

Shaoping Ling

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5476440/publications.pdf>

Version: 2024-02-01

12
papers

960
citations

933264

10
h-index

1199470

12
g-index

13
all docs

13
docs citations

13
times ranked

2185
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence-assisted system for precision diagnosis of PD-L1 expression in non-small cell lung cancer. <i>Modern Pathology</i> , 2022, 35, 403-411.	2.9	28
2	A hierarchical and multi-view registration of serial histopathological images. <i>Pattern Recognition Letters</i> , 2021, 152, 210-217.	2.6	5
3	A standardized pathological proposal for evaluating microvascular invasion of hepatocellular carcinoma: a multicenter study by LCPGC. <i>Hepatology International</i> , 2020, 14, 1034-1047.	1.9	42
4	Is the evolution in tumors Darwinian or non-Darwinian?. <i>National Science Review</i> , 2018, 5, 15-17.	4.6	24
5	Exome sequencing reveals the genetic landscape and frequent inactivation of <i>PCDHB3</i> in Chinese rectal cancers. <i>Journal of Pathology</i> , 2018, 245, 222-234.	2.1	9
6	Integrated genomic analysis identifies deregulated JAK/STAT-MYC-biosynthesis axis in aggressive NK-cell leukemia. <i>Cell Research</i> , 2018, 28, 172-186.	5.7	62
7	The Ecology and Evolution of Cancer: The Ultra-Microevolutionary Process. <i>Annual Review of Genetics</i> , 2016, 50, 347-369.	3.2	86
8	Mutations or copy number losses of <i>CD58</i> and <i>TP53</i> genes in diffuse large B cell lymphoma are independent unfavorable prognostic factors. <i>Oncotarget</i> , 2016, 7, 83294-83307.	0.8	38
9	Extremely high genetic diversity in a single tumor points to prevalence of non-Darwinian cell evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6496-505.	3.3	313
10	Identification of functional cooperative mutations of SETD2 in human acute leukemia. <i>Nature Genetics</i> , 2014, 46, 287-293.	9.4	213
11	Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12042-12047.	3.3	117
12	Population Genetics in Nonmodel Organisms: II. Natural Selection in Marginal Habitats Revealed by Deep Sequencing on Dual Platforms. <i>Molecular Biology and Evolution</i> , 2011, 28, 2833-2842.	3.5	23