

Mong-Hsun Tsai

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

3,118
citations

186265
28
h-index

189892
50
g-index

122
all docs

122
docs citations

122
times ranked

6216
citing authors

#	ARTICLE	IF	CITATIONS
1	miRSystem: An Integrated System for Characterizing Enriched Functions and Pathways of MicroRNA Targets. PLoS ONE, 2012, 7, e42390.	2.5	277
2	Identification of a Novel Biomarker, <i>SEMA5A</i> , for Non-Small Cell Lung Carcinoma in Nonsmoking Women. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2590-2597.	2.5	270
3	Gene Expression Profiling of Breast, Prostate, and Glioma Cells following Single versus Fractionated Doses of Radiation. Cancer Research, 2007, 67, 3845-3852.	0.9	167
4	Deregulated microRNAs in triple-negative breast cancer revealed by deep sequencing. Molecular Cancer, 2015, 14, 36.	19.2	100
5	Gene expression after treatment with hydrogen peroxide, menadione, or t-butyl hydroperoxide in breast cancer cells. Cancer Research, 2002, 62, 6246-54.	0.9	89
6	Age-associated Decrease of Oxidative Repair Enzymes, Human 8-Oxoguanine DNA Glycosylases (hOgg1), in Human Aging. Journal of Radiation Research, 2003, 44, 31-35.	1.6	82
7	A whole genome methylation analysis of systemic lupus erythematosus: hypomethylation of the IL10 and IL1R2 promoters is associated with disease activity. Genes and Immunity, 2012, 13, 214-220.	4.1	79
8	Molecular Characteristics and Metastasis Predictor Genes of Triple-Negative Breast Cancer: A Clinical Study of Triple-Negative Breast Carcinomas. PLoS ONE, 2012, 7, e45831.	2.5	76
9	Integrated Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) Quantitative Proteomic Analysis Identifies Galectin-1 as a Potential Biomarker for Predicting Sorafenib Resistance in Liver Cancer*. Molecular and Cellular Proteomics, 2015, 14, 1527-1545.	3.8	71
10	Integrated Analyses of Copy Number Variations and Gene Expression in Lung Adenocarcinoma. PLoS ONE, 2011, 6, e24829.	2.5	68
11	Dissection of the Kaposi's Sarcoma-Associated Herpesvirus Gene Expression Program by Using the Viral DNA Replication Inhibitor Cidofovir. Journal of Virology, 2004, 78, 13637-13652.	3.4	64
12	De novo transcriptome sequencing of axolotl blastema for identification of differentially expressed genes during limb regeneration. BMC Genomics, 2013, 14, 434.	2.8	63
13	Metastatic Progression of Prostate Cancer Is Mediated by Autonomous Binding of Galectin-4- <i>O</i> -Glycan to Cancer Cells. Cancer Research, 2016, 76, 5756-5767.	0.9	54
14	<i>O</i> -Glycosylation-mediated signaling circuit drives metastatic castration-resistant prostate cancer. FASEB Journal, 2018, 32, 6869-6882.	0.5	49
15	Estimates of Relative Risks for Cancers in a Population after Prolonged Low-Dose-Rate Radiation Exposure: A Follow-up Assessment from 1983 to 2005. Radiation Research, 2008, 170, 143-148.	1.5	47
16	Metabolomic Characterization of Laborers Exposed to Welding Fumes. Chemical Research in Toxicology, 2012, 25, 676-686.	3.3	45
17	DNMT3L promotes quiescence in postnatal spermatogonial progenitor cells. Development (Cambridge), 2014, 141, 2402-2413.	2.5	45
18	MicroRNA-449a Enhances Radiosensitivity in CL1-0 Lung Adenocarcinoma Cells. PLoS ONE, 2013, 8, e62383.	2.5	40

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19	Identification of Gene Expression Biomarkers for Predicting Radiation Exposure. <i>Scientific Reports</i> , 2014, 4, 6293.	3.3	39
20	Reassessment of QTLs for Late Blight Resistance in the Tomato Accession L3708 Using a Restriction Site Associated DNA (RAD) Linkage Map and Highly Aggressive Isolates of <i>Phytophthora infestans</i> . <i>PLoS ONE</i> , 2014, 9, e96417.	2.5	38
21	miR-338-5p inhibits cell proliferation, colony formation, migration and cisplatin resistance in esophageal squamous cancer cells by targeting FERMT2. <i>Carcinogenesis</i> , 2019, 40, 883-892.	2.8	38
22	DBCAT: Database of CpG Islands and Analytical Tools for Identifying Comprehensive Methylation Profiles in Cancer Cells. <i>Journal of Computational Biology</i> , 2011, 18, 1013-1017.	1.6	37
23	Transcriptional responses to ionizing radiation reveal that p53R2 protects against radiation-induced mutagenesis in human lymphoblastoid cells. <i>Oncogene</i> , 2006, 25, 622-632.	5.9	36
24	Comparative Genomics of <i>Rickettsia prowazekii</i> Madrid E and Breinl Strains. <i>Journal of Bacteriology</i> , 2004, 186, 556-565.	2.2	35
25	Transcriptome Analysis of Garlic-Induced Hepatoprotection against Alcoholic Fatty Liver. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 11104-11119.	5.2	35
26	EBARDenovo: highly accurate <i>de novo</i> assembly of RNA-Seq with efficient chimera-detection. <i>Bioinformatics</i> , 2013, 29, 1004-1010.	4.1	33
27	The hypoxia-responsive lncRNA <i>NDRG-OT1</i> promotes NDRG1 degradation via ubiquitin-mediated proteolysis in breast cancer cells. <i>Oncotarget</i> , 2018, 9, 10470-10482.	1.8	33
28	Semaphorin 6A Attenuates the Migration Capability of Lung Cancer Cells via the NRF2/HMOX1 Axis. <i>Scientific Reports</i> , 2019, 9, 13302.	3.3	33
29	ADAM9 Up-Regulates N-Cadherin via miR-218 Suppression in Lung Adenocarcinoma Cells. <i>PLoS ONE</i> , 2014, 9, e94065.	2.5	32
30	MicroRNA-769-3p Down-regulates NDRG1 and Enhances Apoptosis in MCF-7 Cells During Reoxygenation. <i>Scientific Reports</i> , 2014, 4, 5908.	3.3	31
31	Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. <i>Scientific Reports</i> , 2016, 6, 23035.	3.3	31
32	Hypoxia-Induced MALAT1 Promotes the Proliferation and Migration of Breast Cancer Cells by Sponging MiR-3064-5p. <i>Frontiers in Oncology</i> , 2021, 11, 658151.	2.8	29
33	Identification of Potential Plasma Biomarkers for Nonalcoholic Fatty Liver Disease by Integrating Transcriptomics and Proteomics in Laying Hens. <i>Journal of Nutrition</i> , 2017, 147, 293-303.	2.9	28
34	Identification of regulatory SNPs associated with genetic modifications in lung adenocarcinoma. <i>BMC Research Notes</i> , 2015, 8, 92.	1.4	27
35	A standardized herbal extract mitigates tumor inflammation and augments chemotherapy effect of docetaxel in prostate cancer. <i>Scientific Reports</i> , 2017, 7, 15624.	3.3	27
36	Down-Regulation of NDRG1 Promotes Migration of Cancer Cells during Reoxygenation. <i>PLoS ONE</i> , 2011, 6, e24375.	2.5	26

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37	Eight new mitogenomes for exploring the phylogeny and classification of Vetigastropoda. <i>Journal of Molluscan Studies</i> , 2016, 82, 534-541.	1.2	26
38	Smoking and Hepatitis B Virus-Related Hepatocellular Carcinoma Risk: The Mediating Roles of Viral Load and Alanine Aminotransferase. <i>Hepatology</i> , 2019, 69, 1412-1425.	7.3	26
39	Identification of Prognostic Genes for Recurrent Risk Prediction in Triple Negative Breast Cancer Patients in Taiwan. <i>PLoS ONE</i> , 2011, 6, e28222.	2.5	25
40	CellExpress: a comprehensive microarray-based cancer cell line and clinical sample gene expression analysis online system. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	25
41	Autoantibody recognition of an N-terminal epitope of hnRNP L marks the risk for developing HBV-related hepatocellular carcinoma. <i>Journal of Proteomics</i> , 2013, 94, 346-358.	2.4	24
42	Prognostic significance of NPM1 mutation-modulated microRNA-mRNA regulation in acute myeloid leukemia. <i>Leukemia</i> , 2016, 30, 274-284.	7.2	24
43	Duodenal Ulcer-related Antigens from <i>Helicobacter pylori</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1018-1026.	3.8	23
44	Interaction of small RNA and the intron of <i>lMYB1</i> family genes through secondary siRNAs and DNA methylation after wounding. <i>Plant Journal</i> , 2013, 75, 781-794.	5.7	23
45	A Knock-In Npm1 Mutation in Mice Results in Myeloproliferation and Implies a Perturbation in Hematopoietic Microenvironment. <i>PLoS ONE</i> , 2012, 7, e49769.	2.5	21
46	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. <i>GigaScience</i> , 2018, 7, .	6.4	21
47	Incorporation of deep-sea and small-sized species provides new insights into gastropods phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 136-147.	2.7	21
48	A probe-density-based analysis method for array CGH data: simulation, normalization and centralization. <i>Bioinformatics</i> , 2008, 24, 1749-1756.	4.1	20
49	Identification of Methylation-Driven, Differentially Expressed STXBP6 as a Novel Biomarker in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 42573.	3.3	20
50	Different effects of long noncoding RNA <i>NDRG1-OT1</i> fragments on <i>NDRG1</i> transcription in breast cancer cells under hypoxia. <i>RNA Biology</i> , 2018, 15, 1487-1498.	3.1	20
51	<i>Penaeus monodon</i> Thioredoxin Restores the DNA Binding Activity of Oxidized White Spot Syndrome Virus IE1. <i>Antioxidants and Redox Signaling</i> , 2012, 17, 914-926.	5.4	19
52	Aryl Hydrocarbon Receptor Activates <i>NDRG1</i> Transcription under Hypoxia in Breast Cancer Cells. <i>Scientific Reports</i> , 2016, 6, 20808.	3.3	19
53	Transcriptome Changes in Relation to Manic Episode. <i>Frontiers in Psychiatry</i> , 2019, 10, 280.	2.6	18
54	EBV-positive Hodgkin lymphoma is associated with suppression of p21cip1/waf1 and a worse prognosis. <i>Molecular Cancer</i> , 2010, 9, 32.	19.2	17

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55	Zinc Chloride for Odontogenesis of Dental Pulp Stem Cells via Metallothionein Up-regulation. <i>Journal of Endodontics</i> , 2011, 37, 211-216.	3.1	17
56	Gene-expression profiling to identify genes related to spontaneous tumor regression in a canine cancer model. <i>Veterinary Immunology and Immunopathology</i> , 2013, 151, 207-216.	1.2	17
57	The extracellular SEMA domain attenuates intracellular apoptotic signaling of semaphorin 6A in lung cancer cells. <i>Oncogenesis</i> , 2018, 7, 95.	4.9	17
58	iGCâ€”an integrated analysis package of gene expression and copy number alteration. <i>BMC Bioinformatics</i> , 2017, 18, 35.	2.6	16
59	The first complete mitochondrial genome of the sand dollar <i>Sinaechinocyamus mai</i> (Echinoidea:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 16	2.9	16
60	Distinct Signaling Pathways After Higher or Lower Doses of Radiation in Three Closely Related Human Lymphoblast Cell Lines. <i>International Journal of Radiation Oncology Biology Physics</i> , 2010, 76, 212-219.	0.8	15
61	Emergence of differentially regulated pathways associated with the development of regional specificity in chicken skin. <i>BMC Genomics</i> , 2015, 16, 22.	2.8	15
62	SMN is required for the maintenance of embryonic stem cells and neuronal differentiation in mice. <i>Brain Structure and Function</i> , 2015, 220, 1539-1553.	2.3	14
63	An automated microfluidic DNA microarray platform for genetic variant detection in inherited arrhythmic diseases. <i>Analyst, The</i> , 2018, 143, 1367-1377.	3.5	14
64	The chondroprotective effect of diosmin on human articular chondrocytes under oxidative stress. <i>Phytotherapy Research</i> , 2019, 33, 2378-2386.	5.8	13
65	anamiR: integrated analysis of MicroRNA and gene expression profiling. <i>BMC Bioinformatics</i> , 2019, 20, 239.	2.6	13
66	MicroRNA-107 enhances radiosensitivity by suppressing granulins in PC-3 prostate cancer cells. <i>Scientific Reports</i> , 2020, 10, 14584.	3.3	13
67	Abnormal Gene Expression Profiles in Unaffected Parents of Patients with Hereditary-Type Retinoblastoma. <i>Cancer Research</i> , 2006, 66, 3428-3433.	0.9	12
68	Radiation-Induced Changes in Gene-Expression Profiles for the SCC VII Tumor Cells Grown In Vitro and In Vivo. <i>Antioxidants and Redox Signaling</i> , 2006, 8, 1263-1272.	5.4	12
69	Transient DNMT3L Expression Reinforces Chromatin Surveillance to Halt Senescence Progression in Mouse Embryonic Fibroblast. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 103.	3.7	12
70	Uremic Toxin-Producing Bacteroides Species Preval in the Gut Microbiota of Taiwanese CKD Patients: An Analysis Using the New Taiwan Microbiome Baseline. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 726256.	3.9	12
71	Use of Germline Polymorphisms in Predicting Concurrent Chemoradiotherapy Response in Esophageal Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2012, 82, 1996-2003.	0.8	11
72	SNP rs10248565 in HDAC9 as a novel genomic aberration biomarker of lung adenocarcinoma in non-smoking women. <i>Journal of Biomedical Science</i> , 2014, 21, 24.	7.0	11

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73	Identification of Genes with Consistent Methylation Levels across Different Human Tissues. Scientific Reports, 2015, 4, 4351.	3.3	11
74	A Standardized Wedelia chinensis Extract Overcomes the Feedback Activation of HER2/3 Signaling upon Androgen-Ablation in Prostate Cancer. Frontiers in Pharmacology, 2017, 8, 721.	3.5	10
75	Regulatory Mechanisms and Functional Roles of Hypoxia-Induced Long Non-Coding RNA MTORT1 in Breast Cancer Cells. Frontiers in Oncology, 2021, 11, 663114.	2.8	10
76	EasyMAP: A user-friendly online platform for analyzing 16S ribosomal DNA sequencing data. New Biotechnology, 2021, 63, 37-44.	4.4	10
77	To compare the performance of prokaryotic taxonomy classifiers using curated 16S full-length rRNA sequences. Computers in Biology and Medicine, 2022, 145, 105416.	7.0	10
78	DNA (cytosine-5)-methyltransferase 1 as a mediator of mutant p53-determined p16ink4A down-regulation. Journal of Biomedical Science, 2008, 15, 163-168.	7.0	9
79	Identification of a liver cirrhosis signature in plasma for predicting hepatocellular carcinoma risk in a population-based cohort of hepatitis B carriers. Molecular Carcinogenesis, 2014, 53, 58-66.	2.7	9
80	A model-based circular binary segmentation algorithm for the analysis of array CGH data. BMC Research Notes, 2011, 4, 394.	1.4	8
81	Development of a prediction model for radiosensitivity using the expression values of genes and long non-coding RNAs. Oncotarget, 2016, 7, 26739-26750.	1.8	8
82	Identifying the functions and biomarkers of Codonopsis pilosula and Astragalus membranaceus aqueous extracts in hepatic cells. Chinese Medicine, 2019, 14, 10.	4.0	8
83	VariED: the first integrated database of gene annotation and expression profiles for variants related to human diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	7
84	RNASeqR: An R Package for Automated Two-Group RNA-Seq Analysis Workflow. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2023-2031.	3.0	6
85	Semaphorin 5A suppresses the proliferation and migration of lung adenocarcinoma cells. International Journal of Oncology, 2020, 56, 165-177.	3.3	6
86	Individuals' Leukocyte DNA Double-Strand Break Repair as an Indicator of Radiosurgery Responses for Cerebral Arteriovenous Malformations. Journal of Radiation Research, 2004, 45, 269-274.	1.6	5
87	Identification of genes differentially expressed during the growth of Bambusa oldhamii. Plant Physiology and Biochemistry, 2013, 63, 217-226.	5.8	5
88	Deep Sequencing Reveals a MicroRNA Expression Signature in Triple-Negative Breast Cancer. Methods in Molecular Biology, 2018, 1699, 99-111.	0.9	5
89	Macrophage Migration Inhibitory Factor Acts as the Potential Target of a Newly Synthesized Compound, 1-(9- α -methyl-3- α -carbazole)-3, 4-dihydro-1 β -carboline. Scientific Reports, 2019, 9, 2147.	3.3	5
90	CNVIntegrate: the first multi-ethnic database for identifying copy number variations associated with cancer. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	5

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91	The Gut Microbiome, Seleno-Compounds, and Acute Myocardial Infarction. Journal of Clinical Medicine, 2022, 11, 1462.	2.4	5
92	Comparisons and performance evaluations of RNA-seq alignment tools. , 2014, , .		4
93	A reliable multiplex genotyping assay for <scp>HCV</scp> using a suspension bead array. Microbial Biotechnology, 2015, 8, 93-102.	4.2	4
94	Using proteomic profiling to characterize protein signatures of different thymoma subtypes. BMC Cancer, 2019, 19, 796.	2.6	4
95	Mitomycin C treatment induces resistance and enhanced migration via phosphorylated Akt in aggressive lung cancer cells. Oncotarget, 2016, 7, 79995-80007.	1.8	4
96	Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific. Oncotarget, 2015, 6, 19483-19499.	1.8	4
97	Evaluation of Hybridization Conditions for Spotted Oligonucleotide-Based DNA Microarrays. Molecular Biotechnology, 2005, 29, 221-224.	2.4	3
98	Determine the Potency of BCG Vaccines by Flow Cytometer. Biotechnology and Biotechnological Equipment, 2011, 25, 2394-2398.	1.3	3
99	A collaborative study to establish the first National Standard for HIV-1 RNA nucleic acid amplification techniques (NAT) in Taiwan. Journal of Virological Methods, 2013, 191, 122-127.	2.1	3
100	Risk Factors and Genetic Biomarkers of Multiple Primary Cancers in Esophageal Cancer Patients. Frontiers in Oncology, 2020, 10, 585621.	2.8	3
101	Evolutionary Trajectories and Genomic Divergence in Localized Breast Cancers after Ipsilateral Breast Tumor Recurrence. Cancers, 2021, 13, 1821.	3.7	3
102	Overexpression of methylation-driven DCC suppresses proliferation of lung cancer cells. Translational Cancer Research, 2016, 5, 169-175.	1.0	3
103	Novel Tumor-Specific Antigens for Immunotherapy Identified From Multi-omics Profiling in Thymic Carcinomas. Frontiers in Immunology, 2021, 12, 748820.	4.8	3
104	Lidocaine and Bupivacaine Downregulate MYB and DANCR lncRNA by Upregulating miR-187-5p in MCF-7 Cells. Frontiers in Medicine, 2021, 8, 732817.	2.6	3
105	Differential whole-genome doubling and homologous recombination deficiencies across breast cancer subtypes from the Taiwanese population. Communications Biology, 2021, 4, 1052.	4.4	2
106	MiDSysstem: A comprehensive online system for de novo assembly and analysis of microbial genomes. New Biotechnology, 2021, 65, 42-52.	4.4	2
107	IL-27/IL-27RA signaling may modulate inflammation and progression of benign prostatic hyperplasia via suppressing the LPS/TLR4 pathway. Translational Cancer Research, 2020, 9, 4618-4634.	1.0	2
108	Leveraging well-annotated databases for deep learning in biomedical research. Translational Cancer Research, 2020, 9, 7682-7684.	1.0	2

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109	Transcriptome profiling reveals the developmental regulation of NaCl-treated <i>Forcipomyia taiwana</i> eggs. BMC Genomics, 2021, 22, 792.	2.8	2
110	Concurrent analysis of copy number variations and expression profiles to identify genes associated with tumorigenesis and survival outcome in lung adenocarcinoma. , 2010, , .		1
111	High-performance deep learning pipeline predicts individuals in mixtures of DNA using sequencing data. Briefings in Bioinformatics, 2021, 22, .	6.5	1
112	Development of a normalization algorithm for array comparative genomic hybridization. , 2006, , .		0
113	Utilizing Cox regression model to assess the relations between predefined gene sets and the survival outcome of lung adenocarcinoma. , 2010, , .		0
114	Comparison of triple negative breast cancer between Asian and western data sets. , 2010, , .		0
115	Concurrent analysis of copy number variation and gene expression: Application in paired non-smoking female lung cancer patients. , 2010, , .		0
116	Concurrent analysis of copy number variation and gene expression: application in paired non-smoking female lung cancer patients. International Journal of Data Mining and Bioinformatics, 2013, 8, 92.	0.1	0
117	Response to Chen Guan et al.'s comments on our published article "miR-338-5p inhibits cell proliferation, colony formation, migration, and cisplatin resistance in esophageal squamous cancer cells by targeting FERMT2". Carcinogenesis, 2020, 41, 245-245.	2.8	0
118	ATTRACTIVE " An Auto-Updating Database for Experimental Protocols in Regenerative Medicine. IEEE Access, 2021, 9, 75202-75210.	4.2	0
119	MutScape: an analytical toolkit for probing the mutational landscape in cancer genomics. NAR Genomics and Bioinformatics, 2021, 3, lqab099.	3.2	0
120	Extracellular domain of semaphorin 5A serves a tumor-suppressing role by activating interferon signaling pathways in lung adenocarcinoma cells. International Journal of Oncology, 2022, 60, .	3.3	0