

# Quentin Bayard

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2045565/publications.pdf>

Version: 2024-02-01

16  
papers

1,016  
citations

686830

13  
h-index

996533

15  
g-index

16  
all docs

16  
docs citations

16  
times ranked

2057  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational signatures reveal the dynamic interplay of risk factors and cellular processes during liver tumorigenesis. <i>Nature Communications</i> , 2017, 8, 1315.	5.8	228
2	Analysis of Liver Cancer Cell Lines Identifies Agents With Likely Efficacy Against Hepatocellular Carcinoma and Markers of Response. <i>Gastroenterology</i> , 2019, 157, 760-776.	0.6	141
3	Clinical Impact of Genomic Diversity From Early to Advanced Hepatocellular Carcinoma. <i>Hepatology</i> , 2020, 71, 164-182.	3.6	129
4	Cyclin A2/E1 activation defines a hepatocellular carcinoma subclass with a rearrangement signature of replication stress. <i>Nature Communications</i> , 2018, 9, 5235.	5.8	118
5	Adeno-associated virus in the liver: natural history and consequences in tumour development. <i>Gut</i> , 2020, 69, 737-747.	6.1	78
6	Telomere length is key to hepatocellular carcinoma diversity and telomerase addiction is an actionable therapeutic target. <i>Journal of Hepatology</i> , 2021, 74, 1155-1166.	1.8	54
7	Palimpsest: an R package for studying mutational and structural variant signatures along clonal evolution in cancer. <i>Bioinformatics</i> , 2018, 34, 3380-3381.	1.8	53
8	BAP1 mutations define a homogeneous subgroup of hepatocellular carcinoma with fibrolamellar-like features and activated PKA. <i>Journal of Hepatology</i> , 2020, 72, 924-936.	1.8	44
9	Integrated Genomic Analysis Identifies Driver Genes and Cisplatin-Resistant Progenitor Phenotype in Pediatric Liver Cancer. <i>Cancer Discovery</i> , 2021, 11, 2524-2543.	7.7	41
10	Common genetic variation in alcohol-related hepatocellular carcinoma: a case-control genome-wide association study. <i>Lancet Oncology</i> , The, 2022, 23, 161-171.	5.1	36
11	Multi-site tumor sampling highlights molecular intra-tumor heterogeneity in malignant pleural mesothelioma. <i>Genome Medicine</i> , 2021, 13, 113.	3.6	31
12	DNA Methylation Signatures Reveal the Diversity of Processes Remodeling Hepatocellular Carcinoma Methylomes. <i>Hepatology</i> , 2021, 74, 816-834.	3.6	20
13	Recurrent chromosomal rearrangements of <i>ROS1</i> , <i>FRK</i> and <i>IL6</i> activating JAK/STAT pathway in inflammatory hepatocellular adenomas. <i>Gut</i> , 2020, 69, 1667-1676.	6.1	17
14	Bi-allelic hydroxymethylbilane synthase inactivation defines a homogenous clinico-molecular subtype of hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2022, 77, 1038-1046.	1.8	17
15	High Impact: The Role of Promiscuous Binding Sites in Polypharmacology. <i>Molecules</i> , 2019, 24, 2529.	1.7	9
16	Structure, Dynamics, and Impact of Replication Stress-Induced Structural Variants in Hepatocellular Carcinoma. <i>Cancer Research</i> , 2022, 82, 1470-1481.	0.4	0