

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	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
2	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012, 44, 765-769.	9.4	785
3	Exome sequencing identifies frequent mutation of ARID1A in molecular subtypes of gastric cancer. <i>Nature Genetics</i> , 2011, 43, 1219-1223.	9.4	662
4	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433.	2.4	457
5	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
6	Comprehensive analysis of RET and ROS1 rearrangement in lung adenocarcinoma. <i>Modern Pathology</i> , 2015, 28, 468-479.	2.9	114
7	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
8	HIP1 α -ALK, A Novel ALK Fusion Variant that Responds to Crizotinib. <i>Journal of Thoracic Oncology</i> , 2014, 9, 285-294.	0.5	84
9	A Novel Fusion of TPR and ALK in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2014, 9, 563-566.	0.5	83
10	Comprehensive Characterization of Oncogenic Drivers in Asian Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2016, 11, 2129-2140.	0.5	70
11	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
12	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
13	Next generation sequencing reveals genetic landscape of hepatocellular carcinomas. <i>Cancer Letters</i> , 2013, 340, 247-253.	3.2	59
14	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
15	ALK, ROS1 and RET rearrangements in lung squamous cell carcinoma are very rare. <i>Lung Cancer</i> , 2016, 94, 22-27.	0.9	56
16	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014, 103, 189-203.	1.3	49
17	Clinical characteristics associated with ALK rearrangements in never-smokers with pulmonary adenocarcinoma. <i>Lung Cancer</i> , 2014, 83, 259-264.	0.9	30
18	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

#	ARTICLE	IF	CITATIONS
19	<i>SEC31A-ALK</i> Fusion Gene in Lung Adenocarcinoma. Cancer Research and Treatment, 2016, 48, 398-402.	1.3	27
20	Aberrant CDK4 Amplification in Refractory Rhabdomyosarcoma as Identified by Genomic Profiling. Scientific Reports, 2014, 4, 3623.	1.6	25
21	Noninvasive Detection of Hepatocellular Carcinoma with Circulating Tumor DNA Features&Aand Î±-Fetoprotein. Journal of Molecular Diagnostics, 2021, 23, 1174-1184.	1.2	14
22	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
23	Detecting <i>ALK</i> fusions in lung cancer: multiple choice testing?. Lung Cancer Management, 2013, 2, 173-175.	1.5	0
24	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