	1.9	0
793	Low-dose mono(2-ethylhexyl) phthalate promotes ovarian cancer development through PPAR α -dependent PI3K/Akt/NF- κ B pathway. <i>Science of the Total Environment</i> , 2021, 790, 147990.	3.9	24
795	Steroid receptor RNA activator gene footprint in the progression and drug resistance of colorectal cancer through oxidative phosphorylation pathway. <i>Life Sciences</i> , 2021, 285, 119950.	2.0	8
796	Network-adjusted Kendall's Tau Measure for Feature Screening with Application to High-dimensional Survival Genomic Data. <i>Bioinformatics</i> , 2021, 37, 2150-2156.	1.8	4
797	MiRNA based tumor mutation burden diagnostic and prognostic prediction models for endometrial cancer. <i>Bioengineered</i> , 2021, 12, 3603-3620.	1.4	12
798	DNA Methylation Analysis Identifies Patterns in Progressive Glioma Grades to Predict Patient Survival. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1020.	1.8	17
799	MuSA: a graphical user interface for multi-OMICs data integration in radiogenomic studies. <i>Scientific Reports</i> , 2021, 11, 1550.	1.6	13
800	Typical Tumor Immune Microenvironment Status Determine Prognosis in Lung Adenocarcinoma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
801	MITF reprograms the extracellular matrix and focal adhesion in melanoma. <i>ELife</i> , 2021, 10, .	2.8	45
802	Orthodenticle homeobox OTX1 is a potential prognostic biomarker for bladder cancer. <i>Bioengineered</i> , 2021, 12, 6559-6571.	1.4	13

#	ARTICLE	IF	CITATIONS
803	On the impact of batch effect correction in TCGA isomiR expression data. <i>NAR Cancer</i> , 2021, 3, zcab007.	1.6	11
804	Bringing Structural Implications and Deep Learning-Based Drug Identification for <i>KRAS</i> Mutants. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 571-586.	2.5	19
805	Mutation of the Cell Cycle Regulator p27kip1 Drives Pseudohypoxic Pheochromocytoma Development. <i>Cancers</i> , 2021, 13, 126.	1.7	9
806	Comprehensive molecular profiling to predict clinical outcomes in pancreatic cancer. <i>Therapeutic Advances in Medical Oncology</i> , 2021, 13, 175883592110384.	1.4	10
807	N6-methyladenosine (m6A)-mediated messenger RNA signatures and the tumor immune microenvironment can predict the prognosis of hepatocellular carcinoma. <i>Annals of Translational Medicine</i> , 2021, 9, 59-59.	0.7	29
808	Cofilin-1, LIMK1 and SSH1 are differentially expressed in locally advanced colorectal cancer and according to consensus molecular subtypes. <i>Cancer Cell International</i> , 2021, 21, 69.	1.8	10
809	Short H2A histone variants are expressed in cancer. <i>Nature Communications</i> , 2021, 12, 490.	5.8	29
810	Tryptophan metabolism is inversely regulated in the tumor and blood of patients with glioblastoma. <i>Theranostics</i> , 2021, 11, 9217-9233.	4.6	16
811	MMRF-CoMMpass Data Integration and Analysis for Identifying Prognostic Markers. <i>Lecture Notes in Computer Science</i> , 2020, , 564-571.	1.0	4
812	Classifying Breast Cancer Tissue Through DNA Methylation and Clinical Covariate Based Retrieval. <i>Lecture Notes in Computer Science</i> , 2020, , 82-96.	1.0	2
813	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020, 31, 107628.	2.9	186
840	Breast Cancer Subtype by Imbalanced Omics Data through A Deep Learning Fusion Model. , 2020, , .		4
841	Effects of B cell-activating factor on tumor immunity. <i>JCI Insight</i> , 2020, 5, .	2.3	27
842	Targeting the innate immunoreceptor RIG-I overcomes melanoma-intrinsic resistance to T cell immunotherapy. <i>Journal of Clinical Investigation</i> , 2020, 130, 4266-4281.	3.9	27
843	Alterations in TP53 Are a Potential Biomarker of Bladder Cancer Patients Who Benefit From Immune Checkpoint Inhibition. <i>Cancer Control</i> , 2020, 27, 107327482097666.	0.7	25
844	Molecular Biological Features of Nottingham Histological Grade 3 Breast Cancers. <i>Annals of Surgical Oncology</i> , 2020, 27, 4475-4485.	0.7	34
845	An Individualized Immune Prognostic Index is a Superior Predictor of Survival of Hepatocellular Carcinoma. <i>Medical Science Monitor</i> , 2020, 26, e921786.	0.5	8
846	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. <i>F1000Research</i> , 2017, 6, 1558.	0.8	50

#	ARTICLE	IF	CITATIONS
847	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. F1000Research, 0, 7, 439.	0.8	14
848	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	0.8	12
849	CRI iAtlas: an interactive portal for immuno-oncology research. F1000Research, 2020, 9, 1028.	0.8	39
850	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 0, 5, 1542.	0.8	155
851	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 2016, 5, 1542.	0.8	140
852	Deconvolution of heterogeneous tumor samples using partial reference signals. PLoS Computational Biology, 2020, 16, e1008452.	1.5	7
853	Somatic Mutation Patterns in Hemizygous Genomic Regions Unveil Purifying Selection during Tumor Evolution. PLoS Genetics, 2016, 12, e1006506.	1.5	24
854	Comparative transcriptomes of adenocarcinomas and squamous cell carcinomas reveal molecular similarities that span classical anatomic boundaries. PLoS Genetics, 2017, 13, e1006938.	1.5	46
855	Inhibition of the de novo pyrimidine biosynthesis pathway limits ribosomal RNA transcription causing nucleolar stress in glioblastoma cells. PLoS Genetics, 2020, 16, e1009117.	1.5	38
856	Cancer of Unknown Primary (<scp>CUP</scp>): genetic evidence for a novel nosological entity? A case report. EMBO Molecular Medicine, 2020, 12, e11756.	3.3	10
857	Estradiol and progesterone regulate proliferation and apoptosis in colon cancer. Endocrine Connections, 2019, 8, 217-229.	0.8	28
858	The long non-coding RNA H19 suppresses carcinogenesis and chemoresistance in hepatocellular carcinoma. Cell Stress, 2017, 1, 37-54.	1.4	50
859	A genetic variant in microRNA-146a is associated with sporadic breast cancer in a Southern Brazilian Population. Genetics and Molecular Biology, 2019, 42, e20190278.	0.6	7
860	Î”Np63 promotes IGF1 signalling through IRS1 in squamous cell carcinoma. Aging, 2018, 10, 4224-4240.	1.4	12
861	Alternative splicing events are prognostic in hepatocellular carcinoma. Aging, 2019, 11, 4720-4735.	1.4	43
862	A new survival model based on ferroptosis-related genes for prognostic prediction in clear cell renal cell carcinoma. Aging, 2020, 12, 14933-14948.	1.4	67
863	Identification of subtype-specific genes signature by WGCNA for prognostic prediction in diffuse type gastric cancer. Aging, 2020, 12, 17418-17435.	1.4	6
864	Identification of prognostic chromatin-remodeling genes in clear cell renal cell carcinoma. Aging, 2020, 12, 25614-25642.	1.4	4

#	ARTICLE	IF	CITATIONS
865	A pathways-based prediction model for classifying breast cancer subtypes. <i>Oncotarget</i> , 2017, 8, 58809-58822.	0.8	16
866	FGF5 is expressed in melanoma and enhances malignancy <i>in vitro</i> and <i>in vivo</i> . <i>Oncotarget</i> , 2017, 8, 87750-87762.	0.8	25
867	Genes with mutation significance were highly associated with the clinical pattern of patients with breast cancer. <i>Oncotarget</i> , 2017, 8, 98094-98102.	0.8	2
868	B-CAN: a resource sharing platform to improve the operation, visualization and integrated analysis of TCGA breast cancer data. <i>Oncotarget</i> , 2017, 8, 108778-108785.	0.8	3
869	MicroRNA-19a acts as a prognostic marker and promotes prostate cancer progression via inhibiting VPS37A expression. <i>Oncotarget</i> , 2018, 9, 1931-1943.	0.8	20
870	A common molecular signature of intestinal-type gastric carcinoma indicates processes related to gastric carcinogenesis. <i>Oncotarget</i> , 2018, 9, 7359-7371.	0.8	21
871	NFkB hyperactivation causes invasion of esophageal squamous cell carcinoma with EGFR overexpression and p120-catenin down-regulation. <i>Oncotarget</i> , 2018, 9, 11180-11196.	0.8	14
872	Identification of integrin drug targets for 17 solid tumor types. <i>Oncotarget</i> , 2018, 9, 30146-30162.	0.8	16
873	Schwann cell reprogramming and lung cancer progression: a meta-analysis of transcriptome data. <i>Oncotarget</i> , 2019, 10, 7288-7307.	0.8	15
874	Single-cell RNA-seq reveals the immune escape and drug resistance mechanisms of mantle cell lymphoma. <i>Cancer Biology and Medicine</i> , 2020, 17, 726-739.	1.4	25
875	Sequential Inverse Dysregulation of the RNA Helicases DDX3X and DDX3Y Facilitates MYC-Driven Lymphomagenesis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
876	The PI3K and MAPK/p38 pathways control stress granule assembly in a hierarchical manner. <i>Life Science Alliance</i> , 2019, 2, e201800257.	1.3	49
877	Evaluation of colorectal cancer subtypes and cell lines using deep learning. <i>Life Science Alliance</i> , 2019, 2, e201900517.	1.3	65
878	Integrative module analysis of HCC gene expression landscapes. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 1779-1788.	0.8	20
879	Identifying potential prognostic biomarkers in head and neck cancer based on the analysis of microRNA expression profiles in TCGA database. <i>Molecular Medicine Reports</i> , 2020, 21, 1647-1657.	1.1	5
880	Tripartite motif-containing 14 regulates cell proliferation and apoptosis in cervical cancer via the Akt signaling pathway. <i>Molecular Medicine Reports</i> , 2020, 22, 5145-5154.	1.1	13
881	POPDC3 is a potential biomarker for prognosis and radioresistance in patients with head and neck squamous cell carcinoma. <i>Oncology Letters</i> , 2019, 18, 5468-5480.	0.8	8
882	Leveraging methylation to identify the potential causal genes associated with survival in lung adenocarcinoma and lung squamous cell carcinoma. <i>Oncology Letters</i> , 2020, 20, 193-200.	0.8	3

#	ARTICLE	IF	CITATIONS
883	Identification and validation of seven prognostic long non-coding RNAs in oral squamous cell carcinoma. <i>Oncology Letters</i> , 2020, 20, 939-946.	0.8	10
884	Long non-coding RNA metastasis-associated lung adenocarcinoma transcript 1 regulates renal cancer cell migration via cofilin-1. <i>Oncology Letters</i> , 2020, 20, 53.	0.8	7
885	Identification and validation of core genes for serous ovarian adenocarcinoma via bioinformatics analysis. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	5
886	N-glycosylation and receptor tyrosine kinase signaling affect claudin-3 levels in colorectal cancer cells. <i>Oncology Reports</i> , 2020, 44, 1649-1661.	1.2	7
887	A Radiosensitivity Gene Signature and PD-L1 Status Predict Clinical Outcome of Patients with Glioblastoma Multiforme in The Cancer Genome Atlas Dataset. <i>Cancer Research and Treatment</i> , 2020, 52, 530-542.	1.3	13
888	FoxA1 and FoxA2 drive gastric differentiation and suppress squamous identity in NKX2-1-negative lung cancer. <i>ELife</i> , 2018, 7, .	2.8	59
889	CNApp, a tool for the quantification of copy number alterations and integrative analysis revealing clinical implications. <i>ELife</i> , 2020, 9, .	2.8	48
890	Dissecting the DNA binding landscape and gene regulatory network of p63 and p53. <i>ELife</i> , 2020, 9, .	2.8	26
891	Comprehensive genomic analysis of microenvironment phenotypes in ovarian cancer. <i>PeerJ</i> , 2020, 8, e10255.	0.9	4
892	Analysis of genomic variation in lung adenocarcinoma patients revealed the critical role of PI3K complex. <i>PeerJ</i> , 2017, 5, e3216.	0.9	8
893	cRegulome: an R package for accessing microRNA and transcription factor-gene expression correlations in cancer. <i>PeerJ</i> , 2019, 7, e6509.	0.9	1
894	Transcriptional regulation of Bcl-2 gene by the PR/SET domain family member PRDM10. <i>PeerJ</i> , 2019, 7, e6941.	0.9	7
895	Competing endogenous RNA (ceRNA) hypothetical model based on comprehensive analysis of long non-coding RNA expression in lung adenocarcinoma. <i>PeerJ</i> , 2019, 7, e8024.	0.9	16
896	A multiomics comparison between endometrial cancer and serous ovarian cancer. <i>PeerJ</i> , 2020, 8, e8347.	0.9	7
897	Identification of prognostic splicing factors and exploration of their potential regulatory mechanisms in pancreatic adenocarcinoma. <i>PeerJ</i> , 2020, 8, e8380.	0.9	10
898	Genome-wide identification of CpG island methylator phenotype related gene signature as a novel prognostic biomarker of gastric cancer. <i>PeerJ</i> , 2020, 8, e9624.	0.9	11
899	ID3 promotes homologous recombination via non-transcriptional and transcriptional mechanisms and its loss confers sensitivity to PARP inhibition. <i>Nucleic Acids Research</i> , 2021, 49, 11666-11689.	6.5	8
900	Multiomics analysis of tumor mutational burden across cancer types. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5637-5646.	1.9	10

#	ARTICLE	IF	CITATIONS
901	Protein profiling reveals potential isomiR-associated cross-talks among RNAs in cholangiocarcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5722-5734.	1.9	3
902	A methylomics-correlated nomogram predicts the recurrence free survival risk of kidney renal clear cell carcinoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 8559-8576.	1.0	0
903	Colon Cancer Progression Is Reflected to Monotonic Differentiation in Gene Expression and Pathway Deregulation Facilitating Stage-specific Drug Repurposing. <i>Cancer Genomics and Proteomics</i> , 2021, 18, 757-769.	1.0	1
904	lncRNAfunc: a knowledgebase of lncRNA function in human cancer. <i>Nucleic Acids Research</i> , 2022, 50, D1295-D1306.	6.5	63
905	STAT3 as a Potential Target for Tumor Suppressive Effects of 15-Deoxy- $\Delta^{12,14}$ -prostaglandin J_2 in Triple Negative Breast Cancer. <i>Journal of Cancer Prevention</i> , 2021, 26, 207-217.	0.8	3
907	Spatially confined sub-tumor microenvironments in pancreatic cancer. <i>Cell</i> , 2021, 184, 5577-5592.e18.	13.5	182
908	A 6 transcription factors-associated nomogram predicts the recurrence-free survival of thyroid papillary carcinoma. <i>Medicine (United States)</i> , 2021, 100, e27308.	0.4	1
909	Validation of genetic classifiers derived from mouse and human tumors to identify molecular subtypes of colorectal cancer. <i>Human Pathology</i> , 2022, 119, 1-14.	1.1	1
910	PPAR γ^3 Targets-Derived Diagnostic and Prognostic Index for Papillary Thyroid Cancer. <i>Cancers</i> , 2021, 13, 5110.	1.7	1
912	Integrative meta-analysis of gene expression profiles identifies FEN1 and ENDOU as potential diagnostic biomarkers for cervical squamous cell carcinoma. <i>Oncology Letters</i> , 2021, 22, 840.	0.8	6
913	Bayesian log-normal deconvolution for enhanced in silico microdissection of bulk gene expression data. <i>Nature Communications</i> , 2021, 12, 6106.	5.8	7
914	Weighted Gene Co-expression Network Analysis Identifies a Cancer-Associated Fibroblast Signature for Predicting Prognosis and Therapeutic Responses in Gastric Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 744677.	1.6	37
915	Development and Verification of an Autophagy-Related lncRNA Signature to Predict Clinical Outcomes and Therapeutic Responses in Ovarian Cancer. <i>Frontiers in Medicine</i> , 2021, 8, 715250.	1.2	8
916	Epigenetic DNA Modifications Upregulate SPRY2 in Human Colorectal Cancers. <i>Cells</i> , 2021, 10, 2632.	1.8	5
918	Identification of novel subtypes based on ssGSEA in immune-related prognostic signature for tongue squamous cell carcinoma. <i>Cancer Medicine</i> , 2021, 10, 8693-8707.	1.3	21
920	Upregulation of HOX genes promotes cell migration and proliferation in head and neck squamous cell carcinoma. <i>Tumor Biology</i> , 2021, 43, 263-278.	0.8	2
921	International Prognostic Index-Based Immune Prognostic Model for Diffuse Large B-Cell Lymphoma. <i>Frontiers in Immunology</i> , 2021, 12, 732006.	2.2	10
922	Identification of Novel Endogenous Controls for qPCR Normalization in SK-BR-3 Breast Cancer Cell Line. <i>Genes</i> , 2021, 12, 1631.	1.0	2

#	ARTICLE	IF	CITATIONS
923	NOV/CCN3 Promotes Cell Migration and Invasion in Intrahepatic Cholangiocarcinoma via miR-92a-3p. <i>Genes</i> , 2021, 12, 1659.	1.0	6
924	RNF2 ablation reprograms the tumor-immune microenvironment and stimulates durable NK and CD4+ T-cell-dependent antitumor immunity. <i>Nature Cancer</i> , 2021, 2, 1018-1038.	5.7	11
926	Using predictive machine learning models for drug response simulation by calibrating patient-specific pathway signatures. <i>Npj Systems Biology and Applications</i> , 2021, 7, 40.	1.4	4
928	The role of zinc transporter proteins as predictive and prognostic biomarkers of hepatocellular cancer. <i>PeerJ</i> , 2021, 9, e12314.	0.9	5
929	Cellular Origins of EGFR-Driven Lung Cancer Cells Determine Sensitivity to Therapy. <i>Advanced Science</i> , 2021, 8, e2101999.	5.6	13
930	Single-cell RNA sequencing reveals distinct tumor microenvironmental patterns in lung adenocarcinoma. <i>Oncogene</i> , 2021, 40, 6748-6758.	2.6	70
932	Pan-cancer analysis of non-coding transcripts reveals the prognostic onco-lncRNA HOXA10-AS in gliomas. <i>Cell Reports</i> , 2021, 37, 109873.	2.9	13
933	Transcriptomic Analysis Identifies Complement Component 3 as a Potential Predictive Biomarker for Chemotherapy Resistance in Colorectal Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 763652.	1.6	4
934	TNF Patterns and Tumor Microenvironment Characterization in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 754818.	2.2	11
935	DBtRend: A Web-Server of tRNA Expression Profiles from Small RNA Sequencing Data in Humans. <i>Genes</i> , 2021, 12, 1576.	1.0	2
936	Mutations Status of Chemokine Signaling Pathway Predict Prognosis of Immune Checkpoint Inhibitors in Colon Adenocarcinoma. <i>Frontiers in Pharmacology</i> , 2021, 12, 721181.	1.6	5
937	NRIP1 is activated by C-JUN/C-FOS and activates the expression of PGR, ESR1 and CCND1 in luminal A breast cancer. <i>Scientific Reports</i> , 2021, 11, 21159.	1.6	8
938	Whole-exome sequencing identifies biosignatures that predict adverse survival outcomes in surgically treated patients with oral cavity squamous cell carcinoma. <i>Oral Oncology</i> , 2021, 122, 105547.	0.8	3
939	IRIS-TCGA: An Information Retrieval and Integration System for Genomic Data of Cancer. <i>Lecture Notes in Computer Science</i> , 2017, , 160-171.	1.0	1
941	A Novel Synthetic Over-Sampling Technique for Imbalanced Classification of Gene Expressions Using Autoencoders and Swarm Optimization. <i>Lecture Notes in Computer Science</i> , 2018, , 603-615.	1.0	1
960	Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures. <i>F1000Research</i> , 2019, 8, 776.	0.8	9
964	Survival-based bioinformatics analysis to identify hub genes and key pathways in non-small cell lung cancer. <i>Translational Cancer Research</i> , 2019, 8, 1188-1198.	0.4	2
966	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. <i>F1000Research</i> , 0, 8, 776.	0.8	1

#	ARTICLE	IF	CITATIONS
967	miRDriver. , 2019, , .		4
972	Predicting Synthetic Lethal Genetic Interactions in Breast Cancer using Decision Tree. , 2019, , .		1
979	Exomes of Ductal Luminal Breast Cancer Patients from Southwest Colombia: Gene Mutational Profile and Related Expression Alterations. <i>Biomolecules</i> , 2020, 10, 698.	1.8	4
987	NT5DC2 is a novel prognostic marker in human hepatocellular carcinoma. <i>Oncology Letters</i> , 2020, 20, 70.	0.8	7
989	Integrated analysis of whole genome and transcriptome sequencing in a young patient with gastric cancer provides insights for precision therapy. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	0
990	Identification and Validation of a Seizure-Free-Related Gene Signature for Predicting Poor Prognosis in Lower-Grade Gliomas. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7399-7410.	0.8	2
992	m6A-Mediated Tumor Invasion and Methylation Modification in Breast Cancer Microenvironment. <i>Journal of Oncology</i> , 2021, 2021, 1-17.	0.6	10
993	Identification of miR-499a-5p as a Potential Novel Biomarker for Risk Stratification in Endometrial Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 757678.	1.3	9
994	Combined Assessment of the Tumorâ€‘Stroma Ratio and Tumor Immune Cell Infiltrate for Immune Checkpoint Inhibitor Therapy Response Prediction in Colon Cancer. <i>Cells</i> , 2021, 10, 2935.	1.8	12
995	Regulatory T cells promote cancer immune-escape through integrin Î±vÎ²8-mediated TGF-Î² activation. <i>Nature Communications</i> , 2021, 12, 6228.	5.8	58
997	Clinical values and potential pathways of miR-183-5p in gastric cancer: a study based on integrational bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 2123-2131.	0.6	2
998	Identification of Immune-Related Genes for Establishment of Prognostic Index in Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 760079.	1.8	0
999	Identification of modules based on integrative analysis for drug prediction in colorectal cancer. <i>Gene Reports</i> , 2021, 25, 101403.	0.4	0
1000	Genes Associated with Calcium Signaling are Involved in Alcoholâ€‘Induced Breast Cancer Growth. <i>Alcoholism: Clinical and Experimental Research</i> , 2021, 45, 79-91.	1.4	0
1001	Aldehyde Dehydrogenase 1-related Genes in Triple-negative Breast Cancer Investigated Using Network Analysis. <i>Anticancer Research</i> , 2020, 40, 6733-6742.	0.5	2
1002	<p>Screening and Identifying Cisplatin-Related Gene Mutations in Lung Squamous Cell Carcinoma</p>. <i>Pharmacogenomics and Personalized Medicine</i> , 2020, Volume 13, 757-766.	0.4	1
1003	Identification of â€‘regulation of RhoA activity panelâ€‘as a prognostic and predictive biomarker for gastric cancer. <i>Aging</i> , 2021, 13, 714-734.	1.4	1
1004	Comprehensive assessment of PD-L1 and PD-L2 dysregulation in gastrointestinal cancers. <i>Epigenomics</i> , 2020, 12, 2155-2171.	1.0	4

#	ARTICLE	IF	CITATIONS
1006	Integrative analysis of mRNA and miRNA sequencing data for gliomas of various grades. Egyptian Journal of Medical Human Genetics, 2020, 21, .	0.5	2
1008	Analysis of the TCGA Dataset Reveals that Subsites of Laryngeal Squamous Cell Carcinoma Are Molecularly Distinct. Cancers, 2021, 13, 105.	1.7	9
1009	Integrative network analysis identified master regulatory long non-coding RNAs underlying the squamous subtype of pancreatic ductal adenocarcinoma. , 2020, , .		2
1011	A novel strategy for combination of clofarabine and pictilisib is synergistic in gastric cancer. Translational Oncology, 2022, 15, 101260.	1.7	3
1012	Genome-wide Discovery of MicroRNA Biomarkers for Cancer Precision Medicine. RSC Detection Science, 2020, , 1-34.	0.0	1
1013	Screening and identification of genes associated with cell proliferation in cholangiocarcinoma. Aging, 2020, 12, 2626-2646.	1.4	1
1020	The Upregulation of PLXDC2 Correlates with Immune Microenvironment Characteristics and Predicts Prognosis in Gastric Cancer. Disease Markers, 2021, 2021, 1-18.	0.6	3
1021	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. Nature Communications, 2021, 12, 6276.	5.8	89
1022	m5C Regulator-Mediated Methylation Modification Patterns and Tumor Microenvironment Infiltration Characterization in Papillary Thyroid Carcinoma. Frontiers in Oncology, 2021, 11, 729887.	1.3	7
1023	Molecular characterization of metabolic subtypes of gastric cancer based on metabolism-related lncRNA. Scientific Reports, 2021, 11, 21491.	1.6	3
1024	Comprehensive Analysis of m6A RNA Methylation Regulators and the Immune Microenvironment to Aid Immunotherapy in Pancreatic Cancer. Frontiers in Immunology, 2021, 12, 769425.	2.2	21
1025	Charting differentially methylated regions in cancer with Rocker-meth. Communications Biology, 2021, 4, 1249.	2.0	7
1027	C-Myc-activated long non-coding RNA LINC01050 promotes gastric cancer growth and metastasis by sponging miR-7161-3p to regulate SPZ1 expression. Journal of Experimental and Clinical Cancer Research, 2021, 40, 351.	3.5	11
1028	Leveraging biochemical reactions to unravel functional impacts of cancer somatic variants affecting protein interaction interfaces. F1000Research, 0, 10, 1111.	0.8	1
1030	ENPP2 Methylation in Health and Cancer. International Journal of Molecular Sciences, 2021, 22, 11958.	1.8	9
1032	Multi-omics integrative analysis and survival risk model construction of non-small cell lung cancer based on The Cancer Genome Atlas datasets. Oncology Letters, 2020, 20, 58.	0.8	2
1041	CTDPathSim. , 2020, , .		1
1042	CanMod. , 2020, , .		0

#	ARTICLE	IF	CITATIONS
1043	Landscape of transcription and expression regulated by DNA methylation related to age of donor and cell passage in adipose-derived mesenchymal stem cells. <i>Aging</i> , 2020, 12, 21186-21201.	1.4	8
1044	Could microtubule inhibitors be the best choice of therapy in gastric cancer with high immune activity: mutant DYNC1H1 as a biomarker. <i>Aging</i> , 2020, 12, 25101-25119.	1.4	7
1045	Novel methylation-driven genes identified as prognostic indicators for lung squamous cell carcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2019, 11, 1997-2012.	0.0	11
1046	Landscape of active enhancers developed de novo in cirrhosis and conserved in hepatocellular carcinoma. <i>American Journal of Cancer Research</i> , 2020, 10, 3157-3178.	1.4	8
1047	Comprehensive Analysis of Alternative Splicing Signature in Gastric Cancer Prognosis Based on The Cancer Genome Atlas (TCGA) and SpliceSeq Databases. <i>Medical Science Monitor</i> , 2020, 26, e925772.	0.5	0
1048	CARD11 alteration as a candidate biomarker of skin cutaneous melanoma treated with immune checkpoint blockade. <i>American Journal of Translational Research (discontinued)</i> , 2021, 13, 286-300.	0.0	4
1049	Expression and clinical significance of in glioma. <i>International Journal of Clinical and Experimental Pathology</i> , 2021, 14, 938-955.	0.5	0
1050	A Text-Based Computational Framework for Patient-Specific Modeling for Classification of Cancers. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1051	Positive correlation between transcriptomic stemness and PI3K/AKT/mTOR signaling scores in breast cancer, and a counterintuitive relationship with PIK3CA genotype. <i>PLoS Genetics</i> , 2021, 17, e1009876.	1.5	14
1052	Discovery of tumor immune infiltration-related snoRNAs for predicting tumor immune microenvironment status and prognosis in lung adenocarcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6386-6399.	1.9	7
1053	Are we there yet? A machine learning architecture to predict organotropic metastases. <i>BMC Medical Genomics</i> , 2021, 14, 281.	0.7	0
1054	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30
1055	Integrating m6A Regulators-Mediated Methylation Modification Models and Tumor Immune Microenvironment Characterization in Caucasian and Chinese Low-Grade Gliomas. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 725764.	1.8	6
1056	Single-cell RNA-seq highlights a specific carcinoembryonic cluster in ovarian cancer. <i>Cell Death and Disease</i> , 2021, 12, 1082.	2.7	10
1058	Heat shock factor 1 (HSF1) cooperates with estrogen receptor β (ER β) in the regulation of estrogen action in breast cancer cells. <i>ELife</i> , 2021, 10, .	2.8	12
1059	Hypoxic Characteristic Genes Predict Response to Immunotherapy for Urothelial Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 762478.	1.8	8
1060	A Novel Risk-Score Model With Eight MiRNA Signatures for Overall Survival of Patients With Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 741112.	1.1	3
1062	A System Pharmacology Model for Decoding the Synergistic Mechanisms of Compound Kushen Injection in Treating Breast Cancer. <i>Frontiers in Pharmacology</i> , 2021, 12, 723147.	1.6	0

#	ARTICLE	IF	CITATIONS
1063	TP53 Mutation Infers a Poor Prognosis and Is Correlated to Immunocytes Infiltration in Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 759154.	1.8	19
1064	Immune Profiling of Combined Hepatocellular- Cholangiocarcinoma Reveals Distinct Subtypes and Activation of Gene Signatures Predictive of Response to Immunotherapy. <i>Clinical Cancer Research</i> , 2022, 28, 540-551.	3.2	23
1066	Loss of Integrin $\alpha 9 \beta 1$ on Tumor Keratinocytes Enhances the Stromal Vasculature and Growth of Cutaneous Tumors. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1966-1975.e8.	0.3	1
1067	APOBEC Mutagenesis Inhibits Breast Cancer Growth through Induction of T cell-Mediated Antitumor Immune Responses. <i>Cancer Immunology Research</i> , 2022, 10, 70-86.	1.6	20
1068	A Computational Analysis in a Cohort of Parkinson's Disease Patients and Clock-Modified Colorectal Cancer Cells Reveals Common Expression Alterations in Clock-Regulated Genes. <i>Cancers</i> , 2021, 13, 5978.	1.7	14
1072	Identification of the Immune Cell Infiltration Landscape in Hepatocellular Carcinoma to Predict Prognosis and Guide Immunotherapy. <i>Frontiers in Genetics</i> , 2021, 12, 777931.	1.1	7
1073	Multomics subtyping for clinically prognostic cancer subtypes and personalized therapy: A systematic review and meta-analysis. <i>Genetics in Medicine</i> , 2022, 24, 15-25.	1.1	5
1074	The enhanced cell cycle related to the response to adjuvant therapy in pancreatic ductal adenocarcinoma. <i>Genomics</i> , 2021, 114, 95-106.	1.3	1
1076	Coordinated regulation of WNT/ β -catenin, c-Met, and integrin signalling pathways by miR-193b controls triple negative breast cancer metastatic traits. <i>BMC Cancer</i> , 2021, 21, 1296.	1.1	4
1077	Gene Co-Expression Network Characterizing Microenvironmental Heterogeneity and Intercellular Communication in Pancreatic Ductal Adenocarcinoma: Implications of Prognostic Significance and Therapeutic Target. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1078	Patch-Based Convolutional Neural Networks for TCGA-BRCA Breast Cancer Classification. <i>Lecture Notes in Computer Science</i> , 2021, , 29-40.	1.0	0
1079	A Pan-Cancer Analysis of Tumor-Infiltrating B Cell Repertoires. <i>Frontiers in Immunology</i> , 2021, 12, 790119.	2.2	7
1080	Identification of Candidate Gene Signatures and Regulatory Networks in Endometriosis and its Related Infertility by Integrated Analysis. <i>Reproductive Sciences</i> , 2022, 29, 411-426.	1.1	4
1081	Exploiting protein family and protein network data to identify novel drug targets for bladder cancer. <i>Oncotarget</i> , 2022, 13, 105-117.	0.8	2
1082	Network-based prioritization of cancer biomarkers by phenotype-driven module detection and ranking. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 206-217.	1.9	6
1083	Senescence as a dictator of patient outcomes and therapeutic efficacies in human gastric cancer. <i>Cell Death Discovery</i> , 2022, 8, 13.	2.0	21
1084	DEGnext: classification of differentially expressed genes from RNA-seq data using a convolutional neural network with transfer learning. <i>BMC Bioinformatics</i> , 2022, 23, 17.	1.2	15
1085	Construction and validation of a risk scoring model for diffuse large B-cell lymphoma based on ferroptosis-related genes and its association with immune infiltration. <i>Translational Oncology</i> , 2022, 16, 101314.	1.7	12

#	ARTICLE	IF	CITATIONS
1086	Iron-mediated epigenetic activation of NRF2 targets. <i>Journal of Nutritional Biochemistry</i> , 2022, 101, 108929.	1.9	13
1088	Comprehensive Analysis of Alternative Splicing Signature in Gastric Cancer Prognosis Based on The Cancer Genome Atlas (TCGA) and SpliceSeq Databases. <i>Medical Science Monitor</i> , 2020, 26, e925772.	0.5	1
1089	Comprehensive DNA repair gene expression analysis and its prognostic significance in acute myeloid leukemia. <i>Hematology</i> , 2021, 26, 904-913.	0.7	4
1090	CD97 is associated with mitogenic pathway activation, metabolic reprogramming, and immune microenvironment changes in glioblastoma. <i>Scientific Reports</i> , 2022, 12, 1464.	1.6	8
1091	Decreased Expression of ACADSB Predicts Poor Prognosis in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 762629.	1.3	10
1092	KeyPathwayMineR: De Novo Pathway Enrichment in the R Ecosystem. <i>Frontiers in Genetics</i> , 2021, 12, 812853.	1.1	5
1093	Prediction and pan-cancer analysis of mammalian transcripts involved in target directed miRNA degradation. <i>Nucleic Acids Research</i> , 2022, 50, 2019-2035.	6.5	16
1094	Comprehensive Analysis of Copy Number Variation, Nucleotide Mutation, and Transcription Level of PPAR Pathway-Related Genes in Endometrial Cancer. <i>PPAR Research</i> , 2022, 2022, 1-17.	1.1	2
1095	Characterization of m6A regulator-mediated methylation modification patterns and tumor microenvironment infiltration in acute myeloid leukemia. <i>Cancer Medicine</i> , 2022, , .	1.3	5
1096	Immune-related lncRNA classification of head and neck squamous cell carcinoma. <i>Cancer Cell International</i> , 2022, 22, 25.	1.8	8
1098	Relationship between Macrophage and Radiosensitivity in Human Primary and Recurrent Glioblastoma: In Silico Analysis with Publicly Available Datasets. <i>Biomedicines</i> , 2022, 10, 292.	1.4	8
1099	Molecular, Immunological, and Clinical Features Associated With Lymphoid Neogenesis in Muscle Invasive Bladder Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 793992.	2.2	14
1100	STAT3 induces breast cancer growth via ANGPTL4, MMP13 and STC1 secretion by cancer associated fibroblasts. <i>Oncogene</i> , 2022, 41, 1456-1467.	2.6	38
1101	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2022, , .	6.5	5
1102	MicroRNAs as biomarkers for prostate cancer prognosis: a systematic review and a systematic reanalysis of public data. <i>British Journal of Cancer</i> , 2022, 126, 502-513.	2.9	28
1103	Identification of Key Prognostic-Related miRNA-mRNA Pairs in the Progression of Endometrial Carcinoma. <i>Gynecologic and Obstetric Investigation</i> , 2022, , 1-10.	0.7	0
1104	Re-wiring and gene expression changes of AC025034.1 and ATP2B1 play complex roles in early-to-late breast cancer progression. <i>BMC Genomic Data</i> , 2022, 23, 6.	0.7	6
1105	Identification of long non-coding RNAs and RNA binding proteins in breast cancer subtypes. <i>Scientific Reports</i> , 2022, 12, 693.	1.6	14

#	ARTICLE	IF	CITATIONS
1106	Methylation Pattern Mediated by m6A Regulator and Tumor Microenvironment Invasion in Lung Adenocarcinoma. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	1.9	25
1107	Demethylation at enhancer upregulates MCM2 and NUP37 expression predicting poor survival in hepatocellular carcinoma patients. <i>Journal of Translational Medicine</i> , 2022, 20, 49.	1.8	9
1108	PSAT1 gene as a biomarker for targeting triple negative breast cancer in presence of Rapamycin. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2022, 41, 166-182.	0.4	1
1109	Development of an Aging-Related Gene Signature for Predicting Prognosis, Immunotherapy, and Chemotherapy Benefits in Rectal Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 775700.	1.6	4
1110	Patient-Level DNA Damage Repair Pathway Profiles and Anti-Tumor Immunity for Gastric Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 806324.	2.2	6
1111	Circadian Regulation Patterns With Distinct Immune Landscapes in Gliomas Aid in the Development of a Risk Model to Predict Prognosis and Therapeutic Response. <i>Frontiers in Immunology</i> , 2021, 12, 797450.	2.2	7
1113	N6-Methyladenosine-Related lncRNAs as potential biomarkers for predicting prognoses and immune responses in patients with cervical cancer. <i>BMC Genomic Data</i> , 2022, 23, 8.	0.7	9
1114	Pan-Cancer Analyses Reveal Oncogenic Role and Prognostic Value of F-Box Only Protein 22. <i>Frontiers in Oncology</i> , 2021, 11, 790912.	1.3	4
1115	The contribution of uncharted RNA sequences to tumor identity in lung adenocarcinoma. <i>NAR Cancer</i> , 2022, 4, zcac001.	1.6	2
1116	TNF Family-Based Signature Predicts Prognosis, Tumor Microenvironment, and Molecular Subtypes in Bladder Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 800967.	1.8	12
1117	Comprehensive Analysis of Cell Cycle-Related Genes in Patients With Prostate Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 796795.	1.3	3
1118	Follicular Helper T-Cell-Based Classification of Endometrial Cancer Promotes Precise Checkpoint Immunotherapy and Provides Prognostic Stratification. <i>Frontiers in Immunology</i> , 2021, 12, 788959.	2.2	9
1119	Systematic Elucidation of the Aneuploidy Landscape and Identification of Aneuploidy Driver Genes in Prostate Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 723466.	1.8	3
1120	N6-Methyladenosine-Related Gene Expression Signatures for Predicting the Overall Survival and Immune Responses of Patients With Colorectal Cancer. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1121	PBK/TOPK Is a Favorable Prognostic Biomarker Correlated with Antitumor Immunity in Colon Cancers. <i>Biomedicines</i> , 2022, 10, 299.	1.4	3
1122	Integrative Modeling of Multiomics Data for Predicting Tumor Mutation Burden in Patients with Lung Cancer. <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	7
1123	Oncogenic potential of BEST4 in colorectal cancer via activation of PI3K/Akt signaling. <i>Oncogene</i> , 2022, 41, 1166-1177.	2.6	13
1124	Ferroptosis Regulator Modification Patterns and Tumor Microenvironment Immune Infiltration Characterization in Hepatocellular Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 807502.	1.6	4

#	ARTICLE	IF	CITATIONS
1125	Genomic landscape of advanced endometrial cancer analyzed by targeted next-generation sequencing and the cancer genome atlas (TCGA) dataset. <i>Journal of Gynecologic Oncology</i> , 2022, 33, .	1.0	11
1126	The Predictive Value of PAK7 Mutation for Immune Checkpoint Inhibitors Therapy in Non-Small Cell Cancer. <i>Frontiers in Immunology</i> , 2022, 13, 834142.	2.2	4
1127	Characterization of Cell Cycle-Related Competing Endogenous RNAs Using Robust Rank Aggregation as Prognostic Biomarker in Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 2022, 12, 807367.	1.3	3
1128	Analysis of m6A Methylation Modification Patterns and Tumor Immune Microenvironment in Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 785058.	1.8	9
1129	An oncogenic enhancer encodes selective selenium dependency in AML. <i>Cell Stem Cell</i> , 2022, 29, 386-399.e7.	5.2	15
1130	Depiction of Aging-Based Molecular Phenotypes With Diverse Clinical Prognosis and Immunological Features in Gastric Cancer. <i>Frontiers in Medicine</i> , 2021, 8, 792740.	1.2	3
1131	Integrated Analysis of Multi-Omics Data to Identify Prognostic Genes for Pancreatic Cancer. <i>DNA and Cell Biology</i> , 2022, , .	0.9	2
1132	A Tumor Suppressor Gene-Based Prognostic Classifier Predicts Prognosis, Tumor Immune Infiltration, and Small Molecule Compounds in Breast Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 783026.	1.1	2
1133	Identifying Potential Biomarkers of Prognostic Value in Colorectal Cancer via Tumor Microenvironment Data Mining. <i>Frontiers in Genetics</i> , 2021, 12, 787208.	1.1	4
1134	Field cancerization profile-based prognosis signatures lead to more robust risk evaluation in hepatocellular carcinoma. <i>IScience</i> , 2022, 25, 103747.	1.9	4
1135	Knockdown of ATG4A inhibits breast cancer progression and promotes tamoxifen chemosensitivity by suppressing autophagy. <i>Molecular Medicine Reports</i> , 2022, 25, .	1.1	8
1136	Identification of key miRNAs in prostate cancer progression based on miRNA-mRNA network construction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 864-873.	1.9	4
1137	Identification of the hub genes and transcription factorâ€miRNA axes involved in <i>Helicobacter pylori</i> â€associated gastric cancer. <i>Oncology Letters</i> , 2022, 23, 89.	0.8	0
1138	Mycobacterial infection aggravates <i>Helicobacter pylori</i> -induced gastric preneoplastic pathology by redirection of de novo induced Treg cells. <i>Cell Reports</i> , 2022, 38, 110359.	2.9	6
1139	Integrative Analysis of m6A RNA Methylation Regulators and the Tumor Immune Microenvironment in Non-Small-Cell Lung Cancer. <i>Disease Markers</i> , 2022, 2022, 1-34.	0.6	5
1140	SETD2 loss perturbs the kidney cancer epigenetic landscape to promote metastasis and engenders actionable dependencies on histone chaperone complexes. <i>Nature Cancer</i> , 2022, 3, 188-202.	5.7	26
1141	Identification of Key Pathways and Establishment of a Seven-Gene Prognostic Signature in Cervical Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-16.	0.6	6
1142	MHC-II Signature Correlates With Anti-Tumor Immunity and Predicts anti-PD-L1 Response of Bladder Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 757137.	1.8	13

#	ARTICLE	IF	CITATIONS
1143	EZH2 Mediates Proliferation, Migration, and Invasion Promoted by Estradiol in Human Glioblastoma Cells. <i>Frontiers in Endocrinology</i> , 2022, 13, 703733.	1.5	7
1144	PACER lncRNA regulates COX-2 expression in lung cancer cells. <i>Oncotarget</i> , 2022, 13, 291-306.	0.8	5
1145	FCER1G positively relates to macrophage infiltration in clear cell renal cell carcinoma and contributes to unfavorable prognosis by regulating tumor immunity. <i>BMC Cancer</i> , 2022, 22, 140.	1.1	16
1146	Different members of the APOBEC3 family of DNA mutators have opposing associations with the landscape of breast cancer. <i>American Journal of Cancer Research</i> , 2021, 11, 5111-5125.	1.4	1
1147	A value predictive of prostate cancer stemness, tumor immune landscape and immunotherapy response. <i>NAR Cancer</i> , 2022, 4, zcac010.	1.6	7
1148	Cellular and Molecular Effects of Understudied Kinase Pregnancy Upregulated Non-Ubiquitous Calcium-Calmodulin Dependent Kinase (PNCK) in Renal Cell Carcinoma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1149	Different Susceptibilities of Human Melanoma Cell Lines to G2/M Blockage and Cell Death Activation in Response to the Estrogen Receptor β agonist LY500307. <i>Journal of Cancer</i> , 2022, 13, 1573-1587.	1.2	2
1150	Computational analysis of prognosis-related genes in liver cancer. , 2022, , 7-19.		0
1151	Comprehensive assessment of cellular senescence in the tumor microenvironment. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	33
1152	A Study of Feature Selection and Extraction Algorithms for Cancer Subtype Prediction. , 2022, , .		1
1154	Regulatory networks and 5' partner usage of miRNA host gene fusions in breast cancer. <i>International Journal of Cancer</i> , 2022, 151, 95-106.	2.3	5
1155	A novel qualitative signature based on lncRNA pairs for prognosis prediction in hepatocellular carcinoma. <i>Cancer Cell International</i> , 2022, 22, 95.	1.8	8
1156	The methylation of SDC2 and TFPI2 defined three methylator phenotypes of colorectal cancer. <i>BMC Gastroenterology</i> , 2022, 22, 88.	0.8	5
1157	Identification of the Crucial Role of CCL22 in F. nucleatum-Related Colorectal Tumorigenesis that Correlates With Tumor Microenvironment and Immune Checkpoint Therapy. <i>Frontiers in Genetics</i> , 2022, 13, 811900.	1.1	12
1158	Molecular Characterization of m6A Modifications in Non-Clear Cell Renal Cell Carcinoma and Potential Relationship with Pathological Types. <i>International Journal of General Medicine</i> , 2022, Volume 15, 1595-1608.	0.8	0
1159	Early Breast Cancer Evolution by Autosomal Broad Copy Number Alterations. <i>International Journal of Genomics</i> , 2022, 2022, 1-17.	0.8	1
1160	Establishing a Prognostic Model Based on Ulceration and Immune Related Genes in Melanoma Patients and Identification of EIF3B as a Therapeutic Target. <i>Frontiers in Immunology</i> , 2022, 13, 824946.	2.2	5
1162	Deep learning using bulk RNA-seq data expands cell landscape identification in tumor microenvironment. <i>Oncolmmunology</i> , 2022, 11, 2043662.	2.1	5

#	ARTICLE	IF	CITATIONS
1165	Multimiomics Topic Modeling for Breast Cancer Classification. <i>Cancers</i> , 2022, 14, 1150.	1.7	4
1166	A New Prognostic Risk Score: Based on the Analysis of Autophagy-Related Genes and Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 820154.	1.1	6
1167	Construction of a Lactate-Related Prognostic Signature for Predicting Prognosis, Tumor Microenvironment, and Immune Response in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Immunology</i> , 2022, 13, 818984.	2.2	32
1168	Mutational characteristics of young and elderly gastric cancer: a comparative study. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 77-83.	0.6	1
1169	Detection of tumor-specific DNA methylation markers in the blood of patients with pituitary neuroendocrine tumors. <i>Neuro-Oncology</i> , 2022, 24, 1126-1139.	0.6	9
1170	Pan-Cancer Transcriptomic Analysis Identifies PLK1 Crucial for the Tumorigenesis of Clear Cell Renal Cell Carcinoma. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 1099-1116.	1.6	3
1171	Identification of Tumor Antigens and Immune Subtypes in Lung Adenocarcinoma for mRNA Vaccine Development. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 815596.	1.8	7
1172	The Dual Regulation Effects of ESR1/NEDD4L on SLC7A11 in Breast Cancer Under Ionizing Radiation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 772380.	1.8	11
1173	HAUS5 Is A Potential Prognostic Biomarker With Functional Significance in Breast Cancer. <i>Frontiers in Oncology</i> , 2022, 12, 829777.	1.3	6
1174	Identification of Tissue-Specific Gene Clusters Induced by DNA Demethylation in Lung Adenocarcinoma: More Than Germline Genes. <i>Cancers</i> , 2022, 14, 1007.	1.7	7
1176	Ano1 is a Prognostic Biomarker That is Correlated with Immune Infiltration in Colorectal Cancer. <i>International Journal of General Medicine</i> , 2022, Volume 15, 1547-1564.	0.8	2
1177	BTG2 Serves as a Potential Prognostic Marker and Correlates with Immune Infiltration in Lung Adenocarcinoma. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2727-2745.	0.8	7
1178	Multi-omics analyses provide novel biological insights to distinguish lobular ductal types of invasive breast cancers. <i>Breast Cancer Research and Treatment</i> , 2022, 193, 361-379.	1.1	9
1179	Clinical associations of ESR2 (estrogen receptor beta) expression across thousands of primary breast tumors. <i>Scientific Reports</i> , 2022, 12, 4696.	1.6	25
1180	Feature screening for survival trait with application to TCGA high-dimensional genomic data. <i>PeerJ</i> , 2022, 10, e13098.	0.9	1
1181	Morphogen Signals Shaping the Gastric Glands in Health and Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3632.	1.8	3
1182	Analytic approaches to clinical validation of results from preclinical models of glioblastoma: A systematic review. <i>PLoS ONE</i> , 2022, 17, e0264740.	1.1	3
1183	ENPP2 Promoter Methylation Correlates with Decreased Gene Expression in Breast Cancer: Implementation as a Liquid Biopsy Biomarker. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3717.	1.8	9

#	ARTICLE	IF	CITATIONS
1184	Tumor-associated macrophages and risk of recurrence in stage <sc>III</sc> colorectal cancer. <i>Journal of Pathology: Clinical Research</i> , 2022, 8, 307-312.	1.3	5
1185	Development of a miRNA-based classifier for detection of colorectal cancer molecular subtypes. <i>Molecular Oncology</i> , 2022, 16, 2693-2709.	2.1	6
1186	Unraveling the mechanism of alkaloids from <i>Sophora alopecuroides</i> Linn combined with immune checkpoint blockade in the treatment of non-small cell lung cancer based on systems pharmacology. <i>Bioorganic and Medicinal Chemistry</i> , 2022, 64, 116724.	1.4	5
1188	Identification and validation of a seven-gene prognostic marker in colon cancer based on single-cell transcriptome analysis. <i>IET Systems Biology</i> , 2022, 16, 72-83.	0.8	4
1189	Comprehensive Analysis Revealed the Potential Implications of m6A Regulators in Lung Adenocarcinoma. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 806780.	1.6	2
1190	A text-based computational framework for patient -specific modeling for classification of cancers. <i>IScience</i> , 2022, 25, 103944.	1.9	7
1191	The Chaperone Protein GRP78 Promotes Survival and Migration of Head and Neck Cancer After Direct Radiation Exposure and Extracellular Vesicle-Transfer. <i>Frontiers in Oncology</i> , 2022, 12, 842418.	1.3	9
1192	Activation of Drp1 promotes fatty acids-induced metabolic reprogramming to potentiate Wnt signaling in colon cancer. <i>Cell Death and Differentiation</i> , 2022, 29, 1913-1927.	5.0	20
1194	SCAPE: a mixture model revealing single-cell polyadenylation diversity and cellular dynamics during cell differentiation and reprogramming. <i>Nucleic Acids Research</i> , 2022, 50, e66-e66.	6.5	13
1196	Computing microRNA-gene interaction networks in pan-cancer using miRDriver. <i>Scientific Reports</i> , 2022, 12, 3717.	1.6	3
1198	KMT2C methyltransferase domain regulated INK4A expression suppresses prostate cancer metastasis. <i>Molecular Cancer</i> , 2022, 21, 89.	7.9	21
1200	Integrated Multi-Omics Analysis Identified PTPRG and CHL1 as Key Regulators of Immunophenotypes in Clear Cell Renal Cell Carcinoma(ccRCC). <i>Frontiers in Oncology</i> , 2022, 12, 832027.	1.3	7
1202	A single-cell analysis of breast cancer cell lines to study tumour heterogeneity and drug response. <i>Nature Communications</i> , 2022, 13, 1714.	5.8	65
1203	Global DNA methylation profiling reveals chromosomal instability in IDH-mutant astrocytomas. <i>Acta Neuropathologica Communications</i> , 2022, 10, 32.	2.4	6
1204	<i>CIBNplot</i>: Bayesian network plots for enrichment analysis. <i>Bioinformatics</i> , 2022, 38, 2959-2960.	1.8	19
1205	The cancer/testis antigen <i>HORMAD1</i> mediates epithelial-mesenchymal transition to promote tumor growth and metastasis by activating the Wnt/ β -catenin signaling pathway in lung cancer. <i>Cell Death Discovery</i> , 2022, 8, 136.	2.0	9
1206	Quantifying the contribution of transcription factor activity, mutations and microRNAs to CD274 expression in cancer patients. <i>Scientific Reports</i> , 2022, 12, 4374.	1.6	6
1207	Co-occurrence of <i>CDKN2A/B</i> and <i>IFNγ</i> homozygous deletions correlates with an immunosuppressive phenotype and poor prognosis in lung adenocarcinoma. <i>Molecular Oncology</i> , 2022, 16, 1746-1760.	2.1	6

#	ARTICLE	IF	CITATIONS
1209	Molecular Biomarker of Drug Resistance Developed From Patient-Derived Organoids Predicts Survival of Colorectal Cancer Patients. <i>Frontiers in Oncology</i> , 2022, 12, 855674.	1.3	1
1210	Investigating the Clinico-Molecular and Immunological Evolution of Lung Adenocarcinoma Using Pseudotime Analysis. <i>Frontiers in Oncology</i> , 2022, 12, 828505.	1.3	4
1211	The Prognostic Significance and Gene Expression Characteristics of Gastric Signet-Ring Cell Carcinoma: A Study Based on the SEER and TCGA Databases. <i>Frontiers in Surgery</i> , 2022, 9, 819018.	0.6	5
1212	Identification of novel prostate cancer genes in patients stratified by Gleason classification: Role of antitumoral genes. <i>International Journal of Cancer</i> , 2022, 151, 255-264.	2.3	6
1213	Specific human endogenous retroviruses predict metastatic potential in uveal melanoma. <i>JCI Insight</i> , 2022, 7, .	2.3	5
1214	Analysis of Yes-Associated Protein-1 (YAP1) Target Gene Signature to Predict Progressive Breast Cancer. <i>Journal of Clinical Medicine</i> , 2022, 11, 1947.	1.0	2
1215	Solid Tumor Opioid Receptor Expression and Oncologic Outcomes: Analysis of the Cancer Genome Atlas and Genotype Tissue Expression Project. <i>Frontiers in Oncology</i> , 2022, 12, 801411.	1.3	8
1217	Dysregulation of CXCL14 promotes malignant phenotypes of esophageal squamous carcinoma cells via regulating SRC and EGFR signaling. <i>Biochemical and Biophysical Research Communications</i> , 2022, 609, 75-83.	1.0	3
1218	Deep neural network modeling identifies biomarkers of response to immune-checkpoint therapy. <i>IScience</i> , 2022, 25, 104228.	1.9	4
1220	Type 1 conventional dendritic cells maintain and guide the differentiation of precursors of exhausted T _H cells in distinct cellular niches. <i>Immunity</i> , 2022, 55, 656-670.e8.	6.6	41
1221	Prediction of drug candidates for clear cell renal cell carcinoma using a systems biology-based drug repositioning approach. <i>EBioMedicine</i> , 2022, 78, 103963.	2.7	11
1222	GITR/GITRL reverse signalling modulates the proliferation of hepatic progenitor cells by recruiting ANXA2 to phosphorylate ERK1/2 and Akt. <i>Cell Death and Disease</i> , 2022, 13, 297.	2.7	1
1223	Prognostic comparative genes predict targets for sorafenib combination therapies in hepatocellular carcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1752-1763.	1.9	3
1224	The Role of Copy Number Variants in Gene Co-Expression Patterns for Luminal B Breast Tumors. <i>Frontiers in Genetics</i> , 2022, 13, 806607.	1.1	7
1225	Expression Profiles of HOXC6 Predict the Survival of Glioblastoma Patients and Correlate with Cell Cycle. <i>Journal of Oncology</i> , 2022, 2022, 1-17.	0.6	0
1226	cSurvival: a web resource for biomarker interactions in cancer outcomes and in cell lines. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
1227	Typical tumor immune microenvironment status determine prognosis in lung adenocarcinoma. <i>Translational Oncology</i> , 2022, 18, 101367.	1.7	10
1228	A new finding in the key prognosis-related proto-oncogene FYN in hepatocellular carcinoma based on the WGCNA hub-gene screening strategy. <i>BMC Cancer</i> , 2022, 22, 380.	1.1	10

#	ARTICLE	IF	CITATIONS
1229	Discordant prognosis of mismatch repair deficiency in colorectal and endometrial cancer reflects variation in antitumour immune response and immune escape. <i>Journal of Pathology</i> , 2022, 257, 340-351.	2.1	11
1230	Characterization of the treatment-naive immune microenvironment in melanoma with <i>BRAF</i> mutation. , 2022, 10, e004095.		7
1231	CAMOIP: a web server for comprehensive analysis on multi-omics of immunotherapy in pan-cancer. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	52
1232	Diffuse gastric cancer: Emerging mechanisms of tumor initiation and progression. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022, 1877, 188719.	3.3	15
1233	A microRNA panel that regulates proinflammatory cytokines as diagnostic and prognosis biomarkers in colon cancer. <i>Biochemistry and Biophysics Reports</i> , 2022, 30, 101252.	0.7	5
1234	HCNM: Heterogeneous Correlation Network Model for Multi-level Integrative Study of Multi-omics Data for Cancer Subtype Prediction. , 2021, 2021, 1880-1886.		2
1235	Integrated Analysis of Angiogenesis-Mediated Tumor Immune Microenvironment Pattern in Hepatocellular Carcinoma (HCC) and a Novel Prognostic Model Construction to Predict Patient Outcome. <i>Medical Science Monitor</i> , 2021, 27, e934937.	0.5	1
1237	Using MMRFBiolinks R-Package for Discovering Prognostic Markers in Multiple Myeloma. <i>Methods in Molecular Biology</i> , 2022, 2401, 289-314.	0.4	1
1238	REXO4 acts as a biomarker and promotes hepatocellular carcinoma progression. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 3093-3106.	0.6	5
1239	A multiparametric pharmacogenomic strategy for drug repositioning predicts therapeutic efficacy for glioblastoma cell lines. <i>Neuro-Oncology Advances</i> , 2022, 4, vdab192.	0.4	0
1240	An Immune-Related Prognostic Signature for Predicting Clinical Outcomes and Immune Landscape in IDH-Mutant Lower-Grade Gliomas. <i>Journal of Oncology</i> , 2021, 2021, 1-19.	0.6	2
1241	Pan-cancer classification by regularized multi-task learning. <i>Scientific Reports</i> , 2021, 11, 24252.	1.6	7
1242	Molecular drivers of tumor progression in microsatellite stable APC mutation-negative colorectal cancers. <i>Scientific Reports</i> , 2021, 11, 23507.	1.6	3
1244	WNT11/ROR2 signaling is associated with tumor invasion and poor survival in breast cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 395.	3.5	16
1245	Lung Adenocarcinoma Transcriptomic Analysis Predicts Adenylate Kinase Signatures Contributing to Tumor Progression and Negative Patient Prognosis. <i>Metabolites</i> , 2021, 11, 859.	1.3	1
1246	Identifying Cancer Subtypes Using a Residual Graph Convolution Model on a Sample Similarity Network. <i>Genes</i> , 2022, 13, 65.	1.0	8
1247	The Stroma Liquid Biopsy Panel Contains a Stromal-Epithelial Gene Signature Ratio That Is Associated with the Histologic Tumor-Stroma Ratio and Predicts Survival in Colon Cancer. <i>Cancers</i> , 2022, 14, 163.	1.7	4
1248	Genetic and immunologic features of recurrent stage I lung adenocarcinoma. <i>Scientific Reports</i> , 2021, 11, 23690.	1.6	3

#	ARTICLE	IF	CITATIONS
1251	Epigenetic priming in chronic liver disease impacts the transcriptional and genetic landscapes of hepatocellular carcinoma. <i>Molecular Oncology</i> , 2022, 16, 665-682.	2.1	3
1252	Resolving the immune landscape of human prostate at a single-cell level in health and cancer. <i>Cell Reports</i> , 2021, 37, 110132.	2.9	40
1253	STAT3-YAP/TAZ signaling in endothelial cells promotes tumor angiogenesis. <i>Science Signaling</i> , 2021, 14, eabj8393.	1.6	50
1254	Identification of an mRNA isoform switch for HNRNPA1 in breast cancers. <i>Scientific Reports</i> , 2021, 11, 24444.	1.6	5
1255	INTS8 is a therapeutic target for intrahepatic cholangiocarcinoma via the integration of bioinformatics analysis and experimental validation. <i>Scientific Reports</i> , 2021, 11, 23649.	1.6	1
1256	Identification and Validation of Hub Genes Associated with Bladder Cancer by Integrated Bioinformatics and Experimental Assays. <i>Frontiers in Oncology</i> , 2021, 11, 782981.	1.3	11
1257	Tumor microenvironment characterization in esophageal cancer identifies prognostic relevant immune cell subtypes and gene signatures. <i>Aging</i> , 2021, 13, 26118-26136.	1.4	5
1259	Gene expression RNA-sequencing survival analysis of high-grade serous ovarian carcinoma: a comparative study. , 2021, , .		0
1260	SMAD4 mutations do not preclude epithelialâ€mesenchymal transition in colorectal cancer. <i>Oncogene</i> , 2022, 41, 824-837.	2.6	12
1261	Identification of the 7-lncRNA Signature as a Prognostic Biomarker for Acute Myeloid Leukemia. <i>Disease Markers</i> , 2021, 2021, 1-6.	0.6	4
1262	The Sulfotransferase SULT1C2 Is Epigenetically Activated and Transcriptionally Induced by Tobacco Exposure and Is Associated with Patient Outcome in Lung Adenocarcinoma. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 416.	1.2	3
1263	A comprehensive characterization of the transcriptome in enzalutamide resistance prostate cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1782-1782.	0.7	0
1264	ITGB1-DT/ARNTL2 axis may be a novel biomarker in lung adenocarcinoma: a bioinformatics analysis and experimental validation. <i>Cancer Cell International</i> , 2021, 21, 665.	1.8	8
1265	Mining Cancer Cell Line-Based Drugs to Benefit KRAS^(G12D) Pancreatic Adenocarcinoma Patients. , 2021, , .		0
1266	TRMT6/61A-dependent base methylation of tRNA-derived fragments regulates gene-silencing activity and the unfolded protein response in bladder cancer. <i>Nature Communications</i> , 2022, 13, 2165.	5.8	43
1267	Serglycin Is Involved in TGF-Î² Induced Epithelial-Mesenchymal Transition and Is Highly Expressed by Immune Cells in Breast Cancer Tissue. <i>Frontiers in Oncology</i> , 2022, 12, 868868.	1.3	6
1268	Interrogation of cancer gene dependencies reveals paralog interactions of autosome and sex chromosome-encoded genes. <i>Cell Reports</i> , 2022, 39, 110636.	2.9	24
1269	ordinalbayes: Fitting Ordinal Bayesian Regression Models to High-Dimensional Data Using R. <i>Stats</i> , 2022, 5, 371-384.	0.5	0

#	ARTICLE	IF	CITATIONS
1270	GATA3 and MDM2 are synthetic lethal in estrogen receptor-positive breast cancers. <i>Communications Biology</i> , 2022, 5, 373.	2.0	7
1271	Pyroptosis-Related Signature Predicts Prognosis and Immunotherapy Efficacy in Muscle-Invasive Bladder Cancer. <i>Frontiers in Immunology</i> , 2022, 13, 782982.	2.2	19
1272	PTH2R is related to cell proliferation and migration in ovarian cancer: a multi-omics analysis of bioinformatics and experiments. <i>Cancer Cell International</i> , 2022, 22, 148.	1.8	5
1273	Neoantigen-specific CD4+ TÂcells in human melanoma have diverse differentiation states and correlate with CD8+ TÂcell, macrophage, and B cell function. <i>Cancer Cell</i> , 2022, 40, 393-409.e9.	7.7	59
1274	m6Acancer-Net: Identification of m6A-mediated cancer driver genes from gene-site heterogeneous network. <i>Methods</i> , 2022, , .	1.9	1
1275	Immune Landscape in PTEN-Related Glioma Microenvironment: A Bioinformatic Analysis. <i>Brain Sciences</i> , 2022, 12, 501.	1.1	7
1277	Development of a 5-Gene Signature to Evaluate Lung Adenocarcinoma Prognosis Based on the Features of Cancer Stem Cells. <i>BioMed Research International</i> , 2022, 2022, 1-28.	0.9	3
1278	Integrated Network Pharmacology Approach for Drug Combination Discovery: A Multi-Cancer Case Study. <i>Cancers</i> , 2022, 14, 2043.	1.7	10
1279	Osteosarcoma: Novel prognostic biomarkers using circulating and cell-free tumour DNA. <i>European Journal of Cancer</i> , 2022, 168, 1-11.	1.3	8
1440	Cisplatin resistance can be curtailed by blunting Bnip3-mediated mitochondrial autophagy. <i>Cell Death and Disease</i> , 2022, 13, 398.	2.7	20
1441	Constitutive Î²-Catenin Overexpression Represses Lncrna MIR100HG Transcription via HDAC6-Mediated Histone Modification in Colorectal Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 949-959.	1.5	11
1442	Downregulation of KIF15 inhibits the tumorigenesis of non-small-cell lung cancer via inactivating Raf/MEK/ERK signaling.. <i>Histology and Histopathology</i> , 2021, , 18408.	0.5	3
1443	Knockdown of circular RNA hsa_circ_0062270 suppresses the progression of melanoma via downregulation of CDC45.. <i>Histology and Histopathology</i> , 2021, , 18412.	0.5	6
1444	Comprehensive bioinformatic analysis reveals oncogenic role of H2A.Z isoforms in cervical cancer progression.. <i>Iranian Journal of Basic Medical Sciences</i> , 2021, 24, 1470-1481.	1.0	0
1445	Construction and Verification of a Glycolysis-Associated Gene Signature for the Prediction of Overall Survival in Low Grade Glioma. <i>Frontiers in Genetics</i> , 2022, 13, 843711.	1.1	0
1446	MDN1 Mutation Is Associated With High Tumor Mutation Burden and Unfavorable Prognosis in Breast Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 857836.	1.1	2
1447	PersonaDrive: a method for the identification and prioritization of personalized cancer drivers. <i>Bioinformatics</i> , 2022, 38, 3407-3414.	1.8	4
1448	Novel MicroRNA-Regulated Transcript Networks Are Associated with Chemotherapy Response in Ovarian Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4875.	1.8	2

#	ARTICLE	IF	CITATIONS
1449	Identification of Cancer-Associated Fibroblast Subtype of Triple-Negative Breast Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-14.	0.6	8
1450	Obesity-Associated Differentially Methylated Regions in Colon Cancer. <i>Journal of Personalized Medicine</i> , 2022, 12, 660.	1.1	3
1451	Establishment of a lncRNA-Based Prognostic Gene Signature Associated With Altered Immune Responses in HCC. <i>Frontiers in Immunology</i> , 2022, 13, 880288.	2.2	9
1452	m6A Regulator-Mediated Tumour Infiltration and Methylation Modification in Cervical Cancer Microenvironment. <i>Frontiers in Immunology</i> , 2022, 13, 888650.	2.2	15
1453	The Effect of Intratumoral Interrelation among FOXP3+ Regulatory T Cells on Treatment Response and Survival in Triple-Negative Breast Cancer. <i>Cancers</i> , 2022, 14, 2138.	1.7	4
1454	Comprehensive Genome-Scale Analysis of Esophageal Carcinoma With Esophageal Tissue-Resident Micro-Environment Discrepancy. <i>Frontiers in Microbiology</i> , 2022, 13, 859352.	1.5	1
1455	ISL2 is a putative tumor suppressor whose epigenetic silencing reprograms the metabolism of pancreatic cancer. <i>Developmental Cell</i> , 2022, 57, 1331-1346.e9.	3.1	9
1457	Study on the expression and function of chordin in oral squamous cell carcinoma. <i>Oral Diseases</i> , 2023, 29, 2034-2051.	1.5	2
1458	Tumor Purity in Preclinical Mouse Tumor Models. <i>Cancer Research Communications</i> , 2022, 2, 353-365.	0.7	4
1459	Consensus molecular subtype differences linking colon adenocarcinoma and obesity revealed by a cohort transcriptomic analysis. <i>PLoS ONE</i> , 2022, 17, e0268436.	1.1	3
1460	Identification of novel key regulatory lncRNAs in gastric adenocarcinoma. <i>BMC Genomics</i> , 2022, 23, 352.	1.2	8
1461	The LINC01929/miR-6875-5p/ADAMTS12 Axis in the ceRNA Network Regulates the Development of Advanced Bladder Cancer. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	7
1462	ROS-Related miRNAs Regulate Immune Response and Chemoradiotherapy Sensitivity in Hepatocellular Carcinoma by Comprehensive Analysis and Experiment. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-27.	1.9	5
1463	Long Non-Coding RNAs as Potential Regulators of EMT-Related Transcription Factors in Colorectal Cancer—A Systematic Review and Bioinformatics Analysis. <i>Cancers</i> , 2022, 14, 2280.	1.7	10
1464	Activation of the chemokine receptor 3 pathway leads to a better response to immune checkpoint inhibitors in patients with metastatic urothelial carcinoma. <i>Cancer Cell International</i> , 2022, 22, 186.	1.8	4
1465	Development of a prediction model for radiotherapy response among patients with head and neck squamous cell carcinoma based on the tumor immune microenvironment and hypoxia signature. <i>Cancer Medicine</i> , 2022, 11, 4673-4687.	1.3	7
1466	TCR Coexpression Signature Predicts Immunotherapy Resistance in NSCLC. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	2
1467	FAT1 Upregulates in Oral Squamous Cell Carcinoma and Promotes Cell Proliferation via Cell Cycle and DNA Repair. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	8

#	ARTICLE	IF	CITATIONS
1468	Gradient tree boosting and network propagation for the identification of pan-cancer survival networks. STAR Protocols, 2022, 3, 101353.	0.5	0
1470	Identification of genes and pathways associated with sex in Non-smoking lung cancer population. Gene, 2022, 831, 146566.	1.0	4
1471	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559.	5.8	56
1472	F-Box Protein 11 Suppresses Cell Proliferation and Aerobic Glycolysis in Glioblastomas by Mediating the Ubiquitin Degradation of Cdc25A. Journal of Neuropathology and Experimental Neurology, 2022, 81, 511-521.	0.9	1
1473	Albendazole induces immunotherapy response by facilitating ubiquitin-mediated PD-L1 degradation. , 2022, 10, e003819.		13
1474	Transcriptome analysis reveals high tumor heterogeneity with respect to re-activation of stemness and proliferation programs. PLoS ONE, 2022, 17, e0268626.	1.1	0
1475	The role of Jagged1 as a dynamic switch of cancer cell plasticity in PDAC assembloids. Theranostics, 2022, 12, 4431-4445.	4.6	7
1477	Identification of Hub Genes in Colorectal Adenocarcinoma by Integrated Bioinformatics. Frontiers in Cell and Developmental Biology, 2022, 10, .	1.8	2
1479	massiveGST: A Mannâ€“Whitneyâ€“Wilcoxon Gene-Set Test Tool That Gives Meaning to Gene-Set Enrichment Analysis. Entropy, 2022, 24, 739.	1.1	0
1480	The AKT1E17K Allele Promotes Breast Cancer in Mice. Cancers, 2022, 14, 2645.	1.7	1
1481	Comprehensive Pan-Cancer Analysis Reveals the Role of UHRF1-Mediated DNA Methylation and Immune Infiltration in Renal Cell Carcinoma. Journal of Oncology, 2022, 2022, 1-16.	0.6	2
1482	Pan-cancer analyses reveal the genetic and pharmacogenomic landscape of transient receptor potential channels. Npj Genomic Medicine, 2022, 7, .	1.7	8
1483	Identification of Four Novel Prognostic Biomarkers and Construction of Two Nomograms in Adrenocortical Carcinoma: A Multi-Omics Data Study via Bioinformatics and Machine Learning Methods. Frontiers in Molecular Biosciences, 2022, 9, .	1.6	1
1485	Identification of CD8+ T Cell Related Biomarkers in Ovarian Cancer. Frontiers in Genetics, 0, 13, .	1.1	5
1487	Engineered colorectal cancer tissue recapitulates key attributes of a patient-derived xenograft tumor line. Biofabrication, 2022, 14, 045001.	3.7	8
1488	Identification of the Active Compound of Liu Wei Di Huang Wan for Treatment of Gestational Diabetes Mellitus via Network Pharmacology and Molecular Docking. Journal of Diabetes Research, 2022, 2022, 1-13.	1.0	3
1489	Identification of Key Prognostic Genes of Triple Negative Breast Cancer by LASSO-Based Machine Learning and Bioinformatics Analysis. Genes, 2022, 13, 902.	1.0	14
1490	A Genomic Information Management System for Maintaining Healthy Genomic States and Application of Genomic Big Data in Clinical Research. International Journal of Molecular Sciences, 2022, 23, 5963.	1.8	6

#	ARTICLE	IF	CITATIONS
1491	Construction and validation of a two-gene signature based on SUMOylation regulatory genes in non-small cell lung cancer patients. <i>BMC Cancer</i> , 2022, 22, .	1.1	1
1492	Blockade LAT1 Mediates Methionine Metabolism to Overcome Oxaliplatin Resistance under Hypoxia in Renal Cell Carcinoma. <i>Cancers</i> , 2022, 14, 2551.	1.7	2
1493	A local human V β 1 T cell population is associated with survival in nonsmall-cell lung cancer. <i>Nature Cancer</i> , 2022, 3, 696-709.	5.7	39
1494	Overlapping group screening for detection of gene-environment interactions with application to TCGA high-dimensional survival genomic data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
1495	Discovering Common miRNA Signatures Underlying Female-Specific Cancers via a Machine Learning Approach Driven by the Cancer Hallmark ERBB. <i>Biomedicines</i> , 2022, 10, 1306.	1.4	3
1496	Homologous Recombination Pathway Alternation Predicts Prognosis of Colorectal Cancer With Chemotherapy. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	1
1497	A pyroptosis-related gene signature predicts prognosis and immune microenvironment in hepatocellular carcinoma. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	2
1498	Homologous recombination deficiency and molecular subtype are associated with immunogenicity in ovarian cancer. <i>Biomarkers in Medicine</i> , 2022, 16, 771-782.	0.6	1
1500	A Novel Exosome-Relevant Molecular Classification Uncovers Distinct Immune Escape Mechanisms and Genomic Alterations in Gastric Cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
1501	Multi-Omics Integrative Analysis of Lung Adenocarcinoma: An in silico Profiling for Precise Medicine. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	4
1502	Epigenetic Signatures of Centrosomes Are Novel Targets in Cancer Diagnosis: Insights from an Analysis of the Cancer Genome Atlas. <i>Epigenomes</i> , 2022, 6, 14.	0.8	1
1503	Gene Coexpression Network Characterizing Microenvironmental Heterogeneity and Intercellular Communication in Pancreatic Ductal Adenocarcinoma: Implications of Prognostic Significance and Therapeutic Target. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
1507	A potential EBV-related classifier is associated with the efficacy of immunotherapy in gastric cancer. <i>Translational Cancer Research</i> , 2022, 11, 2084-2096.	0.4	3
1508	Expression characteristics of long non-coding RNA in colon adenocarcinoma and its potential value for judging the survival and prognosis of patients: bioinformatics analysis based on The Cancer Genome Atlas database. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 1178-1187.	0.6	7
1509	A review of bioinformatics tools and web servers in different microarray platforms used in cancer research. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 85-164.	1.0	15
1511	KDM6A missense variants hamper H3 histone demethylation in lung squamous cell carcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3151-3160.	1.9	3
1513	Establishment of a reference single-cell RNA sequencing dataset for human pancreatic adenocarcinoma. <i>IScience</i> , 2022, 25, 104659.	1.9	21
1514	Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. <i>Nature Genetics</i> , 2022, 54, 985-995.	9.4	77

#	ARTICLE	IF	CITATIONS
1515	Tissue- and ethnicity-independent hypervariable DNA methylation states show evidence of establishment in the early human embryo. <i>Nucleic Acids Research</i> , 2022, 50, 6735-6752.	6.5	8
1516	HypoxaMIRs: Key Regulators of Hallmarks of Colorectal Cancer. <i>Cells</i> , 2022, 11, 1895.	1.8	4
1517	A novel 7 RNA-based signature for prediction of prognosis and therapeutic responses of wild-type BRAF cutaneous melanoma. <i>Biological Procedures Online</i> , 2022, 24, .	1.4	0
1518	Delineation of Pathogenomic Insights of Breast Cancer in Young Women. <i>Cells</i> , 2022, 11, 1927.	1.8	5
1519	A Whole Exon Screening-Based Score Model Predicts Prognosis and Immune Checkpoint Inhibitor Therapy Effects in Low-Grade Glioma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
1520	APOBEC Alteration Contributes to Tumor Growth and Immune Escape in Pan-Cancer. <i>Cancers</i> , 2022, 14, 2827.	1.7	11
1521	RNF31 inhibition sensitizes tumors to bystander killing by innate and adaptive immune cells. <i>Cell Reports Medicine</i> , 2022, 3, 100655.	3.3	17
1522	Potential Application of Pyroptosis in Kidney Renal Clear Cell Carcinoma Immunotherapy and Targeted Therapy. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
1523	Clustering analysis revealed the autophagy classification and potential autophagy regulators' sensitivity of pancreatic cancer based on multi-omics data. <i>Cancer Medicine</i> , 2023, 12, 733-746.	1.3	5
1524	Comprehensive Analysis Identifies PI3K/Akt Pathway Alterations as an Immune-Related Prognostic Biomarker in Colon Adenocarcinoma Patients Receiving Immune Checkpoint Inhibitor Treatment. <i>Journal of Immunology Research</i> , 2022, 2022, 1-14.	0.9	4
1525	GRHL2 motif is associated with intratumor heterogeneity of cis-regulatory elements in luminal breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, .	2.3	12
1526	Up-Regulation of TRIM32 Associated With the Poor Prognosis of Acute Myeloid Leukemia by Integrated Bioinformatics Analysis With External Validation. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
1527	Novel Diagnostic and Therapeutic Options for KMT2A-Rearranged Acute Leukemias. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	6
1528	Construction of ceRNA Networks Associated With CD8 T Cells in Breast Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	11
1529	Transcriptional and metabolic remodeling in clear cell renal cell carcinoma caused by ATF4 activation and the integrated stress response (ISR). <i>Molecular Carcinogenesis</i> , 2022, 61, 851-864.	1.3	11
1530	ESRRG, ATP4A, and ATP4B as Diagnostic Biomarkers for Gastric Cancer: A Bioinformatic Analysis Based on Machine Learning. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	1
1531	Distinct mechanisms of innate and adaptive immune regulation underlie poor oncologic outcomes associated with KRAS-TP53 co-alteration in pancreatic cancer. <i>Oncogene</i> , 2022, 41, 3640-3654.	2.6	17
1532	Identification of Tumor Antigens and Immune Subtypes of Esophageal Squamous Cell Carcinoma for mRNA Vaccine Development. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4

#	ARTICLE	IF	CITATIONS
1533	Analysis of Melanoma Gene Expression Signatures at the Single-Cell Level Uncovers 45-Gene Signature Related to Prognosis. <i>Biomedicines</i> , 2022, 10, 1478.	1.4	3
1534	The Potential Tumor-Suppressor DHRS7 Inversely Correlates with EGFR Expression in Prostate Cancer Cells and Tumor Samples. <i>Cancers</i> , 2022, 14, 3074.	1.7	2
1535	cGASâ€“STING drives the IL-6-dependent survival of chromosomally instable cancers. <i>Nature</i> , 2022, 607, 366-373.	13.7	132
1537	Transcriptional Plasticity Drives Leukemia Immune Escape. <i>Blood Cancer Discovery</i> , 2022, 3, 394-409.	2.6	8
1538	Adaptive stress response genes associated with breast cancer subtypes and survival outcomes reveal race-related differences. <i>Npj Breast Cancer</i> , 2022, 8, .	2.3	6
1539	A Framework to Predict the Molecular Classification and Prognosis of Breast Cancer Patients and Characterize the Landscape of Immune Cell Infiltration. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-23.	0.7	0
1540	Identification of Immune-Related Hub Genes in Thymoma: Defects in CD247 and Characteristics of Paraneoplastic Syndrome. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1541	Deep learning-based transcription factor activity for stratification of breast cancer patients. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194838.	0.9	1
1542	N6-methyladenosine (m6A) regulator expression pattern correlates with the immune landscape in lung adenocarcinoma. <i>Gene</i> , 2022, 836, 146639.	1.0	2
1543	The comprehensive and systematic identification of BLCA-specific SF-regulated, survival-related AS events. <i>Gene</i> , 2022, 835, 146657.	1.0	5
1544	PLIN2 promotes HCC cells proliferation by inhibiting the degradation of HIF1Î±. <i>Experimental Cell Research</i> , 2022, 418, 113244.	1.2	5
1545	Activating STING1-dependent immune signaling in <i>TP53</i> mutant and wild-type acute myeloid leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
1546	Network-based machine learning approach to predict immunotherapy response in cancer patients. <i>Nature Communications</i> , 2022, 13, .	5.8	56
1547	The immune landscape of solid pediatric tumors. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, .	3.5	13
1548	A Transcription Factor Signature Can Identify the CMS4 Subtype and Stratify the Prognostic Risk of Colorectal Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
1549	TTN mutations predict a poor prognosis in patients with thyroid cancer. <i>Bioscience Reports</i> , 2022, 42, .	1.1	13
1550	Development and validation of a prognostic model for esophageal carcinoma based on immune microenvironment using system bioinformatics. <i>Cancer Medicine</i> , 0, , .	1.3	1
1551	Development of a Prognostic Alternative Splicing Signature Associated With Tumor Microenvironment Immune Profiles in Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0

#	ARTICLE	IF	CITATIONS
1552	High expression of N-type calcium channel indicates a favorable prognosis in gliomas. <i>Medicine (United States)</i> , 2022, 101, e29782.	0.4	1
1553	Integrated Analysis Revealing the Senescence-Mediated Immune Heterogeneity of HCC and Construction of a Prognostic Model Based on Senescence-Related Non-Coding RNA Network. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
1554	DSEATM: drug set enrichment analysis uncovering disease mechanisms by biomedical text mining. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
1555	Molecular subtypes, prognostic and immunotherapeutic relevant gene signatures mediated by DNA methylation regulators in hepatocellular carcinoma. <i>Aging</i> , 2022, 14, 5271-5291.	1.4	3
1556	Impact of 5HydroxyMethylCytosine (5hmC) on reverse/direct association of cell-cycle, apoptosis, and extracellular matrix pathways in gastrointestinal cancers. <i>BMC Genomic Data</i> , 2022, 23, .	0.7	4
1557	A Lesson in Transcriptional Plasticity: Classical Identity Is Silenced, but Not Lost, in Pancreatic Ductal Adenocarcinoma Cell Lines. <i>Gastroenterology</i> , 2022, 163, 1450-1453.e3.	0.6	1
1558	Expression of DNA Helicase Genes Was Correlated with Homologous Recombination Deficiency in Breast Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-7.	0.7	1
1559	Molecular Differences between Squamous Cell Carcinoma and Adenocarcinoma Cervical Cancer Subtypes: Potential Prognostic Biomarkers. <i>Current Oncology</i> , 2022, 29, 4689-4702.	0.9	10
1560	Multi-omics analysis to screen potential therapeutic biomarkers for anti-cancer compounds. <i>Heliyon</i> , 2022, 8, e09616.	1.4	2
1561	Novel Drug Candidate Prediction for Intrahepatic Cholangiocarcinoma via Hub Gene Network Analysis and Connectivity Mapping. <i>Cancers</i> , 2022, 14, 3284.	1.7	11
1562	Comprehensive characterization of enhancer RNA in hepatocellular carcinoma reveals three immune subtypes with implications for immunotherapy. <i>Molecular Therapy - Oncolytics</i> , 2022, 26, 226-244.	2.0	4
1563	Machine Learning-Based Epigenetic Classifiers for Axillary Staging of Patients with ER-Positive Early-Stage Breast Cancer. <i>Annals of Surgical Oncology</i> , 2022, 29, 6407-6414.	0.7	5
1564	Expressional regulation of NKG2DLs is associated with the tumor development and shortened overall survival in lung adenocarcinoma. <i>Immunobiology</i> , 2022, 227, 152239.	0.8	1
1565	High PANX1 Expression Leads to Neutrophil Recruitment and the Formation of a High Adenosine Immunosuppressive Tumor Microenvironment in Basal-like Breast Cancer. <i>Cancers</i> , 2022, 14, 3369.	1.7	5
1566	MAFDash: An easy-to-use dashboard builder for mutation data. <i>F1000Research</i> , 0, 11, 748.	0.8	0
1567	Patient-derived renal cell carcinoma organoids for personalized cancer therapy. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	24
1568	Novel lncRNAs with diagnostic or prognostic value screened out from breast cancer via bioinformatics analyses. <i>PeerJ</i> , 0, 10, e13641.	0.9	4
1569	A comprehensive analysis of ncRNA-mediated interactions reveals potential prognostic biomarkers in prostate adenocarcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3839-3850.	1.9	1

#	ARTICLE	IF	CITATIONS
1570	Molecular landscape of <i>IDH</i> wild type, <i>TERT</i> wild type adult glioblastomas. <i>Brain Pathology</i> , 2022, 32, .	2.1	9
1571	Engineered natural killer cells impede the immunometabolic CD73-adenosine axis in solid tumors. <i>ELife</i> , 0, 11, .	2.8	11
1572	Metabolic modeling-based drug repurposing in Glioblastoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
1573	Characterization of Lactate Metabolism Score in Breast and Thyroid Cancers to Assist Immunotherapy via Large-Scale Transcriptomic Data Analysis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
1574	Construction of a miRNA-Based Nomogram Model to Predict the Prognosis of Endometrial Cancer. <i>Journal of Personalized Medicine</i> , 2022, 12, 1154.	1.1	16
1575	Pan-sarcoma characterization of lncRNAs in the crosstalk of EMT and tumour immunity identifies distinct clinical outcomes and potential implications for immunotherapy. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	3
1576	Characterizing the extracellular matrix transcriptome of cervical, endometrial, and uterine cancers. <i>Matrix Biology Plus</i> , 2022, 15, 100117.	1.9	6
1577	Comprehensive Analysis of the Aberrance and Functional Significance of Ferroptosis in Gastric Cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
1578	Identification of potential biomarkers and survival analysis for oral squamous cell carcinoma: A transcriptomic study. <i>Oral Diseases</i> , 2023, 29, 2658-2666.	1.5	3
1579	Acid-base homeostasis and implications to the phenotypic behaviors of cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, , .	3.0	3
1580	A Novel Ferroptosis-Related Gene Signature to Predict Prognosis of Esophageal Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-14.	0.6	0
1581	An Immune-Related Gene Signature Can Predict Clinical Outcomes and Immunotherapeutic Response in Oral Squamous Cell Carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
1582	Primary cicatricial alopecias are characterized by dysregulation of shared gene expression pathways. , 2022, 1, .		7
1583	The ubiquitin-ligase TRAF6 and TGF β type I receptor form a complex with Aurora kinase B contributing to mitotic progression and cytokinesis in cancer cells. <i>EBioMedicine</i> , 2022, 82, 104155.	2.7	5
1584	Development and Validation of a 6-Gene Hypoxia-Related Prognostic Signature For Cholangiocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
1585	Characterization of the Immune Infiltration Landscape and Identification of Prognostic Biomarkers for Esophageal Cancer. <i>Molecular Biotechnology</i> , 0, , .	1.3	2
1586	Copy Number Variation of Circulating Tumor DNA (ctDNA) Detected Using NIPT in Neoadjuvant Chemotherapy-Treated Ovarian Cancer Patients. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
1587	A Cross-Comparison of High-Throughput Platforms for Circulating MicroRNA Quantification, Agreement in Risk Classification, and Biomarker Discovery in Non-Small Cell Lung Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1

#	ARTICLE	IF	CITATIONS
1588	A Cancer Cellâ€™s Intrinsic GOT2â€™s PPARÎ Axis Suppresses Antitumor Immunity. <i>Cancer Discovery</i> , 2022, 12, 2414-2433.	7.7	20
1589	Identification of Prognostic Genes in Gliomas Based on Increased Microenvironment Stiffness. <i>Cancers</i> , 2022, 14, 3659.	1.7	4
1592	An integrative transcriptome analysis reveals potential predictive, prognostic biomarkers and therapeutic targets in colorectal cancer. <i>BMC Cancer</i> , 2022, 22, .	1.1	19
1594	Stemness-related gene signature for predicting therapeutic response in patients with esophageal cancer. <i>Translational Cancer Research</i> , 2022, 11, 2359-2373.	0.4	1
1595	Metabolic balance in colorectal cancer is maintained by optimal Wnt signaling levels. <i>Molecular Systems Biology</i> , 2022, 18, .	3.2	3
1596	The prognostic value and biological significance of gap junction beta protein 2 (GJB2 or Cx26) in cervical cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	5
1598	RGS1 and related genes as potential targets for immunotherapy in cervical cancer: computational biology and experimental validation. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	15
1599	Selective targeting BMP2 and 4 in SMAD4 negative esophageal adenocarcinoma inhibits tumor growth and aggressiveness in preclinical models. <i>Cellular Oncology (Dordrecht)</i> , 2022, 45, 639-658.	2.1	6
1600	Distinct modulation of IFNÎ3-induced transcription by BET bromodomain and catalytic P300/CBP inhibition in breast cancer. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	1
1602	SETD2 regulates gene transcription patterns and is associated with radiosensitivity in lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
1603	PTPRD and CNTNAP2 as markers of tumor aggressiveness in oligodendrogliomas. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
1604	ALDH1A1 Expression is Enriched in Early Onset Colorectal Cancers. <i>Gastroenterology</i> , 2022, , .	0.6	0
1605	Comprehensive characterization of clonality of driver genes revealing their clinical relevance in colorectal cancer. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	5
1607	Truncated FGFR2 is a clinically actionable oncogene in multiple cancers. <i>Nature</i> , 2022, 608, 609-617.	13.7	31
1608	Induced pluripotent stem cells display a distinct set of MHC I-associated peptides shared by human cancers. <i>Cell Reports</i> , 2022, 40, 111241.	2.9	7
1609	Screening of co-pathogenic genes of non-alcoholic fatty liver disease and hepatocellular carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
1610	Comprehensive exploration of tumor immune microenvironment feature and therapeutic response in colorectal cancer based on a novel immune-related long non-coding RNA prognostic signature. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1611	mintRULS: Prediction of miRNAâ€™s mRNA Target Site Interactions Using Regularized Least Square Method. <i>Genes</i> , 2022, 13, 1528.	1.0	2

#	ARTICLE	IF	CITATIONS
1612	HSF1 Can Prevent Inflammation following Heat Shock by Inhibiting the Excessive Activation of the ATF3 and JUN&FOS Genes. <i>Cells</i> , 2022, 11, 2510.	1.8	3
1613	DNA methylation analysis of normal colon organoids from familial adenomatous polyposis patients reveals novel insight into colon cancer development. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	10
1614	EMT-Related Gene Signature Predicts the Prognosis in Uveal Melanoma Patients. <i>Journal of Oncology</i> , 2022, 2022, 1-19.	0.6	5
1615	Comprehensive Analysis of Histone Modifications in Hepatocellular Carcinoma Reveals Different Subtypes and Key Prognostic Models. <i>Journal of Oncology</i> , 2022, 2022, 1-20.	0.6	0
1616	Identification of Hub Genes of Lung Adenocarcinoma Based on Weighted Gene Co-Expression Network in Chinese Population. <i>Pathology and Oncology Research</i> , 0, 28, .	0.9	1
1617	Lymphocyte antigen 6G6D-mediated modulation through p38 \pm MAPK and DNA methylation in colorectal cancer. <i>Cancer Cell International</i> , 2022, 22, .	1.8	2
1618	Hidden patterns of gene expression provide prognostic insight for colorectal cancer. <i>Cancer Gene Therapy</i> , 2023, 30, 11-21.	2.2	3
1619	M6A Modifier-Mediated Methylation Characterized by Diverse Prognosis, Tumor Microenvironment, and Immunotherapy Response in Hepatocellular Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-25.	0.6	0
1620	Atypical $\text{I}\beta\text{B}$ Bcl3 enhances the generation of the NF- $\text{I}\beta\text{B}$ p52 homodimer. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	4
1621	Utilization of hypoxia-derived gene signatures to predict clinical outcomes and immune checkpoint blockade therapy responses in prostate cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1622	The clonal expression genes associated with poor prognosis of liver cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1623	Oncogenic signaling pathway-related long non-coding RNAs for predicting prognosis and immunotherapy response in breast cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
1624	Translation of the 27-gene immuno-oncology test (IO score) to predict outcomes in immune checkpoint inhibitor treated metastatic urothelial cancer patients. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	6
1625	Gene expression analysis reveals a 5-gene signature for progression-free survival in prostate cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
1626	Subtype and cell type specific expression of lncRNAs provide insight into breast cancer. <i>Communications Biology</i> , 2022, 5, .	2.0	10
1627	Identification of Gender- and Subtype-Specific Gene Expression Associated with Patient Survival in Low-Grade and Anaplastic Glioma in Connection with Steroid Signaling. <i>Cancers</i> , 2022, 14, 4114.	1.7	3
1629	Evolution of intra-tumoral heterogeneity across different pathological stages in papillary thyroid carcinoma. <i>Cancer Cell International</i> , 2022, 22, .	1.8	7
1631	Protocol for stratification of triple-negative breast cancer patients using in silico signaling dynamics. <i>STAR Protocols</i> , 2022, 3, 101619.	0.5	0

#	ARTICLE	IF	CITATIONS
1632	Transformed cells after senescence give rise to more severe tumor phenotypes than transformed non-senescent cells. <i>Cancer Letters</i> , 2022, 546, 215850.	3.2	3
1633	Pan-cancer gene expression analysis: Identification of deregulated autophagy genes and drugs to target them. <i>Gene</i> , 2022, 844, 146821.	1.0	6
1634	Transcriptome Analyses Identify Deregulated MYC in Early Onset Colorectal Cancer. <i>Biomolecules</i> , 2022, 12, 1223.	1.8	6
1635	Comparative whole transcriptome analysis of gene expression in three canine soft tissue sarcoma types. <i>PLoS ONE</i> , 2022, 17, e0273705.	1.1	5
1636	Identification of BRIP1, NSMCE2, ANAPC7, RAD18 and TTL from chromosome segregation gene set associated with hepatocellular carcinoma. <i>Cancer Genetics</i> , 2022, 268-269, 28-36.	0.2	1
1637	Weighted Correlation Network Analysis of Cancer Stem Cell-Related Prognostic Biomarkers in Esophageal Squamous Cell Carcinoma. <i>Technology in Cancer Research and Treatment</i> , 2022, 21, 153303382211170.	0.8	2
1638	SLOAD: a comprehensive database of cancer-specific synthetic lethal interactions for precision cancer therapy via multi-omics analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, .	1.4	5
1639	An Ensemble Framework Integrating Whole Slide Pathological Images and miRNA Data to Predict Radiosensitivity of Breast Cancer Patients. <i>Lecture Notes in Computer Science</i> , 2022, , 757-766.	1.0	0
1640	FOXR2 Is an Epigenetically Regulated Pan-Cancer Oncogene That Activates ETS Transcriptional Circuits. <i>Cancer Research</i> , 2022, 82, 2980-3001.	0.4	7
1641	Comparative single-cell transcriptomes of dose and time dependent epithelialâ€“mesenchymal spectrums. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	8
1642	Identification of m6A modification patterns and development of m6Aâ€“hypoxia prognostic signature to characterize tumor microenvironment in triple-negative breast cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
1643	Identification of Novel tRNA-Leu-CAA-Derived tsRNAs for the Diagnosis and Prognosis of Diffuse Gliomas. <i>Cancer Management and Research</i> , 0, Volume 14, 2609-2623.	0.9	5
1644	Insights into Early Onset Colorectal Cancer through Analysis of Normal Colon Organoids of Familial Adenomatous Polyposis Patients. <i>Cancers</i> , 2022, 14, 4138.	1.7	1
1645	Application of Feature Selection and Deep Learning for Cancer Prediction Using DNA Methylation Markers. <i>Genes</i> , 2022, 13, 1557.	1.0	5
1646	The Ferroptosis Molecular Subtype Reveals Characteristics of the Tumor Microenvironment, Immunotherapeutic Response, and Prognosis in Gastric Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9767.	1.8	2
1647	Hepatogenesis and hepatocarcinogenesis: Alignment of the main signaling pathways. <i>Journal of Cellular Physiology</i> , 0, , .	2.0	3
1648	Identification of candidate biomarkers associated with gastric cancer prognosis based on an integrated bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 1690-1700.	0.6	2
1649	Epithelial-Mesenchymal Transition Gene Signature Is Associated with Neoadjuvant Chemoradiotherapy Resistance and Prognosis of Esophageal Squamous Cell Carcinoma. <i>Disease Markers</i> , 2022, 2022, 1-14.	0.6	2

#	ARTICLE	IF	CITATIONS
1650	Genomic Effect of DNA Methylation on Gene Expression in Colorectal Cancer. <i>Biology</i> , 2022, 11, 1388.	1.3	5
1651	RAS oncogenic activity predicts response to chemotherapy and outcome in lung adenocarcinoma. <i>Nature Communications</i> , 2022, 13, .	5.8	17
1652	Identification of the hub and prognostic genes in liver hepatocellular carcinoma via bioinformatics analysis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	4
1653	Integrated longitudinal analysis of adult grade 4 diffuse gliomas with long-term relapse interval revealed upregulation of TGF- β signaling in recurrent tumors. <i>Neuro-Oncology</i> , 2023, 25, 662-673.	0.6	9
1654	B Cell Receptor Signaling Pathway Mutation as Prognosis Predictor of Immune Checkpoint Inhibitors in Lung Adenocarcinoma by Bioinformatic Analysis. <i>Journal of Inflammation Research</i> , 0, Volume 15, 5541-5555.	1.6	3
1657	Predicting liver cancer on epigenomics data using machine learning. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	0
1658	AR Expression Correlates with Distinctive Clinicopathological and Genomic Features in Breast Cancer Regardless of ESR1 Expression Status. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11468.	1.8	0
1660	Genomic Landscapes and Hallmarks of Mutant RAS in Human Cancers. <i>Cancer Research</i> , 2022, 82, 4058-4078.	0.4	4
1661	Prognostic value of lactate metabolism-related gene expression signature in adult primary gliomas and its impact on the tumor immune microenvironment. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
1662	Dynamic cancer drivers: a causal approach for cancer driver discovery based on bio-pathological trajectories. <i>Briefings in Functional Genomics</i> , 0, , .	1.3	1
1663	The expression and methylation of PITX genes is associated with the prognosis of head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1664	Comprehensive analysis of aerobic glycolysis-related genes for prognosis, immune features and drug treatment strategy in prostate cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
1665	Identification and validation of real hub genes in hepatocellular carcinoma based on weighted gene co-expression network analysis. <i>Cancer Biomarkers</i> , 2022, 35, 227-243.	0.8	3
1667	Analysis of genomes and transcriptomes of clear cell renal cell carcinomas identifies mutations and gene expression changes in the TGF-beta pathway. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
1668	A novel molecular signature identifies mixed subtypes in renal cell carcinoma with poor prognosis and independent response to immunotherapy. <i>Genome Medicine</i> , 2022, 14, .	3.6	11
1669	Identifying key genes of classic papillary thyroid cancer in women aged more than 55 years old using bioinformatics analysis. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	0
1671	Identification of genes with high heterogeneity of expression as a predictor of different prognosis and therapeutic responses in colorectal cancer: a challenge and a strategy. <i>Cancer Cell International</i> , 2022, 22, .	1.8	4
1672	Malignant clonal evolution drives multiple myeloma cellular ecological diversity and microenvironment reprogramming. <i>Molecular Cancer</i> , 2022, 21, .	7.9	12

#	ARTICLE	IF	CITATIONS
1673	Impaired expression of serine/arginine protein kinase 2 (SRPK2) affects melanoma progression. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
1675	CGV: Cancer Genome Viewer, a web service for integrative cancer genome and pharmacogenomic data analysis. <i>Bioinformatics</i> , 0, , .	1.8	0
1676	Evaluating the role of IDO1 macrophages in immunotherapy using scRNA-seq and bulk-seq in colorectal cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
1677	A metabolism-associated gene signature for prognosis prediction of hepatocellular carcinoma. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	5
1678	Removing unwanted variation from large-scale RNA sequencing data with PRPS. <i>Nature Biotechnology</i> , 2023, 41, 82-95.	9.4	20
1679	An EMT-based risk score thoroughly predicts the clinical prognosis, tumor immune microenvironment and molecular subtypes of bladder cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
1680	Analyzing integrated network of methylation and gene expression profiles in lung squamous cell carcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1681	Circular RNA hsa_circ_0062682 Binds to YBX1 and Promotes Oncogenesis in Hepatocellular Carcinoma. <i>Cancers</i> , 2022, 14, 4524.	1.7	5
1683	Gene Expression and DNA Methylation in Human Papillomavirus Positive and Negative Head and Neck Squamous Cell Carcinomas. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10967.	1.8	3
1685	Applications for open access normalized synthesis in metastatic prostate cancer trials. <i>Frontiers in Artificial Intelligence</i> , 0, 5, .	2.0	0
1686	TRAF3IP3 promotes glioma progression through the ERK signaling pathway. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
1687	Unveiling the molecular features, relevant immune and clinical characteristics of SIGLEC15 in thyroid cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
1688	A Genomically and Clinically Annotated Patient-Derived Xenograft Resource for Preclinical Research in Non- Small Cell Lung Cancer. <i>Cancer Research</i> , 2022, 82, 4126-4138.	0.4	7
1689	Comparison of the mutational profiles of neuroendocrine breast tumours, invasive ductal carcinomas and pancreatic neuroendocrine carcinomas. <i>Oncogenesis</i> , 2022, 11, .	2.1	1
1690	DSTYK inhibition increases the sensitivity of lung cancer cells to T cell-mediated cytotoxicity. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	6
1691	High-dimensional genomic feature selection with the ordered stereotype logit model. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
1692	Transformer for Gene Expression Modeling (T-GEM): An Interpretable Deep Learning Model for Gene Expression-Based Phenotype Predictions. <i>Cancers</i> , 2022, 14, 4763.	1.7	8
1693	Accurate detection of benign and malignant renal tumor subtypes with MethylBoostER: An epigenetic marker-driven learning framework. <i>Science Advances</i> , 2022, 8, .	4.7	1

#	ARTICLE	IF	CITATIONS
1694	CiberAMP: An R Package to Identify Differential mRNA Expression Linked to Somatic Copy Number Variations in Cancer Datasets. <i>Biology</i> , 2022, 11, 1411.	1.3	0
1695	Identification of a novel m5C/m6A-related gene signature for predicting prognosis and immunotherapy efficacy in lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
1696	A lactate-related LncRNA model for predicting prognosis, immune landscape and therapeutic response in breast cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
1697	DNA methylation regulator-mediated modification pattern defines tumor microenvironment immune infiltration landscape in colon cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
1699	Ferroptosis-related gene signature predicts prognosis in kidney renal papillary cell carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
1701	Macrophage-related molecular subtypes in lung adenocarcinoma identify novel tumor microenvironment with prognostic and therapeutic implications. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1702	Systematic analysis of cancer-specific synthetic lethal interactions provides insight into personalized anticancer therapy. <i>FEBS Journal</i> , 2023, 290, 1531-1548.	2.2	2
1703	Immune activation is essential for the antitumor activity of EZH2 inhibition in urothelial carcinoma. <i>Science Advances</i> , 2022, 8, .	4.7	13
1704	A meta-learning approach to improving radiation response prediction in cancers. <i>Computers in Biology and Medicine</i> , 2022, 150, 106163.	3.9	5
1705	PSG7 indicates that age at diagnosis is associated with papillary thyroid carcinoma: A study based on the cancer genome atlas data. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1706	A transcriptional network of cell cycle dysregulation in noninvasive papillary urothelial carcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
1707	KrÄppel-like factor 7 influences translation and pathways involved in ribosomal biogenesis in breast cancer. <i>Breast Cancer Research</i> , 2022, 24, .	2.2	5
1708	Elevated CDK5R1 expression associated with poor prognosis, proliferation, and drug resistance in colorectal and breast malignancies: CDK5R1 as an oncogene in cancers. <i>Chemico-Biological Interactions</i> , 2022, 368, 110190.	1.7	0
1709	Constructing Integrative Cerna Networks and Finding Prognostic Biomarkers in Renal Cell Carcinoma. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, , 1-10.	1.9	1
1710	Identifying common signatures and potential therapeutic biomarkers in COPD and lung cancer using miRNA-mRNA co-expression networks. <i>Informatics in Medicine Unlocked</i> , 2022, 34, 101115.	1.9	1
1711	Hsa_Circ_0066351 Acts as a Prognostic and Immunotherapeutic Biomarker in Colorectal Cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
1713	Senescence Rewires Microenvironment Sensing to Facilitate Antitumor Immunity. <i>Cancer Discovery</i> , 2023, 13, 432-453.	7.7	46
1715	MiR-140 leads to MRE11 downregulation and ameliorates oxaliplatin treatment and therapy response in colorectal cancer patients. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4

#	ARTICLE	IF	CITATIONS
1717	Transcriptome-based network analysis related to M2-like tumor-associated macrophage infiltration identified VARS1 as a potential target for improving melanoma immunotherapy efficacy. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	6
1718	Molecular Classification of Colorectal Cancer by microRNA Profiling: Correlation with the Consensus Molecular Subtypes (CMS) and Validation of miR-30b Targets. <i>Cancers</i> , 2022, 14, 5175.	1.7	3
1719	CmirC: an integrated database of clustered miRNAs co-localized with copy number variations in cancer. <i>Functional and Integrative Genomics</i> , 2022, 22, 1229-1241.	1.4	2
1720	RNA m5C regulator-mediated modification patterns and the cross-talk between tumor microenvironment infiltration in gastric cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
1721	Differential Expression in the Tumor Microenvironment of mRNAs Closely Associated with Colorectal Cancer Metastasis. <i>Annals of Surgical Oncology</i> , 0, , .	0.7	0
1722	Deciphering the action mechanism of paeoniflorin in suppressing pancreatic cancer: A network pharmacology study and experimental validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
1723	miR-20b-5p is a novel biomarker for detecting prostate cancer. <i>Oncology Letters</i> , 2022, 24, .	0.8	2
1725	Decoding the colorectal cancer ecosystem emphasizes the cooperative role of cancer cells, TAMs and CAFs in tumor progression. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	2
1726	The cholesterol transport protein GRAMD1C regulates autophagy initiation and mitochondrial bioenergetics. <i>Nature Communications</i> , 2022, 13, .	5.8	12
1727	BIC: a database for the transcriptional landscape of bacteria in cancer. <i>Nucleic Acids Research</i> , 0, , .	6.5	3
1728	Single-cell transcriptomic analysis highlights origin and pathological process of human endometrioid endometrial carcinoma. <i>Nature Communications</i> , 2022, 13, .	5.8	13
1729	In silico characterization of competing endogenous RNA network in glioblastoma multiforme with a systems biology approach. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
1730	Non-genetic stratification reveals epigenetic heterogeneity and identifies vulnerabilities of glycolysis addiction in lung adenocarcinoma subtype. <i>Oncogenesis</i> , 2022, 11, .	2.1	0
1731	TRPV1 Is a Potential Tumor Suppressor for Its Negative Association with Tumor Proliferation and Positive Association with Antitumor Immune Responses in Pan-Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-15.	0.6	3
1732	Identification of a novel signature with prognostic value in triple-negative breast cancer through clinico-transcriptomic analysis. <i>Annals of Translational Medicine</i> , 2022, 10, 1095-1095.	0.7	1
1733	The prognostic value and molecular properties of tertiary lymphoid structures in oesophageal squamous cell carcinoma. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	13
1734	Scinderin Is a Novel Oncogene for Its Correlates with Poor Prognosis, Immune Infiltrates and Matrix Metalloproteinase-2/9 (MMP2/9) in Glioma. <i>Brain Sciences</i> , 2022, 12, 1415.	1.1	1
1735	Identification of a novel ceRNA network related to prognosis and immunity in HNSCC based on integrated bioinformatic investigation. <i>Scientific Reports</i> , 2022, 12, .	1.6	1

#	ARTICLE	IF	CITATIONS
1736	Necroptosis-related lncRNAs: Combination of bulk and single-cell sequencing reveals immune landscape alteration and a novel prognosis stratification approach in lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
1737	Comprehensive Characterization of the Regulatory Landscape of Adrenocortical Carcinoma: Novel Transcription Factors and Targets Associated with Prognosis. <i>Cancers</i> , 2022, 14, 5279.	1.7	5
1738	A Hypoxia-Related Prognostic Model Predicts Overall Survival and Treatment Response in Hepatocellular Carcinoma. <i>Bioscience Reports</i> , 0, , .	1.1	0
1739	Function and prognostic value of N6-methyladenosine-modified RNAs in lung adenocarcinoma. <i>Journal of Gene Medicine</i> , 2023, 25, .	1.4	1
1740	The cell-free DNA methylome captures distinctions between localized and metastatic prostate tumors. <i>Nature Communications</i> , 2022, 13, .	5.8	25
1741	c-Mpl-del, a c-Mpl alternative splicing isoform, promotes AMKL progression and chemoresistance. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	2
1743	Fusion gene recurrence in non-small cell lung cancers and its association with cigarette smoke exposure. <i>Translational Lung Cancer Research</i> , 2022, 11, 2022-2039.	1.3	1
1744	COL11A1 as an novel biomarker for breast cancer with machine learning and immunohistochemistry validation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	10
1745	Construction and validation of a m6A RNA methylation and ferroptosis-related prognostic model for pancreatic cancer by integrated bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 2553-2564.	0.6	3
1746	Pan-cancer analyses of classical protein tyrosine phosphatases and phosphatase-targeted therapy in cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
1747	Endometrial cancer prognosis prediction using correlation models based on CDK family genes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1748	miR-148a-3p and DDX6 functional link promotes survival of myeloid leukemia cells. <i>Blood Advances</i> , 2023, 7, 3846-3861.	2.5	2
1749	PLPP2: Potential therapeutic target of breast cancer in PLPP family. <i>Immunobiology</i> , 2022, 227, 152298.	0.8	1
1750	Biomarkers discovery for endometrial cancer: A graph convolutional sample network method. <i>Computers in Biology and Medicine</i> , 2022, 150, 106200.	3.9	2
1751	Targeting cancer glycosylation repolarizes tumor-associated macrophages allowing effective immune checkpoint blockade. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	49
1752	Integrated analysis of the genomic and transcriptional profile of gliomas with isocitrate dehydrogenase-1 and tumor protein 53 mutations. <i>International Journal of Immunopathology and Pharmacology</i> , 2022, 36, 039463202211392.	1.0	0
1753	GLassonet: Identifying Discriminative Gene Sets Among Molecular Subtypes of Breast Cancer. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1905-1916.	1.9	2
1754	Significance of Chr9p22.1-p21.3 Deletion in Cancer Development: A Pan-cancer <i>In Silico</i> Analysis. <i>Anticancer Research</i> , 2022, 42, 5291-5304.	0.5	2

#	ARTICLE	IF	CITATIONS
1755	Metabolism-associated molecular classification of gastric adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
1756	Single-cell RNA sequencing reveals cellular and molecular reprogramming landscape of gliomas and lung cancer brain metastases. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	12
1758	SLC11A1 associated with tumor microenvironment is a potential biomarker of prognosis and immunotherapy efficacy for colorectal cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
1759	Expression pattern of secretory-cell-related transcriptional signatures in colon adenocarcinomas defines tumor microenvironment characteristics and correlates with clinical outcomes. <i>Molecular Oncology</i> , 2023, 17, 499-517.	2.1	1
1760	Novel T-cell signature based on cell pair algorithm predicts survival and immunotherapy response for patients with bladder urothelial carcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
1761	Molecular subtyping of esophageal squamous cell carcinoma by large-scale transcriptional profiling: Characterization, therapeutic targets, and prognostic value. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
1762	Increased levels of microRNA-320 in blood serum and plasma is associated with imminent and advanced lung cancer. <i>Molecular Oncology</i> , 2023, 17, 312-327.	2.1	1
1763	An Enhancer Demethylator Phenotype Converged to Immune Dysfunction and Resistance to Immune Checkpoint Inhibitors in Clear-Cell Renal Cell Carcinomas. <i>Clinical Cancer Research</i> , 2023, 29, 1279-1291.	3.2	4
1765	Connecting multiple microenvironment proteomes uncovers the biology in head and neck cancer. <i>Nature Communications</i> , 2022, 13, .	5.8	4
1766	Cellular and molecular effects of PNCK, a non-canonical kinase target in renal cell carcinoma. <i>IScience</i> , 2022, 25, 105621.	1.9	2
1767	Identifying Diagnostic and Prognostic Differentially Expressed Genes of Gastric Cancer Based on Bioinformatics Analyses of RNA-seq Data. <i>Genetic Testing and Molecular Biomarkers</i> , 2022, 26, 512-521.	0.3	1
1768	Prognosis Risk Model Based on Necroptosis-Related Signature for Bladder Cancer. <i>Genes</i> , 2022, 13, 2120.	1.0	0
1769	The tRNA-Cys-GCA Derived tsRNAs Suppress Tumor Progression of Gliomas via Regulating VAV2. <i>Disease Markers</i> , 2022, 2022, 1-16.	0.6	4
1770	A novel DNA damage repair-related signature for predicting prognosis and treatment response in non-small lung cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
1771	The expression changes of transcription factors including ANKZF1, LEF1, CASZ1, and ATOH1 as a predictor of survival rate in colorectal cancer: a large-scale analysis. <i>Cancer Cell International</i> , 2022, 22, .	1.8	4
1772	Sequential gene expression analysis of cervical malignant transformation identifies RFC4 as a novel diagnostic and prognostic biomarker. <i>BMC Medicine</i> , 2022, 20, .	2.3	2
1773	Sprouty4 is epigenetically upregulated in human colorectal cancer. <i>Epigenetics</i> , 2023, 18, .	1.3	3
1774	TIMEDB: tumor immune micro-environment cell composition database with automatic analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2023, 51, D1417-D1424.	6.5	7

#	ARTICLE	IF	CITATIONS
1777	Landscape of the intratumoral microenvironment in bladder cancer: Implications for prognosis and immunotherapy. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 74-85.	1.9	1
1778	Proteomic profiling of canine fibrosarcoma and adjacent peritumoral tissue. <i>Neoplasia</i> , 2023, 35, 100858.	2.3	2
1779	Omics-based identification of an NRF2-related auranofin resistance signature in cancer: Insights into drug repurposing. <i>Computers in Biology and Medicine</i> , 2023, 152, 106347.	3.9	4
1780	Cancer subtyping with heterogeneous multi-omics data via hierarchical multi-kernel learning. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	2
1781	Leveraging biochemical reactions to unravel functional impacts of cancer somatic variants affecting protein interaction interfaces. <i>F1000Research</i> , 0, 10, 1111.	0.8	0
1783	Exploring the Role of the Inhibitor of Apoptosis BIRC6 in Breast Cancer: A Database Analysis. <i>JCO Clinical Cancer Informatics</i> , 2022, , .	1.0	0
1784	Oral Lichen Planus and Oral Squamous Cell Carcinoma share key oncogenic signatures. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
1785	Cuprotosis Patterns Are Associated with Tumor Mutation Burden and Immune Landscape in Lung Adenocarcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-12.	0.6	4
1786	Multi-omics consensus portfolio to refine the classification of lung adenocarcinoma with prognostic stratification, tumor microenvironment, and unique sensitivity to first-line therapies. <i>Translational Lung Cancer Research</i> , 2022, 11, 2243-2260.	1.3	1
1787	Identification of prognostically significant DNA methylation signatures in patients with various breast cancer types. <i>Bulletin of Russian State Medical University</i> , 2022, , .	0.3	0
1788	Screening for Biomarkers for Progression from Oral Leukoplakia to Oral Squamous Cell Carcinoma and Evaluation of Diagnostic Efficacy by Multiple Machine Learning Algorithms. <i>Cancers</i> , 2022, 14, 5808.	1.7	3
1790	A Model-Based Prognostic Predictor for Urothelial Bladder Carcinoma Through the Integrated Bioinformatics Analysis. , 2022, , .		0
1791	Loss of NF1 in Melanoma Confers Sensitivity to SYK Kinase Inhibition. <i>Cancer Research</i> , 2023, 83, 316-331.	0.4	4
1792	MYC regulates a pan-cancer network of co-expressed oncogenic splicing factors. <i>Cell Reports</i> , 2022, 41, 111704.	2.9	19
1793	Construction of the model for predicting prognosis by key genes regulating EGFR-TKI resistance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1794	Multimiomics of Colorectal Cancer Organoids Reveals Putative Mediators of Cancer Progression Resulting from SMAD4 Inactivation. <i>Journal of Proteome Research</i> , 2023, 22, 138-151.	1.8	8
1795	Genome-wide methylation profiling identify hypermethylated HOXL subclass genes as potential markers for esophageal squamous cell carcinoma detection. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	3
1796	The characterization of tumor microenvironment infiltration and the construction of predictive index based on cuproptosis-related gene in primary lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3

#	ARTICLE	IF	CITATIONS
1797	PDPN contributes to constructing immunosuppressive microenvironment in IDH wildtype glioma. <i>Cancer Gene Therapy</i> , 2023, 30, 345-357.	2.2	5
1798	Leveraging biochemical reactions to unravel functional impacts of cancer somatic variants affecting protein interaction interfaces. <i>F1000Research</i> , 0, 10, 1111.	0.8	0
1799	SETD7 Expression Is Associated with Breast Cancer Survival Outcomes for Specific Molecular Subtypes: A Systematic Analysis of Publicly Available Datasets. <i>Cancers</i> , 2022, 14, 6029.	1.7	2
1800	Transcriptomics indicate nuclear division and cell adhesion not recapitulated in MCF7 and MCF10A compared to luminal A breast tumours. <i>Scientific Reports</i> , 2022, 12, .	1.6	15
1802	Integrative network analysis reveals subtype-specific long non-coding RNA regulatory mechanisms in head and neck squamous cell carcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 535-549.	1.9	4
1803	m ⁶ A RNA methylation regulators predict prognosis and indicate characteristics of tumour microenvironment infiltration in acute myeloid leukaemia. <i>Epigenetics</i> , 0, , 1-20.	1.3	2
1804	DRAGON: Determining Regulatory Associations using Graphical models on multi-Omic Networks. <i>Nucleic Acids Research</i> , 2023, 51, e15-e15.	6.5	5
1805	Intratumoral Gene Transfer of mRNAs Encoding IL12 in Combination with Decoy-Resistant IL18 Improves Local and Systemic Antitumor Immunity. <i>Cancer Immunology Research</i> , 2023, 11, 184-198.	1.6	7
1807	Integrated analysis of necroptosis-related genes for evaluating immune infiltration and colon cancer prognosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
1810	Elucidating the Genetic Landscape of Oral Leukoplakia to Predict Malignant Transformation. <i>Clinical Cancer Research</i> , 2023, 29, 602-613.	3.2	6
1811	ncâ€RNAâ€mediated high expression of CDK6 correlates with poor prognosis and immune infiltration in pancreatic cancer. <i>Cancer Medicine</i> , 0, , .	1.3	1
1812	A Race-Specific, DNA Methylation Analysis of Aging in Normal Rectum: Implications for the Biology of Aging and Its Relationship to Rectal Cancer. <i>Cancers</i> , 2023, 15, 45.	1.7	6
1814	Cancer cell-derived type I interferons instruct tumor monocyte polarization. <i>Cell Reports</i> , 2022, 41, 111769.	2.9	8
1815	Identification and validation of a pyroptosis-related prognostic model for colorectal cancer. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	5
1816	Histopathologic and proteogenomic heterogeneity reveals features of clear cell renal cell carcinoma aggressiveness. <i>Cancer Cell</i> , 2023, 41, 139-163.e17.	7.7	43
1818	Evaluation and Comparison of Multi-Omics Data Integration Methods for Subtyping of Cutaneous Melanoma. <i>Biomedicines</i> , 2022, 10, 3240.	1.4	3
1819	RIPOR2 Expression Decreased by HPV-16 E6 and E7 Oncoproteins: An Opportunity in the Search for Prognostic Biomarkers in Cervical Cancer. <i>Cells</i> , 2022, 11, 3942.	1.8	4
1820	Comprehensive analysis of hypoxia-related genes for prognosis, immune features, and drugs treatment strategy in gastric cancer using bulk and single-cell RNA-sequencing. <i>Scientific Reports</i> , 2022, 12, .	1.6	0

#	ARTICLE	IF	CITATIONS
1821	Noninvasive detection of brain gliomas using plasma cell-free DNA 5-hydroxymethylcytosine sequencing. <i>International Journal of Cancer</i> , 2023, 152, 1707-1718.	2.3	3
1822	Role of IL4 and GMCSF in Predicting Survival in Esophageal Cancer. <i>Journal of the American College of Surgeons</i> , 2023, 236, 107-115.	0.2	2
1823	Personalized immune subtypes based on machine learning predict response to checkpoint blockade in gastric cancer. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	0
1824	Construction and validation of a novel signature based on epithelial-mesenchymal transition-related genes to predict prognosis and immunotherapy response in hepatocellular carcinoma by comprehensive analysis of the tumor microenvironment. <i>Functional and Integrative Genomics</i> , 2023, 23, , .	1.4	9
1826	Characterization of cellular senescence patterns predicts the prognosis and therapeutic response of hepatocellular carcinoma. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	5
1827	Modulation of gene expression associated with copy number variation identifies key regulatory programs in high-grade serous ovarian carcinoma. <i>Advances in Cancer Biology Metastasis</i> , 2023, , 100088.	1.1	0
1829	SARS-CoV-2 replicates and displays oncolytic properties in clear cell and papillary renal cell carcinoma. <i>PLoS ONE</i> , 2023, 18, e0279578.	1.1	11
1831	Multi-Omics Data Analysis for Cancer Research: Colorectal Cancer, Liver Cancer and Lung Cancer. <i>Translational Bioinformatics</i> , 2023, , 77-99.	0.0	0
1833	Identification of tumour antigens and immune subtypes in the development of an anti-cancer vaccine for endometrial carcinoma. <i>Scandinavian Journal of Immunology</i> , 0, , .	1.3	0
1834	Cuproptosis-associated CDKN2A is targeted by plicamycin to regulate the microenvironment in patients with head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1835	LNCAROD promotes the proliferation and migration of gastric cancer: a bioinformatics analysis and experimental validation. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	3
1836	Spatial transcriptome analysis of long non-coding RNAs reveals tissue specificity and functional roles in cancer. <i>Journal of Zhejiang University: Science B</i> , 2023, 24, 15-31.	1.3	3
1837	MTA2 is one of 14 Transcription factors predicting recurrence free survival in gastric cancer and promotes cancer progression by targeting MCM5. <i>Journal of Cancer</i> , 2023, 14, 262-274.	1.2	3
1839	Comprehensive analysis of immune-related lncRNAs and their clinical relevance in gastric adenocarcinoma. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	2
1840	Identification of the ageing-related prognostic gene signature, and the associated regulation axis in skin cutaneous melanoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
1841	A novel pyroptosis scoring model was associated with the prognosis and immune microenvironment of esophageal squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
1843	Using Single-Cell RNA Sequencing and MicroRNA Targeting Data to Improve Colorectal Cancer Survival Prediction. <i>Cells</i> , 2023, 12, 228.	1.8	5
1844	Fast, accurate, and racially unbiased pan-cancer tumor-only variant calling with tabular machine learning. <i>Npj Precision Oncology</i> , 2023, 7, .	2.3	2

#	ARTICLE	IF	CITATIONS
1846	Integrated multi-omics profiling yields a clinically relevant molecular classification for esophageal squamous cell carcinoma. <i>Cancer Cell</i> , 2023, 41, 181-195.e9.	7.7	30
1847	High-expression of the innate-immune related gene <i>UNC93B1</i> predicts inferior outcomes in acute myeloid leukemia. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
1850	Screening and identifying a novel M-MDSCs-related gene signature for predicting prognostic risk and immunotherapeutic responses in patients with lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
1851	A classification method of gastric cancer subtype based on residual graph convolution network. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1852	Prognosis, immune microenvironment, and personalized treatment prediction in Rho GTPase-activating protein 4-mutant cervical cancer: Computer strategies for precision oncology. <i>Life Sciences</i> , 2023, 315, 121360.	2.0	0
1853	Identification of a robust scoring system based on metabolic genes followed by in-depth validation of <i>ATP1A3</i> in glioma. <i>Life Sciences</i> , 2023, 315, 121377.	2.0	1
1854	<i>CHRNA1</i> and its correlated-myogenesis/cell cycle genes are prognosis-related markers of metastatic melanoma. <i>Biochemistry and Biophysics Reports</i> , 2023, 33, 101425.	0.7	1
1855	Analysis of endometrial carcinoma TCGA reveals differences in DNA methylation in tumors from Black and White women. <i>Gynecologic Oncology</i> , 2023, 170, 1-10.	0.6	4
1857	5-Methylcytosine (m5C) Modification Patterns and Tumor Immune Infiltration Characteristics in Clear Cell Renal Cell Carcinoma. <i>Current Oncology</i> , 2023, 30, 559-574.	0.9	2
1858	<i>DNAH7</i> mutations benefit colorectal cancer patients receiving immune checkpoint inhibitors. <i>Annals of Translational Medicine</i> , 2022, 10, 1335-1335.	0.7	1
1859	Cell-type Deconvolution and Age Estimation Using DNA Methylation Reveals NK Cell Deficiency in the Hepatocellular Carcinoma Microenvironment. , 2022, , .		0
1860	Towards resolution of the intron retention paradox in breast cancer. <i>Breast Cancer Research</i> , 2022, 24, .	2.2	3
1861	Functional Validation of the Putative Oncogenic Activity of <i>PLAU</i> . <i>Biomedicines</i> , 2023, 11, 102.	1.4	1
1862	Pan-cancer Landscape of Programmed Death Ligand-1 and Programmed Death Ligand-2 Structural Variations. <i>JCO Precision Oncology</i> , 2023, , .	1.5	1
1863	Arginine limitation drives a directed codon-dependent DNA sequence evolution response in colorectal cancer cells. <i>Science Advances</i> , 2023, 9, .	4.7	8
1864	<i>SOCS1</i> Deficiency Promotes Hepatocellular Carcinoma via <i>SOCS3</i> -Dependent <i>CDKN1A</i> Induction and <i>NRF2</i> Activation. <i>Cancers</i> , 2023, 15, 905.	1.7	4
1865	Single-cell analysis reveals prognostic fibroblast subpopulations linked to molecular and immunological subtypes of lung cancer. <i>Nature Communications</i> , 2023, 14, .	5.8	17
1867	In silico identification and biological evaluation of a selective <i>MAP4K4</i> inhibitor against pancreatic cancer. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2023, 38, .	2.5	2

#	ARTICLE	IF	CITATIONS
1869	Tumor Microenvironment and Genes Affecting the Prognosis of Temozolomide-Treated Glioblastoma. <i>Journal of Personalized Medicine</i> , 2023, 13, 188.	1.1	2
1870	Pan-cancer landscape of protein activities identifies drivers of signalling dysregulation and patient survival. <i>Molecular Systems Biology</i> , 2023, 19, .	3.2	10
1871	CAFncAPA: a knowledgebase for systematic functional annotations of APA events in human cancers. <i>NAR Cancer</i> , 2023, 5, .	1.6	1
1873	Modeling tumour heterogeneity of PD-L1 expression in tumour progression and adaptive therapy. <i>Journal of Mathematical Biology</i> , 2023, 86, .	0.8	0
1874	ANXA10 is a prognostic biomarker and suppressor of hepatocellular carcinoma: a bioinformatics analysis and experimental validation. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
1875	Epigenetic dysregulation-mediated COL12A1 upregulation predicts worse outcome in intrahepatic cholangiocarcinoma patients. <i>Clinical Epigenetics</i> , 2023, 15, .	1.8	5
1876	Pan-cancer onco-signatures reveal a novel mitochondrial subtype of luminal breast cancer with specific regulators. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	0
1877	Tastin promotes non-small-cell lung cancer progression through the ErbB4, PI3K/AKT, and ERK1/2 pathways. <i>Experimental Biology and Medicine</i> , 2023, 248, 519-531.	1.1	7
1880	BASP1 is a prognostic biomarker associated with immunotherapeutic response in head and neck squamous cell carcinoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	3
1881	Persistent mutation burden drives sustained anti-tumor immune responses. <i>Nature Medicine</i> , 2023, 29, 440-449.	15.2	35
1882	Chromobox proteins in cancer: Multifaceted functions and strategies for modulation (Review). <i>International Journal of Oncology</i> , 2023, 62, .	1.4	4
1883	Mutational Impacts on the N and C Terminal Domains of the MUC5B Protein: A Transcriptomics and Structural Biology Study. <i>ACS Omega</i> , 2023, 8, 3726-3735.	1.6	3
1884	Multi-region sampling with paired sample sequencing analyses reveals sub-groups of patients with novel patient-specific dysregulation in Hepatocellular Carcinoma. <i>BMC Cancer</i> , 2023, 23, .	1.1	3
1885	Identification of Potential Diagnostic and Prognostic Biomarkers for Gastric Cancer Based on Bioinformatic Analysis. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2023, , .	0.6	0
1886	A methylomics-associated nomogram predicts the overall survival risk of stage III to IV ovarian cancer. <i>Medicine (United States)</i> , 2023, 102, e32766.	0.4	0
1887	Investigation of the efficacy and pharmacological mechanism of Danhong injections for treating chronic obstructive pulmonary disease: A PRISMA-compliant meta-analysis and network pharmacology analysis. <i>Medicine (United States)</i> , 2023, 102, e32846.	0.4	0
1888	The Characteristics of Tumor Microenvironment Predict Survival and Response to Immunotherapy in Adrenocortical Carcinomas. <i>Cells</i> , 2023, 12, 755.	1.8	5
1889	Scaffold coupling: ERK activation by trans-phosphorylation across different scaffold protein species. <i>Science Advances</i> , 2023, 9, .	4.7	1

#	ARTICLE	IF	CITATIONS
1891	Probabilistic canonical correlation analysis for sparse count data. <i>Journal of Statistical Research</i> , 2023, 56, 75-100.	0.0	0
1892	<sc>eaQTLdb</sc> : An atlas of enhancer activity quantitative trait loci across cancer types. <i>International Journal of Cancer</i> , 0, , .	2.3	0
1893	OncorTT: Predicting novel oncology-related therapeutic targets using BERT embeddings and omics features. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
1894	Multi-omics integration method based on attention deep learning network for biomedical data classification. <i>Computer Methods and Programs in Biomedicine</i> , 2023, 231, 107377.	2.6	8
1895	Integrated Metabolomic and Transcriptomic Analysis of Modified Nucleosides for Biomarker Discovery in Clear Cell Renal Cell Carcinoma. <i>Cells</i> , 2023, 12, 1102.	1.8	3
1897	The Interaction between Intratumoral Microbiome and Immunity Is Related to the Prognosis of Ovarian Cancer. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	7
1898	A Tumor Microenvironment-Driven Network Regulated by STAT3 and p65 Negatively Controls the Enrichment of Cancer Stem Cells in Human HR+/HER2 ⁺ Breast Cancer. <i>Cancers</i> , 2023, 15, 2255.	1.7	1
1900	Identifying cancer driver genes using a two-stage random walk with restart on a gene interaction network. <i>Computers in Biology and Medicine</i> , 2023, 158, 106810.	3.9	0
1901	Deciphering the immune heterogeneity dominated by natural killer cells with prognostic and therapeutic implications in hepatocellular carcinoma. <i>Computers in Biology and Medicine</i> , 2023, 158, 106872.	3.9	2
1902	Gender differences in smoking-induced changes in the tumor immune microenvironment. <i>Archives of Biochemistry and Biophysics</i> , 2023, 739, 109579.	1.4	1
1903	Integrated multiomics analyses unveil the implication of a costimulatory molecule score on tumor aggressiveness and immune evasion in breast cancer: A large-scale study through over 8,000 patients. <i>Computers in Biology and Medicine</i> , 2023, 159, 106866.	3.9	0
1904	The prognostic value of hedgehog signaling in bladder cancer by integrated bioinformatics. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
1905	Multi-omics profiling of papillary thyroid microcarcinoma reveals different somatic mutations and a unique transcriptomic signature. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	2
1910	Risk scoring based on DNA methylation-driven related DEGs for colorectal cancer prognosis with systematic insights. <i>Life Sciences</i> , 2023, 316, 121413.	2.0	3
1911	Predicting latent lncRNA and cancer metastatic event associations via variational graph auto-encoder. <i>Methods</i> , 2023, 211, 1-9.	1.9	0
1912	CD8 ⁺ CD226 ^{high} T cells in liver metastases dictate the prognosis of colorectal cancer patients treated with chemotherapy and radical surgery. , 2023, 20, 365-378.		2
1913	Mutated axon guidance gene <sc><i>PLXNB2</i></sc> sustains growth and invasiveness of stem cells isolated from cancers of unknown primary. <i>EMBO Molecular Medicine</i> , 2023, 15, .	3.3	4
1915	Identification and validation of a novel prognostic model based on platinum resistance-related genes in bladder cancer. <i>International Braz J Urol: Official Journal of the Brazilian Society of Urology</i> , 2023, 49, 61-88.	0.7	2

#	ARTICLE	IF	CITATIONS
1916	Longitudinal DNA methylation analysis of adult-type IDH-mutant gliomas. <i>Acta Neuropathologica Communications</i> , 2023, 11, .	2.4	2
1918	Fatty acid synthase as a new therapeutic target for HER2-positive gastric cancer. <i>Cellular Oncology (Dordrecht)</i> , 2023, 46, 661-676.	2.1	1
1919	Multi-omics analysis unravels the underlying mechanisms of poor prognosis and differential therapeutic responses of solid predominant lung adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
1920	Open-source curation of a pancreatic ductal adenocarcinoma gene expression analysis platform (pdacR) supports a two-subtype model. <i>Communications Biology</i> , 2023, 6, .	2.0	4
1921	Genomic and microenvironmental heterogeneity shaping epithelial-to-mesenchymal trajectories in cancer. <i>Nature Communications</i> , 2023, 14, .	5.8	16
1922	Single-cell RNA sequencing reveals the effects of chemotherapy on human pancreatic adenocarcinoma and its tumor microenvironment. <i>Nature Communications</i> , 2023, 14, .	5.8	29
1923	Body Composition and Metabolic Dysfunction Really Matter for the Achievement of Better Outcomes in High-Grade Serous Ovarian Cancer. <i>Cancers</i> , 2023, 15, 1156.	1.7	4
1924	Integrative analysis of DNA methylation and gene expression through machine learning identifies stomach cancer diagnostic and prognostic biomarkers. <i>Journal of Cellular and Molecular Medicine</i> , 2023, 27, 714-726.	1.6	1
1925	Why loss of Y? A pan-cancer genome analysis of tumors with loss of Y chromosome. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 1573-1583.	1.9	3
1926	Gibbs process distinguishes survival and reveals contact-inhibition genes in Glioblastoma multiforme. <i>PLoS ONE</i> , 2023, 18, e0277176.	1.1	2
1927	PTPN18 Serves as a Potential Oncogene for Glioblastoma by Enhancing Immune Suppression. <i>Oxidative Medicine and Cellular Longevity</i> , 2023, 2023, 1-21.	1.9	0
1928	A Transcriptomic and Reverse-Engineering Strategy Reveals Molecular Signatures of Arachidonic Acid Metabolism in 12 Cancers. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 127-138.	1.0	2
1929	RNA-Seq Analysis of Clinical Samples from TCGA Reveal Molecular Signatures for Ovarian Cancer. <i>Cancer Investigation</i> , 2023, 41, 394-404.	0.6	1
1931	Dynamic network biomarker to determine the critical point of breast cancer stage progression. <i>Breast Cancer</i> , 2023, 30, 453-465.	1.3	1
1932	Prognostic Significance of Amino Acid Metabolism-Related Genes in Prostate Cancer Retrieved by Machine Learning. <i>Cancers</i> , 2023, 15, 1309.	1.7	3
1933	In silico designed mRNA vaccines targeting CA-125 neoantigen in breast and ovarian cancer. <i>Vaccine</i> , 2023, 41, 2073-2083.	1.7	7
1935	A Survival Model Based on the ASB Genes and Used to Predict the Prognosis of Kidney Renal Clear Cell Carcinoma. <i>Genetical Research</i> , 2023, 2023, 1-11.	0.3	0
1937	Construction of a TTN Mutation-Based Prognostic Model for Evaluating Immune Microenvironment, Cancer Stemness, and Outcomes of Colorectal Cancer Patients. <i>Stem Cells International</i> , 2023, 2023, 1-21.	1.2	2

#	ARTICLE	IF	CITATIONS
1938	A comprehensive pan-cancer analysis reveals cancer-associated robust isomiR expression landscapes in miRNA arm switching. <i>Molecular Genetics and Genomics</i> , 0, , .	1.0	0
1939	Molecular phenotypic linkage between N6-methyladenosine methylation and tumor immune microenvironment in hepatocellular carcinoma. <i>Journal of Cancer Research and Clinical Oncology</i> , 0, , .	1.2	0
1940	Exploring Prognosis, Tumor Microenvironment and Tumor Immune Infiltration in Hepatocellular Carcinoma Based on ATF/CREB Transcription Factor Family Gene-Related Model. <i>Journal of Hepatocellular Carcinoma</i> , 0, Volume 10, 327-345.	1.8	2
1941	Contrast subgraphs allow comparing homogeneous and heterogeneous networks derived from omics data. <i>GigaScience</i> , 2022, 12, .	3.3	3
1942	Clinicopathological significance of peritumoral alveolar macrophages in patients with resected early-stage lung squamous cell carcinoma. <i>Cancer Immunology, Immunotherapy</i> , 2023, 72, 2205-2215.	2.0	2
1943	Identification of a necroptosis-related gene signature as a novel prognostic biomarker of cholangiocarcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
1944	Pan-Cancer Analysis Reveals Functional Similarity of Three lncRNAs across Multiple Tumors. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4796.	1.8	1
1945	Tumor senescence leads to poor survival and therapeutic resistance in human breast cancer. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
1946	N6-methyladenosine related gene expression signatures for predicting the overall survival and immune responses of patients with colorectal cancer. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
1947	Deciphering comprehensive features of tumor microenvironment controlled by chromatin regulators to predict prognosis and guide therapies in uterine corpus endometrial carcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
1949	The landscape of human p53-regulated long non-coding RNAs reveals critical host gene co-regulation. <i>Molecular Oncology</i> , 2023, 17, 1263-1279.	2.1	3
1950	Detection of Stage-wise Biomarkers in Lung Adenocarcinoma Using Multiplex Analysis. <i>Current Bioinformatics</i> , 2023, 18, .	0.7	0
1953	Tumor MK2 transcript levels are associated with improved response to chemotherapy and patient survival in non-small cell lung cancer. <i>Physiological Genomics</i> , 2023, 55, 168-178.	1.0	0
1955	<i>TLN1</i> contains a cancer-associated cassette exon that alters talin-1 mechanosensitivity. <i>Journal of Cell Biology</i> , 2023, 222, .	2.3	1
1956	Correlation of tumor mutational burden with prognosis and immune infiltration in lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
1960	Pan-cancer investigation of C-to-U editing reveals its important role in cancer development and new targets for cancer treatment. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
1961	Identification and Characterization of Metabolic Subtypes of Endometrial Cancer Using a Systems-Level Approach. <i>Metabolites</i> , 2023, 13, 409.	1.3	1
1962	Identification of IRAK1BP1 as a candidate prognostic factor in lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1

#	ARTICLE	IF	CITATIONS
1963	Myo1e overexpression in lung adenocarcinoma is associated with increased risk of mortality. Scientific Reports, 2023, 13, .	1.6	2
1964	Integrating bulk and single-cell RNA sequencing data reveals the relationship between intratumor microbiome signature and host metabolic heterogeneity in breast cancer. Frontiers in Immunology, 0, 14, .	2.2	5
1965	Visualizing genomic characteristics across an RNA-Seq based reference landscape of normal and neoplastic brain. Scientific Reports, 2023, 13, .	1.6	4
1966	Single-cell profiling of the copy-number heterogeneity in colorectal cancer. Chinese Medical Journal, 2023, 136, 707-718.	0.9	0
1969	Integrative analysis revealed that distinct cuprotosis patterns reshaped tumor microenvironment and responses to immunotherapy of colorectal cancer. Frontiers in Immunology, 0, 14, .	2.2	2
1970	An <i>in silico</i> approach to the identification of diagnostic and prognostic markers in low-grade gliomas. PeerJ, 0, 11, e15096.	0.9	1
1971	Heterogeneity of tumor immune microenvironment of EGFR/ALK-positive tumors versus EGFR/ALK-negative tumors in resected brain metastases from lung adenocarcinoma. , 2023, 11, e006243.		7
1972	ELK3-CXCL16 axis determines natural killer cell cytotoxicity via the chemotactic activity of CXCL16 in triple negative breast cancer. OncoImmunology, 2023, 12, .	2.1	2
1974	Definition of a Novel Immunogenic Cell Death-Relevant Gene Signature Associated with Immune Landscape in Gastric Cancer. Biochemical Genetics, 2023, 61, 2092-2115.	0.8	2
1975	Attenuation of cancer proliferation by suppression of glypican-1 and its pleiotropic effects in neoplastic behavior. Oncotarget, 2023, 14, 219-235.	0.8	1
1976	Machine learning based combination of multi-omics data for subgroup identification in non-small cell lung cancer. Scientific Reports, 2023, 13, .	1.6	8
1977	Identification and validation of <i>NFIA</i> as a novel prognostic marker in renal cell carcinoma. Journal of Pathology: Clinical Research, 2023, 9, 261-272.	1.3	0
1978	NaRnEA: An Information Theoretic Framework for Gene Set Analysis. Entropy, 2023, 25, 542.	1.1	2
1979	Identification of Mir-182-3p/FLI-1 Axis as a Key Signaling in Immune Response in Cervical Cancer: A Comprehensive Bioinformatic Analysis. International Journal of Molecular Sciences, 2023, 24, 6032.	1.8	1
1980	Comprehensive analyses of A 12-metabolism-associated gene signature and its connection with tumor metastases in clear cell renal cell carcinoma. BMC Cancer, 2023, 23, .	1.1	1
1981	Th2 cells infiltrating high-grade serous ovarian cancer: a feature that may account for the poor prognosis. Journal of Gynecologic Oncology, 2023, 34, .	1.0	3
1982	Predator: Predicting the impact of cancer somatic mutations on protein-protein interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, , 1-10.	1.9	1
1983	Comprehensive characterization of ferroptosis in hepatocellular carcinoma revealing the association with prognosis and tumor immune microenvironment. Frontiers in Oncology, 0, 13, .	1.3	1

#	ARTICLE	IF	CITATIONS
1984	FAK suppresses antigen processing and presentation to promote immune evasion in pancreatic cancer. <i>Gut</i> , 2024, 73, 131-155.	6.1	7
1985	LRP1B mutation is associated with tumor immune microenvironment and progression-free survival in lung adenocarcinoma treated with immune checkpoint inhibitors. <i>Translational Lung Cancer Research</i> , 2023, 12, 510-529.	1.3	2
1986	NF- κ B Activator 1 downregulation in macrophages activates STAT3 to promote adenoma-adenocarcinoma transition and immunosuppression in colorectal cancer. <i>BMC Medicine</i> , 2023, 21, .	2.3	5
1987	NCAPG as a novel prognostic biomarker in numerous cancers: a meta-analysis and bioinformatics analysis. <i>Aging</i> , 2023, 15, 2503-2524.	1.4	1
1989	Prognostic value of autophagy-related genes based on single-cell RNA-sequencing in colorectal cancer. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
1990	Identification of distinct tumor cell patterns with single-cell RNA sequencing integrating primary lung adenocarcinoma and brain metastasis tumor. <i>Translational Lung Cancer Research</i> , 2023, 12, 547-565.	1.3	1
1991	Identifying Key Regulators of Keratinization in Lung Squamous Cell Cancer Using Integrated TCGA Analysis. <i>Cancers</i> , 2023, 15, 2066.	1.7	1
1992	Transcriptomic data in tumor-adjacent normal tissues harbor prognostic information on multiple cancer types. <i>Cancer Medicine</i> , 0, , .	1.3	0
1993	Spatial probabilistic mapping of metabolite ensembles in mass spectrometry imaging. <i>Nature Communications</i> , 2023, 14, .	5.8	7
1994	Subtype classification based on t cell proliferation-related regulator genes and risk model for predicting outcomes of lung adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
1995	Smoking-related epigenetic modifications are associated with the prognosis and chemotherapeutics of patients with bladder cancer. <i>International Journal of Immunopathology and Pharmacology</i> , 2023, 37, 039463202311667.	1.0	1
1996	Molecular Subtyping and Survival Analysis of Osteosarcoma Reveals Prognostic Biomarkers and Key Canonical Pathways. <i>Cancers</i> , 2023, 15, 2134.	1.7	4
1997	Rewiring of miRNA-mRNA bipartite co-expression network as a novel way to understand the prostate cancer related players. <i>Systems Biology in Reproductive Medicine</i> , 0, , 1-12.	1.0	0
1998	The landscape of objective response rate of anti-PD-1/L1 monotherapy across 31 types of cancer: a system review and novel biomarker investigating. <i>Cancer Immunology, Immunotherapy</i> , 2023, 72, 2483-2498.	2.0	1
1999	Intratumoral microbiota is associated with prognosis in patients with adrenocortical carcinoma. , 2023, 2, .		6
2000	ZAP70 interaction with 13 mRNAs as a potential immunotherapeutic target for endometrial cancer. <i>Oncology Letters</i> , 2023, 25, .	0.8	0
2001	Synthetic miR-21 decoy circularized by tRNA splicing mechanism inhibited tumorigenesis in glioblastoma in-vitro and in-vivo models. <i>Molecular Therapy - Nucleic Acids</i> , 2023, 32, 432-444.	2.3	3
2002	Identification of natural killer cell associated subtyping and gene signature to predict prognosis and drug sensitivity of lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0

#	ARTICLE	IF	CITATIONS
2004	The cancer testis antigen TDRD1 regulates prostate cancer proliferation by associating with the snRNP biogenesis machinery. <i>Oncogene</i> , 2023, 42, 1821-1831.	2.6	1
2007	TP53 mutation-related senescence is an indicator of hepatocellular carcinoma patient outcomes from multiomics profiles. , 2023, 2, .		0
2008	Pan-cancer analysis reveals IGFL2 as a potential target for cancer prognosis and immunotherapy. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
2009	Unveiling DNA damage repair-based molecular subtypes, tumor microenvironment and pharmacogenomic landscape in gastric cancer. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
2010	DNA Methylation Landscapes of Prostate Cancer Brain Metastasis Are Shaped by Early Driver Genetic Alterations. <i>Cancer Research</i> , 2023, 83, 1203-1213.	0.4	3
2011	Investigation of Diagnostic and Prognostic Value of CLEC4M of Non-Small Cell Lung Carcinoma Associated with Immune Microenvironment. <i>International Journal of General Medicine</i> , 0, Volume 16, 1317-1332.	0.8	0
2012	Integrated bioinformatic analysis of mitochondrial metabolism-related genes in acute myeloid leukemia. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
2013	Integrative analysis of TP53 mutations in lung adenocarcinoma for immunotherapies and prognosis. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
2015	Prognostic model development for classification of colorectal adenocarcinoma by using machine learning model based on feature selection technique boruta. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
2017	Common genetic variations in telomere length genes and lung cancer: a Mendelian randomisation study and its novel application in lung tumour transcriptome. <i>ELife</i> , 0, 12, .	2.8	3
2018	Machine Learning Predicts the Oxidative Stress Subtypes Provide an Innovative Insight into Colorectal Cancer. <i>Oxidative Medicine and Cellular Longevity</i> , 2023, 2023, 1-12.	1.9	1
2019	Study on biomarkers in endometrial cancer using transcriptome data: A machine learning approach. , 2023, , 311-327.		0
2114	A Drug Repurposing Pipeline Based on Bladder Cancer Integrated Proteotranscriptomics Signatures. <i>Methods in Molecular Biology</i> , 2023, , 59-99.	0.4	0
2320	What can we learn about acid-base transporters in cancer from studying somatic mutations in their genes?. <i>Pflugers Archiv European Journal of Physiology</i> , 0, , .	1.3	1
2427	Identification of subtype-specific master regulatory long non-coding RNAs of gastric cancer through a network-based approach. , 2023, , .		0
2470	Analysing Severity of Breast Cancer using RNA Sequencing Data. , 2023, , .		0