

Ting-Wen Chen

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

2,250
citations

331538

21
h-index

243529

44
g-index

60
all docs

60
docs citations

60
times ranked

5120
citing authors

#	ARTICLE	IF	CITATIONS
1	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
2	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
3	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
4	Gut microbiota modulates COPD pathogenesis: role of anti-inflammatory <i>Parabacteroides goldsteinii</i> lipopolysaccharide. <i>Gut</i> , 2022, 71, 309-321.	6.1	126
5	APOBEC3A is an oral cancer prognostic biomarker in Taiwanese carriers of an APOBEC deletion polymorphism. <i>Nature Communications</i> , 2017, 8, 465.	5.8	89
6	MicroRNA-223 and microRNA-92a in stool and plasma samples act as complementary biomarkers to increase colorectal cancer detection. <i>Oncotarget</i> , 2016, 7, 10663-10675.	0.8	81
7	MiR-31-5p-ACOX1 Axis Enhances Tumorigenic Fitness in Oral Squamous Cell Carcinoma Via the Promigratory Prostaglandin E2. <i>Theranostics</i> , 2018, 8, 486-504.	4.6	80
8	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	9.4	75
9	Arm Selection Preference of MicroRNA-193a Varies in Breast Cancer. <i>Scientific Reports</i> , 2016, 6, 28176.	1.6	67
10	ChIPseek, a web-based analysis tool for ChIP data. <i>BMC Genomics</i> , 2014, 15, 539.	1.2	57
11	FastAnnotator- an efficient transcript annotation web tool. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	51
12	Genetic Indicators of Drug Resistance in the Highly Repetitive Genome of <i>Trichomonas vaginalis</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1658-1672.	1.1	44
13	Whole Genome DNA Methylation Analysis of Obstructive Sleep Apnea: <i>IL1R2</i> , <i>NPR2</i> , <i>AR</i> , <i>SP140</i> Methylation and Clinical Phenotype. <i>Sleep</i> , 2016, 39, 743-755.	0.6	42
14	MicroRNA expression profiles in human breast cancer cells after multifraction and single-dose radiation treatment. <i>Oncology Reports</i> , 2014, 31, 2147-2156.	1.2	37
15	Histidine-Dependent Protein Methylation Is Required for Compartmentalization of CTP Synthase. <i>Cell Reports</i> , 2018, 24, 2733-2745.e7.	2.9	36
16	Integrated analyses utilizing metabolomics and transcriptomics reveal perturbation of the polyamine pathway in oral cavity squamous cell carcinoma. <i>Analytica Chimica Acta</i> , 2019, 1050, 113-122.	2.6	34
17	Comprehensive microRNA profiling of prostate cancer cells after ionizing radiation treatment. <i>Oncology Reports</i> , 2014, 31, 1067-1078.	1.2	33
18	Emerging role of microRNAs in modulating endothelin-1 expression in gastric cancer. <i>Oncology Reports</i> , 2015, 33, 485-493.	1.2	32

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19	FunctionAnnotator, a versatile and efficient web tool for non-model organism annotation. <i>Scientific Reports</i> , 2017, 7, 10430.	1.6	29
20	Genome-wide gene expression array identifies novel genes related to disease severity and excessive daytime sleepiness in patients with obstructive sleep apnea. <i>PLoS ONE</i> , 2017, 12, e0176575.	1.1	25
21	Inactivation of the tight junction gene CLDN11 by aberrant hypermethylation modulates tubulins polymerization and promotes cell migration in nasopharyngeal carcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 102.	3.5	25
22	Synbiotics Alleviate the Gut Indole Load and Dysbiosis in Chronic Kidney Disease. <i>Cells</i> , 2021, 10, 114.	1.8	25
23	Tigecycline-non-susceptible hypervirulent <i>Klebsiella pneumoniae</i> strains in Taiwan. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 309-317.	1.3	23
24	Novel Role for miR-1290 in Host Species Specificity of Influenza A Virus. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 10-23.	2.3	20
25	Whole Genome DNA Methylation Analysis of Active Pulmonary Tuberculosis Disease Identifies Novel Epigenotypes: PARP9/miR-505/RASGRP4/GNG12 Gene Methylation and Clinical Phenotypes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3180.	1.8	20
26	TACCO, a Database Connecting Transcriptome Alterations, Pathway Alterations and Clinical Outcomes in Cancers. <i>Scientific Reports</i> , 2019, 9, 3877.	1.6	19
27	Murine Renal Transcriptome Profiles Upon Leptospiral Infection: Implications for Chronic Kidney Diseases. <i>Journal of Infectious Diseases</i> , 2018, 218, 1411-1423.	1.9	18
28	Epigenome-wide association study on asthma and chronic obstructive pulmonary disease overlap reveals aberrant DNA methylations related to clinical phenotypes. <i>Scientific Reports</i> , 2021, 11, 5022.	1.6	17
29	Responding to a Zoonotic Emergency with Multi-omics Research: <i>Pentatrichomonas hominis</i> Hydrogenosomal Protein Characterization with Use of RNA Sequencing and Proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 662-669.	1.0	14
30	Mutant p53 Attenuates Oxidative Phosphorylation and Facilitates Cancer Stemness through Downregulating miR-200c/PCK2 Axis in Basal-Like Breast Cancer. <i>Molecular Cancer Research</i> , 2021, 19, 1900-1916.	1.5	14
31	DODO: an efficient orthologous genes assignment tool based on domain architectures. Domain based ortholog detection. <i>BMC Bioinformatics</i> , 2010, 11, S6.	1.2	13
32	Interrogation of alternative splicing events in duplicated genes during evolution. <i>BMC Genomics</i> , 2011, 12, S16.	1.2	13
33	CMPD: cancer mutant proteome database. <i>Nucleic Acids Research</i> , 2015, 43, D849-D855.	6.5	13
34	Increase in Akkermansiaceae in Gut Microbiota of Prostate Cancer-Bearing Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9626.	1.8	13
35	Potential impact on kidney infection: a whole-genome analysis of <i>Leptospira santarosai</i> serovar Shermani. <i>Emerging Microbes and Infections</i> , 2014, 3, 1-11.	3.0	12
36	Evaluation and Application of the Strand-Specific Protocol for Next-Generation Sequencing. <i>BioMed Research International</i> , 2015, 2015, 1-8.	0.9	11

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37	MicroRNA Sequencing Analysis in Obstructive Sleep Apnea and Depression: Anti-Oxidant and MAOA-Inhibiting Effects of miR-15b-5p and miR-92b-3p through Targeting PTGS1-NF- κ B-SP1 Signaling. <i>Antioxidants</i> , 2021, 10, 1854.	2.2	10
38	Meta-analytical biomarker search of EST expression data reveals three differentially expressed candidates. <i>BMC Genomics</i> , 2012, 13, S12.	1.2	9
39	Co-modulated behavior and effects of differentially expressed miRNA in colorectal cancer. <i>BMC Genomics</i> , 2013, 14, S12.	1.2	9
40	Is the whole greater than the sum of its parts? De novo assembly strategies for bacterial genomes based on paired-end sequencing. <i>BMC Genomics</i> , 2015, 16, 648.	1.2	8
41	Characterization of Copy Number Variations in Oral Cavity Squamous Cell Carcinoma Reveals a Novel Role for MLLT3 in Cell Invasiveness. <i>Oncologist</i> , 2019, 24, e1388-e1400.	1.9	8
42	Transcriptomic signatures of exacerbated progression in leptospirosis subclinical chronic kidney disease with secondary nephrotoxic injury. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 320, F1001-F1018.	1.3	8
43	OMICS in Ecology: Systems Level Analyses of <i>Halobacterium salinarum</i> Reveal Large-scale Temperature-Mediated Changes and a Requirement of CctA for Thermotolerance. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 65-80.	1.0	7
44	Vanno: A Visualization-Aided Variant Annotation Tool. <i>Human Mutation</i> , 2015, 36, 167-174.	1.1	6
45	PARRoT- a homology-based strategy to quantify and compare RNA-sequencing from non-model organisms. <i>BMC Bioinformatics</i> , 2016, 17, 513.	1.2	6
46	Involvement of Differentially Expressed microRNAs in the PEGylated Liposome Encapsulated 188Rhenium-Mediated Suppression of Orthotopic Hypopharyngeal Tumor. <i>Molecules</i> , 2020, 25, 3609.	1.7	6
47	Brachytherapy Approach Using ¹⁷⁷ Lu Conjugated Gold Nanostars and Evaluation of Biodistribution, Tumor Retention, Dosimetry and Therapeutic Efficacy in Head and Neck Tumor Model. <i>Pharmaceutics</i> , 2021, 13, 1903.	2.0	6
48	Characterization of Recurrent Relevant Genes Reveals a Novel Role of RPL36A in Radioresistant Oral Squamous Cell Carcinoma. <i>Cancers</i> , 2021, 13, 5623.	1.7	6
49	CPAP: Cancer Panel Analysis Pipeline. <i>Human Mutation</i> , 2013, 34, 1340-1346.	1.1	3
50	Illuminating lncRNA Function Through Target Prediction. <i>Methods in Molecular Biology</i> , 2021, 2372, 263-295.	0.4	3
51	ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. <i>DNA Research</i> , 2017, 24, 327-332.	1.5	2
52	Complete Genome Sequence of a New Halophilic Archaeon, <i>Haloarcula taiwanensis</i> , Isolated from a Solar Saltern in Southern Taiwan. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
53	Melanin production as a visual indicator of conjugal transfer in <i>Streptomyces</i> . <i>Journal of Applied Genetics</i> , 2020, 61, 299-301.	1.0	1
54	Survival-related genes are diversified across cancers but generally enriched in cancer hallmark pathways. <i>BMC Genomics</i> , 2021, 22, 918.	1.2	1

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55	Implication of the IL-10-Expression Signature in the Pathogenicity of <i>Leptospira</i> -Infected Macrophages. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
56	VIP DB – A viral protein domain usage and distribution database. <i>Genomics</i> , 2012, 100, 149-156.	1.3	0
57	Abstract 1104: MicroRNA miR-31 regulates oral squamous cell carcinoma cell migration by targeting critical enzyme of peroxisomal lipid metabolism. , 2016, , .		0