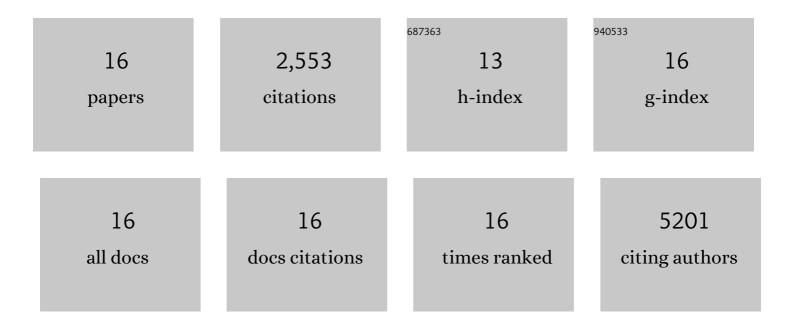
Kim Wong

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2866295/publications.pdf Version: 2024-02-01



KIM WONC

#	Article	IF	CITATIONS
1	The mutational landscape of melanoma brain metastases presenting as the first visceral site of recurrence. British Journal of Cancer, 2021, 124, 156-160.	6.4	21
2	Cut-like homeobox 1 (CUX1) tumor suppressor gene haploinsufficiency induces apoptosis evasion to sustain myeloid leukemia. Nature Communications, 2021, 12, 2482.	12.8	14
3	The clinicopathologic spectrum and genomic landscape of de-/trans-differentiated melanoma. Modern Pathology, 2021, 34, 2009-2019.	5.5	18
4	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature Communications, 2020, 11, 4306.	12.8	26
5	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. Nature Communications, 2020, 11, 1407.	12.8	13
6	<i>In situ</i> CRISPR as9 base editing for the development of genetically engineered mouse models of breast cancer. EMBO Journal, 2020, 39, e102169.	7.8	40
7	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
8	Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. Nature Communications, 2019, 10, 353.	12.8	99
9	Association of the <i>POT1</i> Germline Missense Variant p.178T With Familial Melanoma. JAMA Dermatology, 2019, 155, 604.	4.1	34
10	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	21.4	169
11	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease–Associated Colorectal Cancers. Clinical Cancer Research, 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. PLoS ONE, 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. Genome Biology, 2016, 17, 167.	8.8	70
14	The fine-scale architecture of structural variants in 17 mouse genomes. Genome Biology, 2012, 13, R18.	9.6	47
15	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	27.8	1,461
16	Sequence-based characterization of structural variation in the mouse genome. Nature, 2011, 477, 326-329.	27.8	299