

Maoshan Chen

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

6,746
citations

201674

27
h-index

168389

53
g-index

61
all docs

61
docs citations

61
times ranked

10215
citing authors

#	ARTICLE	IF	CITATIONS
1	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	27.8	1,966
2	Extracellular vesicles in cancer – implications for future improvements in cancer care. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 617-638.	27.6	1,020
3	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	5.5	832
4	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5135-5140.	7.1	674
5	Integrated Profiling of MicroRNAs and mRNAs: MicroRNAs Located on Xq27.3 Associate with Clear Cell Renal Cell Carcinoma. <i>PLoS ONE</i> , 2010, 5, e15224.	2.5	573
6	Deep Sequencing of RNA from Three Different Extracellular Vesicle (EV) Subtypes Released from the Human LIM1863 Colon Cancer Cell Line Uncovers Distinct Mirna-Enrichment Signatures. <i>PLoS ONE</i> , 2014, 9, e110314.	2.5	181
7	Exosomes Derived from Human Primary and Metastatic Colorectal Cancer Cells Contribute to Functional Heterogeneity of Activated Fibroblasts by Reprogramming Their Proteome. <i>Proteomics</i> , 2019, 19, e1800148.	2.2	108
8	Secreted primary human malignant mesothelioma exosome signature reflects oncogenic cargo. <i>Scientific Reports</i> , 2016, 6, 32643.	3.3	85
9	Extracellular vesicles: their role in cancer biology and epithelial–mesenchymal transition. <i>Biochemical Journal</i> , 2017, 474, 21-45.	3.7	81
10	Intact TP-53 function is essential for sustaining durable responses to BH3-mimetic drugs in leukemias. <i>Blood</i> , 2021, 137, 2721-2735.	1.4	75
11	Transcriptome and long noncoding RNA sequencing of three extracellular vesicle subtypes released from the human colon cancer LIM1863 cell line. <i>Scientific Reports</i> , 2016, 6, 38397.	3.3	72
12	Comparative mRNA and microRNA Expression Profiling of Three Genitourinary Cancers Reveals Common Hallmarks and Cancer-Specific Molecular Events. <i>PLoS ONE</i> , 2011, 6, e22570.	2.5	69
13	Identification of Serum microRNA Biomarkers for Tuberculosis Using RNA-seq. <i>PLoS ONE</i> , 2014, 9, e88909.	2.5	69
14	Distinct shed microvesicle and exosome microRNA signatures reveal diagnostic markers for colorectal cancer. <i>PLoS ONE</i> , 2019, 14, e0210003.	2.5	67
15	YBX1/YB-1 induces partial EMT and tumourigenicity through secretion of angiogenic factors into the extracellular microenvironment. <i>Oncotarget</i> , 2015, 6, 13718-13730.	1.8	66
16	Myoepithelial cell-specific expression of stefin A as a suppressor of early breast cancer invasion. <i>Journal of Pathology</i> , 2017, 243, 496-509.	4.5	44
17	A new look at adenovirus splicing. <i>Virology</i> , 2014, 456-457, 329-341.	2.4	42
18	Secreted midbody remnants are a class of extracellular vesicles molecularly distinct from exosomes and microparticles. <i>Communications Biology</i> , 2021, 4, 400.	4.4	41

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19	Neoadjuvant Chemotherapy Creates Surgery Opportunities For Inoperable Locally Advanced Breast Cancer. <i>Scientific Reports</i> , 2017, 7, 44673.	3.3	40
20	miRNA Genes of an Invasive Vector Mosquito, <i>Aedes albopictus</i> . <i>PLoS ONE</i> , 2013, 8, e67638.	2.5	38
21	Genome-Wide Transcriptome and Antioxidant Analyses on Gamma-Irradiated Phases of <i>Deinococcus radiodurans</i> R1. <i>PLoS ONE</i> , 2014, 9, e85649.	2.5	37
22	Fluctuating expression of microRNAs in adenovirus infected cells. <i>Virology</i> , 2015, 478, 99-111.	2.4	37
23	Chronic methamphetamine interacts with BDNF Val66Met to remodel psychosis pathways in the mesocorticolimbic proteome. <i>Molecular Psychiatry</i> , 2021, 26, 4431-4447.	7.9	37
24	A Systematic Analysis on DNA Methylation and the Expression of Both mRNA and microRNA in Bladder Cancer. <i>PLoS ONE</i> , 2011, 6, e28223.	2.5	35
25	Unique proteome signature of post-chemotherapy ovarian cancer ascites-derived tumor cells. <i>Scientific Reports</i> , 2016, 6, 30061.	3.3	33
26	Transcriptome Analysis of <i>Taxillus chinensis</i> (DC.) Danser Seeds in Response to Water Loss. <i>PLoS ONE</i> , 2017, 12, e0169177.	2.5	31
27	Complement and coagulation cascades pathway correlates with chemosensitivity and overall survival in patients with soft tissue sarcoma. <i>European Journal of Pharmacology</i> , 2020, 879, 173121.	3.5	31
28	Distinct temporal changes in host cell lncRNA expression during the course of an adenovirus infection. <i>Virology</i> , 2016, 492, 242-250.	2.4	30
29	Surfaceome of Exosomes Secreted from the Colorectal Cancer Cell Line SW480: Peripheral and Integral Membrane Proteins Analyzed by Proteolysis and TX114. <i>Proteomics</i> , 2019, 19, e1700453.	2.2	30
30	Circulating Tumour DNA Analysis for Tumour Genome Characterisation and Monitoring Disease Burden in Extramedullary Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1858.	4.1	28
31	Astrocytes derived from ASD individuals alter behavior and destabilize neuronal activity through aberrant Ca ²⁺ signaling. <i>Molecular Psychiatry</i> , 2022, 27, 2470-2484.	7.9	26
32	Deep parallel sequencing reveals conserved and novel miRNAs in gill and hepatopancreas of giant freshwater prawn. <i>Fish and Shellfish Immunology</i> , 2013, 35, 1061-1069.	3.6	22
33	Proteomic profiling reveals key cancer progression modulators in shed microvesicles released from isogenic human primary and metastatic colorectal cancer cell lines. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140171.	2.3	22
34	Utility of Circulating Cell-Free RNA Analysis for the Characterization of Global Transcriptome Profiles of Multiple Myeloma Patients. <i>Cancers</i> , 2019, 11, 887.	3.7	20
35	An automated approach for global identification of sRNA-encoding regions in RNA-Seq data from <i>Mycobacterium tuberculosis</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2016, 48, 544-553.	2.0	18
36	Knockdown of stem cell regulator Oct4A in ovarian cancer reveals cellular reprogramming associated with key regulators of cytoskeleton-extracellular matrix remodelling. <i>Scientific Reports</i> , 2017, 7, 46312.	3.3	18

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37	Liquid biopsy: an evolving paradigm for the biological characterisation of plasma cell disorders. <i>Leukemia</i> , 2021, 35, 2771-2783.	7.2	17
38	Comprehensive transcriptomics and proteomics analyses of pollinated and parthenocarpic litchi (<i>Litchi chinensis</i> Sonn.) fruits during early development. <i>Scientific Reports</i> , 2017, 7, 5401.	3.3	15
39	Identification of adenovirus-encoded small RNAs by deep RNA sequencing. <i>Virology</i> , 2013, 442, 148-155.	2.4	14
40	iTRAQ-Based Proteomics Identification of Serum Biomarkers of Two Chronic Hepatitis B Subtypes Diagnosed by Traditional Chinese Medicine. <i>BioMed Research International</i> , 2016, 2016, 1-29.	1.9	14
41	SMAP: a streamlined methylation analysis pipeline for bisulfite sequencing. <i>GigaScience</i> , 2015, 4, 29.	6.4	13
42	Human myeloma cell- and plasma-derived extracellular vesicles contribute to functional regulation of stromal cells. <i>Proteomics</i> , 2021, 21, e2000119.	2.2	13
43	Transcriptomic and proteomic analyses reveal new insights into the regulation of immune pathways during adenovirus type 2 infection. <i>BMC Microbiology</i> , 2019, 19, 15.	3.3	10
44	Non-Specific Immunity Associated Gut Microbiome in <i>Aristichthys nobilis</i> under Different Rearing Strategies. <i>Genes</i> , 2021, 12, 916.	2.4	10
45	Human Plasma Extracellular Vesicle Isolation and Proteomic Characterization for the Optimization of Liquid Biopsy in Multiple Myeloma. <i>Methods in Molecular Biology</i> , 2021, 2261, 151-191.	0.9	8
46	Deep sequencing identifies regulated small RNAs in <i>Dugesia japonica</i> . <i>Molecular Biology Reports</i> , 2013, 40, 4075-4081.	2.3	7
47	Data on the expression of cellular lncRNAs in human adenovirus infected cells. <i>Data in Brief</i> , 2016, 8, 1263-1279.	1.0	6
48	Thyroid hemigenesis and Hashimoto's thyroiditis diagnostic and treatment pitfalls. <i>World Journal of Surgical Oncology</i> , 2017, 15, 182.	1.9	5
49	Transglutaminase-2, RNA-binding proteins and mitochondrial proteins selectively traffic to MDCK cell-derived microvesicles following H-Ras-induced epithelial-mesenchymal transition. <i>Proteomics</i> , 2021, 21, 2000221.	2.2	5
50	Potential biomarkers for inherited thrombocytopenia 2 identified by plasma proteomics. <i>Platelets</i> , 2022, 33, 443-450.	2.3	4
51	TOP2A expression predicts responsiveness to carfilzomib in myeloma and informs novel combinatorial strategies for enhanced proteasome inhibitor cell killing. <i>Leukemia and Lymphoma</i> , 2021, 62, 337-347.	1.3	2
52	Dynamic transcriptome analysis identifies genes related to fatty acid biosynthesis in the seeds of <i>Prunus pedunculata</i> Pall. <i>BMC Plant Biology</i> , 2021, 21, 152.	3.6	2
53	Generation of the human induced pluripotent stem cell line (SHAMUi001-A) carrying the heterozygous c.128G>T mutation in the 5'-UTR of the ANKRD26 gene. <i>Stem Cell Research</i> , 2020, 48, 102002.	0.7	1
54	Analysis of Annotated and Unannotated Long Noncoding RNAs from Exosome Subtypes Using Next-Generation RNA Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2254, 195-218.	0.9	1

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55	Molecular Characterization of LRB7 Gene and a Water Channel Protein TIP2 in <i>Chorispora bungeana</i> . <i>BioMed Research International</i> , 2016, 2016, 1-11.	1.9	0
56	CPLSTool: A Framework to Generate Automatic Bioinformatics Pipelines. <i>Biomedical Journal of Scientific & Technical Research</i> , 2018, 11, .	0.1	0
57	EloA promotes HEL polyploidization upon PMA stimulation through enhanced ERK1/2 activity. <i>Platelets</i> , 2022, 33, 755-763.	2.3	0
58	Editorial: Understanding the RNA Species in the Extracellular Vesicles of Multiple Myeloma. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	0