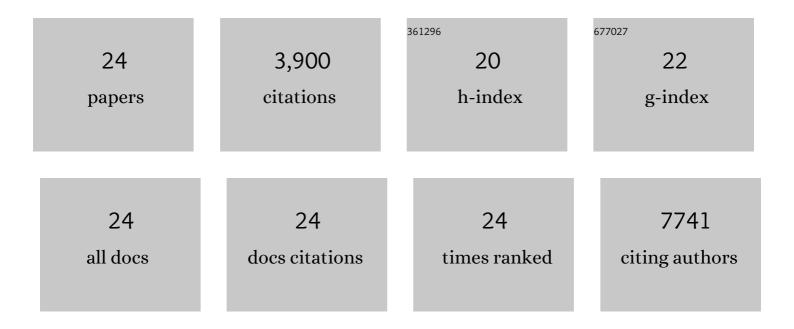
Mao Mao

List of Publications by Year in descending order

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

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#	Article	IF	CITATIONS
19	Next generation sequencing reveals genetic landscape of hepatocellular carcinomas. Cancer Letters, 2013, 340, 247-253.	3.2	59
20	Detecting <i>ALK</i> fusions in lung cancer: multiple choice testing?. Lung Cancer Management, 2013, 2, 173-175.	1.5	0
21	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. Genome Research, 2013, 23, 1422-1433.	2.4	457
22	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769.	9.4	785
23	Exome sequencing identifies frequent mutation of ARID1A in molecular subtypes of gastric cancer. Nature Genetics, 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. PLoS ONE, 2011, 6, e20090.	1.1	68