

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	Potential biomarkers for inherited thrombocytopenia 2 identified by plasma proteomics. Platelets, 2022, 33, 443-450.	2.3	4
2	EloA promotes HEL polyploidization upon PMA stimulation through enhanced ERK1/2 activity. Platelets, 2022, 33, 755-763.	2.3	0
3	Astrocytes derived from ASD individuals alter behavior and destabilize neuronal activity through aberrant Ca ²⁺ signaling. Molecular Psychiatry, 2022, 27, 2470-2484.	7.9	26
4	Chronic methamphetamine interacts with BDNF Val66Met to remodel psychosis pathways in the mesocorticolimbic proteome. Molecular Psychiatry, 2021, 26, 4431-4447.	7.9	37
5	TOP2A expression predicts responsiveness to carfilzomib in myeloma and informs novel combinatorial strategies for enhanced proteasome inhibitor cell killing. Leukemia and Lymphoma, 2021, 62, 337-347.	1.3	2
6	Human Plasma Extracellular Vesicle Isolation and Proteomic Characterization for the Optimization of Liquid Biopsy in Multiple Myeloma. Methods in Molecular Biology, 2021, 2261, 151-191.	0.9	8
7	Human myeloma cell- and plasma-derived extracellular vesicles contribute to functional regulation of stromal cells. Proteomics, 2021, 21, e2000119.	2.2	13
8	Dynamic transcriptome analysis identifies genes related to fatty acid biosynthesis in the seeds of Prunus pedunculata Pall. BMC Plant Biology, 2021, 21, 152.	3.6	2
9	Transglutaminase-2, RNA-binding proteins and mitochondrial proteins selectively traffic to MDCK cell-derived microvesicles following H-Ras-induced epithelial-mesenchymal transition. Proteomics, 2021, 21, 2000221.	2.2	5
10	Secreted midbody remnants are a class of extracellular vesicles molecularly distinct from exosomes and microparticles. Communications Biology, 2021, 4, 400.	4.4	41
11	Intact TP-53 function is essential for sustaining durable responses to BH3-mimetic drugs in leukemias. Blood, 2021, 137, 2721-2735.	1.4	75
12	Non-Specific Immunity Associated Gut Microbiome in Aristichthys nobilis under Different Rearing Strategies. Genes, 2021, 12, 916.	2.4	10
13	Liquid biopsy: an evolving paradigm for the biological characterisation of plasma cell disorders. Leukemia, 2021, 35, 2771-2783.	7.2	17
14	Analysis of Annotated and Unannotated Long Noncoding RNAs from Exosome Subtypes Using Next-Generation RNA Sequencing. Methods in Molecular Biology, 2021, 2254, 195-218.	0.9	1
15	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. Stem Cell Research, 2020, 48, 102002.	0.7	1
16	Complement and coagulation cascades pathway correlates with chemosensitivity and overall survival in patients with soft tissue sarcoma. European Journal of Pharmacology, 2020, 879, 173121.	3.5	31
17	Utility of Circulating Cell-Free RNA Analysis for the Characterization of Global Transcriptome Profiles of Multiple Myeloma Patients. Cancers, 2019, 11, 887.	3.7	20
18	Surfaceome of Exosomes Secreted from the Colorectal Cancer Cell Line SW480: Peripheral and Integral Membrane Proteins Analyzed by Proteolysis and TX114. Proteomics, 2019, 19, e1700453.	2.2	30

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19	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
20	Distinct shed microvesicle and exosome microRNA signatures reveal diagnostic markers for colorectal cancer. <i>PLoS ONE</i> , 2019, 14, e0210003.	2.5	67
21	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
22	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
23	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
24	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
25	CPLSTool: A Framework to Generate Automatic Bioinformatics Pipelines. <i>Biomedical Journal of Scientific & Technical Research</i> , 2018, 11, .	0.1	0
26	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
27	Neoadjuvant Chemotherapy Creates Surgery Opportunities For Inoperable Locally Advanced Breast Cancer. <i>Scientific Reports</i> , 2017, 7, 44673.	3.3	40
28	Extracellular vesicles: their role in cancer biology and epithelial–mesenchymal transition. <i>Biochemical Journal</i> , 2017, 474, 21-45.	3.7	81
29	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
30	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
31	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
32	Thyroid hemiagenesis and Hashimoto’s thyroiditis diagnostic and treatment pitfalls. <i>World Journal of Surgical Oncology</i> , 2017, 15, 182.	1.9	5
33	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
34	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
35	Secreted primary human malignant mesothelioma exosome signature reflects oncogenic cargo. <i>Scientific Reports</i> , 2016, 6, 32643.	3.3	85
36	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

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37	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
38	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
39	Data on the expression of cellular lncRNAs in human adenovirus infected cells. <i>Data in Brief</i> , 2016, 8, 1263-1279.	1.0	6
40	Unique proteome signature of post-chemotherapy ovarian cancer ascites-derived tumor cells. <i>Scientific Reports</i> , 2016, 6, 30061.	3.3	33
41	Fluctuating expression of microRNAs in adenovirus infected cells. <i>Virology</i> , 2015, 478, 99-111.	2.4	37
42	SMAP: a streamlined methylation analysis pipeline for bisulfite sequencing. <i>GigaScience</i> , 2015, 4, 29.	6.4	13
43	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
44	Identification of Serum microRNA Biomarkers for Tuberculosis Using RNA-seq. <i>PLoS ONE</i> , 2014, 9, e88909.	2.5	69
45	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
46	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
47	A new look at adenovirus splicing. <i>Virology</i> , 2014, 456-457, 329-341.	2.4	42
48	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
49	Deep sequencing identifies regulated small RNAs in <i>Dugesia japonica</i> . <i>Molecular Biology Reports</i> , 2013, 40, 4075-4081.	2.3	7
50	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	5.5	832
51	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
52	Identification of adenovirus-encoded small RNAs by deep RNA sequencing. <i>Virology</i> , 2013, 442, 148-155.	2.4	14
53	miRNA Genes of an Invasive Vector Mosquito, <i>Aedes albopictus</i> . <i>PLoS ONE</i> , 2013, 8, e67638.	2.5	38
54	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	27.8	1,966

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55	Comparative mRNA and microRNA Expression Profiling of Three Genitourinary Cancers Reveals Common Hallmarks and Cancer-Specific Molecular Events. PLoS ONE, 2011, 6, e22570.	2.5	69
56	A Systematic Analysis on DNA Methylation and the Expression of Both mRNA and microRNA in Bladder Cancer. PLoS ONE, 2011, 6, e28223.	2.5	35
57	Integrated Profiling of MicroRNAs and mRNAs: MicroRNAs Located on Xq27.3 Associate with Clear Cell Renal Cell Carcinoma. PLoS ONE, 2010, 5, e15224.	2.5	573
58	Editorial: Understanding the RNA Species in the Extracellular Vesicles of Multiple Myeloma. Frontiers in Oncology, 0, 12, .	2.8	0