

Chia-Chin Wu

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

18,667
citations

257450

24
h-index

315739

38
g-index

44
all docs

44
docs citations

44
times ranked

35058
citing authors

#	ARTICLE	IF	CITATIONS
1	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
2	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	28.9	2,562
3	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	28.9	2,435
4	Depletion of Carcinoma-Associated Fibroblasts and Fibrosis Induces Immunosuppression and Accelerates Pancreas Cancer with Reduced Survival. <i>Cancer Cell</i> , 2014, 25, 719-734.	16.8	1,892
5	Epithelial-to-mesenchymal transition is dispensable for metastasis but induces chemoresistance in pancreatic cancer. <i>Nature</i> , 2015, 527, 525-530.	27.8	1,725
6	Epithelial-to-mesenchymal transition induces cell cycle arrest and parenchymal damage in renal fibrosis. <i>Nature Medicine</i> , 2015, 21, 998-1009.	30.7	736
7	Generation and testing of clinical-grade exosomes for pancreatic cancer. <i>JCI Insight</i> , 2018, 3, .	5.0	520
8	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	416
9	Targeting YAP-Dependent MDSC Infiltration Impairs Tumor Progression. <i>Cancer Discovery</i> , 2016, 6, 80-95.	9.4	404
10	Genomic deletion of malic enzyme 2 confers collateral lethality in pancreatic cancer. <i>Nature</i> , 2017, 542, 119-123.	27.8	209
11	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. <i>Nature Medicine</i> , 2018, 24, 1047-1057.	30.7	175
12	Immuno-genomic landscape of osteosarcoma. <i>Nature Communications</i> , 2020, 11, 1008.	12.8	143
13	Targeting Vascular Pericytes in Hypoxic Tumors Increases Lung Metastasis via Angiopoietin-2. <i>Cell Reports</i> , 2015, 10, 1066-1081.	6.4	132
14	Synthetic vulnerabilities of mesenchymal subpopulations in pancreatic cancer. <i>Nature</i> , 2017, 542, 362-366.	27.8	105
15	Identification of Functional Heterogeneity of Carcinoma-Associated Fibroblasts with Distinct IL6-Mediated Therapy Resistance in Pancreatic Cancer. <i>Cancer Discovery</i> , 2022, 12, 1580-1597.	9.4	100
16	Truncating PREX2 mutations activate its GEF activity and alter gene expression regulation in NRAS-mutant melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1296-305.	7.1	59
17	GeneNetwork: an interactive tool for reconstruction of genetic networks using microarray data. <i>Bioinformatics</i> , 2004, 20, 3691-3693.	4.1	57
18	Grey input-output analysis and its application for environmental cost allocation. <i>European Journal of Operational Research</i> , 2003, 145, 175-201.	5.7	54

#	ARTICLE	IF	CITATIONS
19	Genes suppressed by DNA methylation in non-small cell lung cancer reveal the epigenetics of epithelial-mesenchymal transition. <i>BMC Genomics</i> , 2014, 15, 1079.	2.8	45
20	Genomic profiling of dedifferentiated liposarcoma compared to matched well-differentiated liposarcoma reveals higher genomic complexity and a common origin. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002386.	1.2	45
21	Multimomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. <i>Genome Biology</i> , 2020, 21, 271.	8.8	36
22	Genomics and the Immune Landscape of Osteosarcoma. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1258, 21-36.	1.6	31
23	Prediction of human functional genetic networks from heterogeneous data using RVM-based ensemble learning. <i>Bioinformatics</i> , 2010, 26, 807-813.	4.1	28
24	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association. <i>Nature Communications</i> , 2022, 13, 42.	12.8	27
25	Global strategy for optimizing textile dyeing manufacturing process via GA-based grey nonlinear integer programming. <i>Computers and Chemical Engineering</i> , 2003, 27, 833-854.	3.8	25
26	Identification of cancer fusion drivers using network fusion centrality. <i>Bioinformatics</i> , 2013, 29, 1174-1181.	4.1	22
27	TARGETgene: A Tool for Identification of Potential Therapeutic Targets in Cancer. <i>PLoS ONE</i> , 2012, 7, e43305.	2.5	19
28	The androgen receptor is a therapeutic target in desmoplastic small round cell sarcoma. <i>Nature Communications</i> , 2022, 13, .	12.8	14
29	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. <i>Acta Neuropathologica</i> , 2021, 142, 565-590.	7.7	12
30	Unique somatic variants in DNA from urine exosomes of individuals with bladder cancer. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 22, 360-376.	4.1	10
31	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. <i>PLoS Computational Biology</i> , 2018, 14, e1006266.	3.2	8
32	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold. <i>Npj Precision Oncology</i> , 2022, 6, 21.	5.4	7
33	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. <i>Journal of Thoracic Disease</i> , 2020, 12, 1952-1959.	1.4	6
34	Evaluation of environmentally benign production program in the textile-dyeing industry (I): an input-output analysis. <i>Civil Engineering and Environmental Systems</i> , 2007, 24, 275-298.	0.9	4
35	Evaluation of environmentally benign production program in the textile-dyeing industry (II): a multi-objective programming approach. <i>Civil Engineering and Environmental Systems</i> , 2008, 25, 1-28.	0.9	4
36	Targeting YAP-dependent MDSC infiltration impairs tumor progression. , 2015, 3, .		0

#	ARTICLE	IF	CITATIONS
37	Abstract 109: Network-based model to identify potential therapeutic targets in breast, colon, and lung cancers. , 2010, , .		0
38	Abstract 3183: Breast Cancer MethylSeq: Analysis of bisulfite converted breast cancer genomes using microdroplet-based targeted sequencing. , 2012, , .		0
39	Abstract 156: Integrated exome and transcriptome sequencing of primary lung cancers and paired distant metastases. , 2016, , .		0
40	Abstract 1291: Notch2 inhibition as a therapeutic intervention in osteosarcoma. , 2019, , .		0