

Yi-Mi Wu

List of Publications by Year in descending order

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41
papers

10,665
citations

331642

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302107

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times ranked

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#	ARTICLE	IF	CITATIONS
1	Homozygous ATM mutation due to germline uniparental isodisomy in patient with T acute lymphoblastic leukemia and hepatosplenic T-cell lymphoma. <i>Cancer Genetics</i> , 2022, 266-267, 15-18.	0.4	0
2	Targeting transcriptional regulation of SARS-CoV-2 entry factors <i>ACE2</i> and <i>TMPRSS2</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	142
3	Assessment of Clinical Benefit of Integrative Genomic Profiling in Advanced Solid Tumors. <i>JAMA Oncology</i> , 2021, 7, 525-533.	7.1	65
4	Cancer Cell Intrinsic and Immunologic Phenotypes Determine Clinical Outcomes in Basal-like Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 3079-3093.	7.0	8
5	Unusual clinical behavior of a very late retinoblastoma relapse in a patient with a germline RB mutation. <i>Pediatric Blood and Cancer</i> , 2021, 68, e29064.	1.5	1
6	Clinical Features and Outcomes of Patients with Myelofibrosis and RAS Pathway Activating Mutations at the University of Michigan. <i>Blood</i> , 2021, 138, 4643-4643.	1.4	0
7	Clinical Sequencing of High-Grade Undifferentiated Sarcomas: A Case Series and Report of an Aggressive Primary Cardiac Tumor With Multiple Oncogenic Drivers. <i>JCO Precision Oncology</i> , 2020, 4, 1061-1069.	3.0	1
8	Index of Cancer-Associated Fibroblasts Is Superior to the Epithelialâ€“Mesenchymal Transition Score in Prognosis Prediction. <i>Cancers</i> , 2020, 12, 1718.	3.7	18
9	Double-Negative Prostate Cancer Masquerading as a Squamous Cancer of Unknown Primary: A Clinicopathologic and Genomic Sequencing-Based Case Study. <i>JCO Precision Oncology</i> , 2020, 4, 1386-1392.	3.0	4
10	Role of Aneuploidy in Transcriptional Regulation and Clinical Prognosis in Relapsed and/or Refractory Multiple Myeloma (RRMM). <i>Blood</i> , 2020, 136, 45-46.	1.4	1
11	Integrative Exome and Transcriptome Analysis of Conjunctival Melanoma and Its Potential Application for Personalized Therapy. <i>JAMA Ophthalmology</i> , 2019, 137, 1444.	2.5	29
12	Distinct structural classes of activating FOXA1 alterations in advanced prostate cancer. <i>Nature</i> , 2019, 571, 413-418.	27.8	192
13	The Landscape of Circular RNA in Cancer. <i>Cell</i> , 2019, 176, 869-881.e13.	28.9	1,095
14	Metastatic castration resistant prostate cancer with squamous cell, small cell, and sarcomatoid elementsâ€“a clinicopathologic and genomic sequencing-based discussion. <i>Medical Oncology</i> , 2019, 36, 27.	2.5	8
15	Aneuploidy Is Associated with Inferior Survival in Relapsed Refractory Multiple Myeloma Patients. <i>Blood</i> , 2019, 134, 4360-4360.	1.4	3
16	Clinical validation of the Tempus xO assay. <i>Oncotarget</i> , 2018, 9, 25826-25832.	1.8	43
17	Clinically Integrated Sequencing Alters Therapy in Children and Young Adults With High-Risk Glial Brain Tumors. <i>JCO Precision Oncology</i> , 2018, 2, 1-34.	3.0	10
18	Inactivation of CDK12 Delineates a Distinct Immunogenic Class of Advanced Prostate Cancer. <i>Cell</i> , 2018, 173, 1770-1782.e14.	28.9	400

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19	Clinical characteristics and whole exome/transcriptome sequencing of coexisting chronic myeloid leukemia and myelofibrosis. American Journal of Hematology, 2017, 92, 555-561.	4.1	12
20	Integrative clinical genomics of metastatic cancer. Nature, 2017, 548, 297-303.	27.8	685
21	Blood-brain barrier-adapted precision medicine therapy for pediatric brain tumors. Translational Research, 2017, 188, 27.e1-27.e14.	5.0	12
22	Clinical application of comprehensive next generation sequencing in the management of metastatic cancer in adults.. Journal of Clinical Oncology, 2017, 35, 101-101.	1.6	7
23	Next generation sequencing of extraskeletal myxoid chondrosarcoma. Oncotarget, 2017, 8, 21770-21777.	1.8	20
24	Identification of clinically actionable pharmacogenetic variants during tumor genetic profiling in pediatric cancer patients.. Journal of Clinical Oncology, 2016, 34, 1583-1583.	1.6	2
25	Characterizing and targeting <i>PDGFRA</i> alterations in pediatric high-grade glioma. Oncotarget, 2016, 7, 65696-65706.	1.8	55
26	A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine. Oncotarget, 2016, 7, 52888-52899.	1.8	18
27	A subset of solitary fibrous tumors express nuclear PAX8 and PAX2: a potential diagnostic pitfall. Histology and Histopathology, 2016, 31, 223-30.	0.7	6
28	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	28.9	2,660
29	The landscape of antisense gene expression in human cancers. Genome Research, 2015, 25, 1068-1079.	5.5	150
30	The landscape of long noncoding RNAs in the human transcriptome. Nature Genetics, 2015, 47, 199-208.	21.4	2,410
31	ERG/AKR1C3/AR Constitutes a Feed-Forward Loop for AR Signaling in Prostate Cancer Cells. Clinical Cancer Research, 2015, 21, 2569-2579.	7.0	60
32	Targeting the MLL complex in castration-resistant prostate cancer. Nature Medicine, 2015, 21, 344-352.	30.7	165
33	The use of exome capture RNA-seq for highly degraded RNA with application to clinical cancer sequencing. Genome Research, 2015, 25, 1372-1381.	5.5	139
34	Integrative Clinical Sequencing in the Management of Refractory or Relapsed Cancer in Youth. JAMA - Journal of the American Medical Association, 2015, 314, 913.	7.4	333
35	The Distinctive Mutational Spectra of Polyomavirus-Negative Merkel Cell Carcinoma. Cancer Research, 2015, 75, 3720-3727.	0.9	276
36	Clinical impact of high-throughput sequencing in patients with advanced cancer: Lessons learned from the Michigan Oncology Sequencing Center.. Journal of Clinical Oncology, 2015, 33, 11057-11057.	1.6	2

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37	Prostate cancer cellâ€‘stromal cell crosstalk via FGFR1 mediates antitumor activity of dovitinib in bone metastases. <i>Science Translational Medicine</i> , 2014, 6, 252ra122.	12.4	86
38	Transcriptome meta-analysis of lung cancer reveals recurrent aberrations in NRG1 and Hippo pathway genes. <i>Nature Communications</i> , 2014, 5, 5893.	12.8	121
39	Therapeutic targeting of BET bromodomain proteins in castration-resistant prostate cancer. <i>Nature</i> , 2014, 510, 278-282.	27.8	811
40	Comprehensive molecular profiling of pretreatment metastatic castration resistant prostate cancer (CRPC): Secondary data from NCI 9012, a randomized ETS fusion-stratified phase II trial.. <i>Journal of Clinical Oncology</i> , 2014, 32, e16038-e16038.	1.6	1
41	Identification of Targetable FGFR Gene Fusions in Diverse Cancers. <i>Cancer Discovery</i> , 2013, 3, 636-647.	9.4	614