

Jian Bai

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

344
citations

1307594

7
h-index

1058476

14
g-index

19
all docs

19
docs citations

19
times ranked

614
citing authors

#	ARTICLE	IF	CITATIONS
1	Common Postzygotic Mutational Signatures in Healthy Adult Tissues Related to Embryonic Hypoxia. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 177-191.	6.9	1
2	Genome-scale profiling of circulating cell-free DNA signatures for early detection of hepatocellular carcinoma in cirrhotic patients. <i>Cell Research</i> , 2021, 31, 589-592.	12.0	59
3	Influence of low tumor content on tumor mutational burden estimation by whole-exome sequencing and targeted panel sequencing. <i>Clinical and Translational Medicine</i> , 2021, 11, e415.	4.0	7
4	The Landscape of Cell-Free HBV Integrations and Mutations in Cirrhosis and Hepatocellular Carcinoma Patients. <i>Clinical Cancer Research</i> , 2021, 27, 3772-3783.	7.0	21
5	Durable Response to the Combination of Atezolizumab With Platinum-Based Chemotherapy in an Untreated Non-Smoking Lung Adenocarcinoma Patient With BRAF V600E Mutation: A Case Report. <i>Frontiers in Oncology</i> , 2021, 11, 634920.	2.8	7
6	Identification of Somatic Mutations in Papanicolaou Smear DNA and Plasma Circulating Cell-Free DNA for Detection of Endometrial and Epithelial Ovarian Cancers: A Pilot Study. <i>Frontiers in Oncology</i> , 2020, 10, 582546.	2.8	4
7	Neoantigen Tracking: Tracking Neoantigens by Personalized Circulating Tumor DNA Sequencing during Checkpoint Blockade Immunotherapy in Non-small Cell Lung Cancer (Adv. Sci. 9/2020). <i>Advanced Science</i> , 2020, 7, 2070047.	11.2	0
8	Tracking Neoantigens by Personalized Circulating Tumor DNA Sequencing during Checkpoint Blockade Immunotherapy in Non-small Cell Lung Cancer. <i>Advanced Science</i> , 2020, 7, 1903410.	11.2	30
9	Abstract 4597: 5-Hydroxymethylcytosine signatures in cell-free DNA as a potential biomarker for colorectal cancer and precancerous adenoma. , 2020, , .		0
10	A Reference System for BRCA Mutation Detection Based on Next-Generation Sequencing in the Chinese Population. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 677-686.	2.8	7
11	Germline Mutations in Cancer Susceptibility Genes in a Large Series of Unselected Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2017, 23, 6113-6119.	7.0	159
12	Retinol dehydrogenase-10 promotes development and progression of human glioma via the TWEAK-NF- κ B axis. <i>Oncotarget</i> , 2017, 8, 105262-105275.	1.8	6
13	Discovery of potential colorectal cancer serum biomarkers through quantitative proteomics on the colonic tissue interstitial fluids from the AOM-DSS mouse model. <i>Journal of Proteomics</i> , 2016, 132, 31-40.	2.4	28
14	Abstract 2397: Mutation signatures and intratumor heterogeneity of esophageal squamous cell carcinoma in a Chinese cohort. , 2016, , .		0
15	An Old Story Retold: Loss of G1 Control Defines A Distinct Genomic Subtype of Esophageal Squamous Cell Carcinoma. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 258-270.	6.9	7
16	Abstract 4797: Mutation signature and intratumor heterogeneity of esophageal squamous cell carcinoma in a Chinese cohort. <i>Cancer Research</i> , 2015, 75, 4797-4797.	0.9	1
17	Positive selection signals of hepatitis B virus and their association with disease stages and viral genotypes. <i>Infection, Genetics and Evolution</i> , 2013, 19, 176-187.	2.3	7
18	Abstract C03: A comprehensive study of genomic alterations reveals deregulation of the cell cycle in most esophageal squamous cell carcinomas. , 2013, , .		0