Chih-Hung Chou

List of Publications by Year
in descending order

33 papers	6,329 citations	331259 21 h-index	395343 33 g-index
33 all docs	33 docs citations	33 times ranked	12224 citing authors

#	Article	IF	Citations
1	DNMT3b protects centromere integrity by restricting R-loop-mediated DNA damage. Cell Death and Disease, 2022, 13, .	2.7	7
2	Source identification of HIV-1 transmission in three lawsuits Using Ultra-Deep pyrosequencing and phylogenetic analysis. Journal of Microbiology, Immunology and Infection, 2021, 54, 596-605.	1.5	3
3	Circulating <scp>microRNAs</scp> Associated With Reversible Cerebral Vasoconstriction Syndrome. Annals of Neurology, 2021, 89, 459-473.	2.8	23
4	QRICH1 dictates the outcome of ER stress through transcriptional control of proteostasis. Science, 2021, 371, .	6.0	73
5	Role of endothelial cells in pulmonary fibrosis via SREBP2 activation. JCI Insight, 2021, 6, .	2.3	21
6	miRTarBase 2020: updates to the experimentally validated microRNA–target interaction database. Nucleic Acids Research, 2020, 48, D148-D154.	6.5	762
7	Multi-omics profiling reveals microRNA-mediated insulin signaling networks. BMC Bioinformatics, 2020, 21, 389.	1.2	3
8	Control of matrix stiffness promotes endodermal lineage specification by regulating SMAD2/3 via lncRNA LINC00458. Science Advances, 2020, 6, eaay0264.	4.7	45
9	Micro <scp>RNA</scp> â€483 amelioration of experimental pulmonary hypertension. EMBO Molecular Medicine, 2020, 12, e11303.	3.3	35
10	Enterotype-based Analysis of Gut Microbiota along the Conventional Adenoma-Carcinoma Colorectal Cancer Pathway. Scientific Reports, 2019, 9, 10923.	1.6	46
11	Bone marrow concentrate-induced mesenchymal stem cell conditioned medium facilitates wound healing and prevents hypertrophic scar formation in a rabbit ear model. Stem Cell Research and Therapy, 2019, 10, 275.	2.4	34
12	Mechanical stretch induces hair regeneration through the alternative activation of macrophages. Nature Communications, 2019, 10, 1524.	5.8	106
13	Pilot Study to Establish a Novel Five-Gene Biomarker Panel for Predicting Lymph Node Metastasis in Patients With Early Stage Endometrial Cancer. Frontiers in Oncology, 2019, 9, 1508.	1.3	15
14	miRTarBase update 2018: a resource for experimentally validated microRNA-target interactions. Nucleic Acids Research, 2018, 46, D296-D302.	6.5	1,591
15	Extension of C. elegans lifespan using the Â·NO-delivery dinitrosyl iron complexes. Journal of Biological Inorganic Chemistry, 2018, 23, 775-784.	1.1	17
16	Integrated MicroRNA–mRNA Analysis Reveals miR-204 Inhibits Cell Proliferation in Gastric Cancer by Targeting CKS1B, CXCL1 and GPRC5A. International Journal of Molecular Sciences, 2018, 19, 87.	1.8	41
17	A Three–MicroRNA Signature as a Potential Biomarker for the Early Detection of Oral Cancer. International Journal of Molecular Sciences, 2018, 19, 758.	1.8	69
18	The aquatic animalsâ€™ transcriptome resource for comparative functional analysis. BMC Genomics, 2018, 19, 103.	1.2	5

#	ARTICLE	IF	CITATIONS
19	MicroRNA-224 down-regulates Glycine N-methyltransferase gene expression in Hepatocellular Carcinoma. Scientific Reports, 2018, 8, 12284.	1.6	19
20	Î±-ketoglutarate orchestrates macrophage activation through metabolic and epigenetic reprogramming. Nature Immunology, 2017, 18, 985-994.	7.0	715
21	Haptoglobin expression correlates with tumor differentiation and five-year overall survival rate in hepatocellular carcinoma. PLoS ONE, 2017, 12, e0171269.	1.1	38
22	Characterization of the Drug Resistance Profiles of Patients Infected with CRF07_BC Using Phenotypic Assay and Ultra-Deep Pyrosequencing. PLoS ONE, 2017, 12, e0170420.	1.1	1
23	DDX3 Represses Stemness by Epigenetically Modulating Tumor-suppressive miRNAs in Hepatocellular Carcinoma. Scientific Reports, 2016, 6, 28637.	1.6	29
24	Transcriptome sequencing based annotation and homologous evidence based scaffolding of Anguilla japonica draft genome. BMC Genomics, 2016, 17, 13.	1.2	9
25	miRTarBase 2016: updates to the experimentally validated miRNA-target interactions database. Nucleic Acids Research, 2016, 44, D239-D247.	6.5	1,331
26	Expanding genotype/phenotype of neuromuscular diseases by comprehensive target capture/NGS. Neurology: Genetics, 2015, 1, e14.	0.9	48
27	Integrated analyses to reconstruct microRNA-mediated regulatory networks in mouse liver using high-throughput profiling. BMC Genomics, 2015, 16, S12.	1.2	12
28	MethHC: a database of DNA methylation and gene expression in human cancer. Nucleic Acids Research, 2015, 43, D856-D861.	6.5	261
29	The evolutionary dynamics of tRNA-gene copy number and codon-use in E. coli.. BMC Evolutionary Biology, 2015, 15, 163.	3.2	26
30	miRTarBase update 2014: an information resource for experimentally validated miRNA-target interactions. Nucleic Acids Research, 2014, 42, D78-D85.	6.5	710
31	A computational approach for identifying microRNA-target interactions using high-throughput CLIP and PAR-CLIP sequencing. BMC Genomics, 2013, 14, S2.	1.2	53
32	sRNAMap: genomic maps for small non-coding RNAs, their regulators and their targets in microbial genomes. Nucleic Acids Research, 2009, 37, D150-D154.	6.5	81
33	FMM: a web server for metabolic pathway reconstruction and comparative analysis. Nucleic Acids Research, 2009, 37, W129-W134.	6.5	100