

Arnoud Boot

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

4,328
citations

430843

18
h-index

315719

38
g-index

44
all docs

44
docs citations

44
times ranked

8959
citing authors

#	ARTICLE	IF	CITATIONS
1	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	27.8	2,104
2	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	9.4	637
3	Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	272
4	Somatic POLE proofreading domain mutation, immune response, and prognosis in colorectal cancer: a retrospective, pooled biomarker study. <i>The Lancet Gastroenterology and Hepatology</i> , 2016, 1, 207-216.	8.1	227
5	Genomic and Transcriptomic Profiling of Combined Hepatocellular and Intrahepatic Cholangiocarcinoma Reveals Distinct Molecular Subtypes. <i>Cancer Cell</i> , 2019, 35, 932-947.e8.	16.8	182
6	In-depth characterization of the cisplatin mutational signature in human cell lines and in esophageal and liver tumors. <i>Genome Research</i> , 2018, 28, 654-665.	5.5	126
7	Genome-scale mutational signatures of aflatoxin in cells, mice, and human tumors. <i>Genome Research</i> , 2017, 27, 1475-1486.	5.5	90
8	Associations of polymorphisms of eight muscle- or metabolism-related genes with performance in Mount Olympus marathon runners. <i>Journal of Applied Physiology</i> , 2010, 108, 567-574.	2.5	65
9	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
10	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5833-5846.	8.2	58
11	Characterization of colibactin-associated mutational signature in an Asian oral squamous cell carcinoma and in other mucosal tumor types. <i>Genome Research</i> , 2020, 30, 803-813.	5.5	32
12	Tumor LINE-1 Methylation Level in Association with Survival of Patients with Stage II Colon Cancer. <i>International Journal of Molecular Sciences</i> , 2017, 18, 36.	4.1	29
13	BRAF mutation-specific promoter methylation of FOX genes in colorectal cancer. <i>Clinical Epigenetics</i> , 2013, 5, 2.	4.1	27
14	Imprinted survival genes preclude loss of heterozygosity of chromosome 7 in cancer cells. <i>Journal of Pathology</i> , 2016, 240, 72-83.	4.5	27
15	The mutational landscape of early and typical onset oral tongue squamous cell carcinoma. <i>Cancer</i> , 2021, 127, 544-553.	4.1	27
16	HLA-G protein expression in colorectal cancer evaluated by immunohistochemistry and western blot analysis: Its expression characteristics remain enigmatic. <i>Clinical Immunology</i> , 2018, 194, 80-86.	3.2	26
17	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. <i>Scientific Reports</i> , 2015, 5, 16286.	3.3	24
18	A tumor-associated splice-isoform of <i>MAP2K7</i> drives dedifferentiation in MBNL1-low cancers via JNK activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16391-16400.	7.1	23

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19	Recurrent mutations in topoisomerase II α cause a previously undescribed mutator phenotype in human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	22
20	Monoallelic NTHL1 Loss-of-Function Variants and Risk of Polyposis and Colorectal Cancer. <i>Gastroenterology</i> , 2020, 159, 2241-2243.e6.	1.3	20
21	ROS-induced near-homozygous genomes in thyroid cancer. <i>Endocrine-Related Cancer</i> , 2018, 25, 83-97.	3.1	18
22	Synergistic effects of the sesquiterpene lactone, EPD, with cisplatin and paclitaxel in ovarian cancer cells. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 38.	8.6	17
23	Recurrent APC Splice Variant c.835-8A>G in Patients With Unexplained Colorectal Polyposis Fulfilling the Colibactin Mutational Signature. <i>Gastroenterology</i> , 2020, 159, 1612-1614.e5.	1.3	17
24	The Homeobox Gene MEIS1 Is Methylated in BRAFp.V600E Mutated Colon Tumors. <i>PLoS ONE</i> , 2013, 8, e79898.	2.5	11
25	Characterization of novel low passage primary and metastatic colorectal cancer cell lines. <i>Oncotarget</i> , 2016, 7, 14499-14509.	1.8	11
26	Evidence for genetic association between chromosome 1q loci and predisposition to colorectal neoplasia. <i>British Journal of Cancer</i> , 2017, 117, 1215-1223.	6.4	10
27	Methylation associated transcriptional repression of ELOVL5 in novel colorectal cancer cell lines. <i>PLoS ONE</i> , 2017, 12, e0184900.	2.5	10
28	Highly recurrent CBS epimutations in gastric cancer CpG island methylator phenotypes and inflammation. <i>Genome Biology</i> , 2021, 22, 167.	8.8	10
29	Promoter methylation and mRNA expression of HLA-G in relation to HLA-G protein expression in colorectal cancer. <i>Human Immunology</i> , 2016, 77, 764-772.	2.4	9
30	Toward clinical understanding of aristolochic acid upper-tract urothelial carcinoma. <i>Theranostics</i> , 2020, 10, 5578-5580.	10.0	9
31	Accuracy of mutational signature software on correlated signatures. <i>Scientific Reports</i> , 2022, 12, 390.	3.3	6
32	Whole exome sequencing identifies clinically relevant mutational signatures in resected hepatocellular carcinoma. <i>Liver Cancer International</i> , 2020, 1, 25-35.	1.3	5
33	Mutational analysis of driver genes defines the colorectal adenoma: in situ carcinoma transition. <i>Scientific Reports</i> , 2022, 12, 2570.	3.3	5
34	Allelic Switching of DLX5, GRB10, and SVOPL during Colorectal Cancer Tumorigenesis. <i>International Journal of Genomics</i> , 2019, 2019, 1-10.	1.6	4
35	Multiple neoplasia in a patient with Citelman syndrome harboring germline monoallelic MUTYH mutation. <i>Npj Genomic Medicine</i> , 2020, 5, 39.	3.8	3
36	Chemosensitivity of BRCA1-Mutated Ovarian Cancer Cells and Established Cytotoxic Agents. <i>International Journal of Gynecological Cancer</i> , 2017, 27, 1571-1578.	2.5	2

#	ARTICLE	IF	CITATIONS
37	Mutational processes in cancer preferentially affect binding of particular transcription factors. Scientific Reports, 2021, 11, 3339.	3.3	2