

# Mao Mao

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

3,900  
citations

361296

20  
h-index

677027

22  
g-index

24  
all docs

24  
docs citations

24  
times ranked

7741  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct mutations and lineages of SARS-CoV-2 virus in the early phase of COVID-19 pandemic and subsequent 1-year global expansion. <i>Journal of Medical Virology</i> , 2022, 94, 2035-2049.	2.5	7
2	Whole-genome sequencing as an alternative to analyze copy number abnormalities in acute myeloid leukemia and myelodysplastic syndrome. <i>Leukemia and Lymphoma</i> , 2022, 63, 2301-2310.	0.6	0
3	Noninvasive Detection of Hepatocellular Carcinoma with Circulating Tumor DNA Features and $\alpha$ -Fetoprotein. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1174-1184.	1.2	14
4	Comprehensive Characterization of Oncogenic Drivers in Asian Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2016, 11, 2129-2140.	0.5	70
5	ALK, ROS1 and RET rearrangements in lung squamous cell carcinoma are very rare. <i>Lung Cancer</i> , 2016, 94, 22-27.	0.9	56
6	&lt;i>&gt;SEC31A-ALK&lt;/i>; Fusion Gene in Lung Adenocarcinoma. <i>Cancer Research and Treatment</i> , 2016, 48, 398-402.	1.3	27
7	Comprehensive analysis of RET and ROS1 rearrangement in lung adenocarcinoma. <i>Modern Pathology</i> , 2015, 28, 468-479.	2.9	114
8	HIP1-ALK, A Novel ALK Fusion Variant that Responds to Crizotinib. <i>Journal of Thoracic Oncology</i> , 2014, 9, 285-294.	0.5	84
9	Clinical characteristics associated with ALK rearrangements in never-smokers with pulmonary adenocarcinoma. <i>Lung Cancer</i> , 2014, 83, 259-264.	0.9	30
10	A Single-Tube Multiplexed Assay for Detecting ALK, ROS1, and RET Fusions in Lung Cancer. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 229-243.	1.2	105
11	Whole-genome sequencing and comprehensive molecular profiling identify new driver mutations in gastric cancer. <i>Nature Genetics</i> , 2014, 46, 573-582.	9.4	895
12	Test of Four Colon Cancer Risk-Scores in Formalin Fixed Paraffin Embedded Microarray Gene Expression Data. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	3.0	30
13	Patterns of somatic alterations between matched primary and metastatic colorectal tumors characterized by whole-genome sequencing. <i>Genomics</i> , 2014, 104, 234-241.	1.3	58
14	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014, 103, 189-203.	1.3	49
15	A Novel Fusion of TPR and ALK in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2014, 9, 563-566.	0.5	83
16	Aberrant CDK4 Amplification in Refractory Rhabdomyosarcoma as Identified by Genomic Profiling. <i>Scientific Reports</i> , 2014, 4, 3623.	1.6	25
17	Genomic landscape of copy number aberrations enables the identification of oncogenic drivers in hepatocellular carcinoma. <i>Hepatology</i> , 2013, 58, 706-717.	3.6	159
18	Multiplexed Gene Expression and Fusion Transcript Analysis to Detect ALK Fusions in Lung Cancer. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 51-61.	1.2	63

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19	Next generation sequencing reveals genetic landscape of hepatocellular carcinomas. <i>Cancer Letters</i> , 2013, 340, 247-253.	3.2	59
20	Detecting <i>ALK</i> fusions in lung cancer: multiple choice testing?. <i>Lung Cancer Management</i> , 2013, 2, 173-175.	1.5	0
21	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433.	2.4	457
22	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012, 44, 765-769.	9.4	785
23	Exome sequencing identifies frequent mutation of <i>ARID1A</i> in molecular subtypes of gastric cancer. <i>Nature Genetics</i> , 2011, 43, 1219-1223.	9.4	662
24	Predictive Genes in Adjacent Normal Tissue Are Preferentially Altered by sCNV during Tumorigenesis in Liver Cancer and May Rate Limiting. <i>PLoS ONE</i> , 2011, 6, e20090.	1.1	68