

Kim Wong

List of Publications by Year in descending order

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16
papers

2,553
citations

687363

13
h-index

940533

16
g-index

16
all docs

16
docs citations

16
times ranked

5201
citing authors

#	ARTICLE	IF	CITATIONS
1	The mutational landscape of melanoma brain metastases presenting as the first visceral site of recurrence. <i>British Journal of Cancer</i> , 2021, 124, 156-160.	6.4	21
2	Cut-like homeobox 1 (CUX1) tumor suppressor gene haploinsufficiency induces apoptosis evasion to sustain myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2482.	12.8	14
3	The clinicopathologic spectrum and genomic landscape of de-/trans-differentiated melanoma. <i>Modern Pathology</i> , 2021, 34, 2009-2019.	5.5	18
4	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , 2020, 11, 4306.	12.8	26
5	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. <i>Nature Communications</i> , 2020, 11, 1407.	12.8	13
6	<i>In situ</i> CRISPR-Cas9 base editing for the development of genetically engineered mouse models of breast cancer. <i>EMBO Journal</i> , 2020, 39, e102169.	7.8	40
7	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	12.8	205
8	Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. <i>Nature Communications</i> , 2019, 10, 353.	12.8	99
9	Association of the <i>POT1</i> Germline Missense Variant p.I78T With Familial Melanoma. <i>JAMA Dermatology</i> , 2019, 155, 604.	4.1	34
10	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	21.4	169
11	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease-Associated Colorectal Cancers. <i>Clinical Cancer Research</i> , 2018, 24, 5133-5142.	7.0	26
12	Generation and Characterisation of a Pax8-CreERT2 Transgenic Line and a Slc22a6-CreERT2 Knock-In Line for Inducible and Specific Genetic Manipulation of Renal Tubular Epithelial Cells. <i>PLoS ONE</i> , 2016, 11, e0148055.	2.5	11
13	Deep genome sequencing and variation analysis of 13 inbred mouse strains defines candidate phenotypic alleles, private variation and homozygous truncating mutations. <i>Genome Biology</i> , 2016, 17, 167.	8.8	70
14	The fine-scale architecture of structural variants in 17 mouse genomes. <i>Genome Biology</i> , 2012, 13, R18.	9.6	47
15	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011, 477, 289-294.	27.8	1,461
16	Sequence-based characterization of structural variation in the mouse genome. <i>Nature</i> , 2011, 477, 326-329.	27.8	299