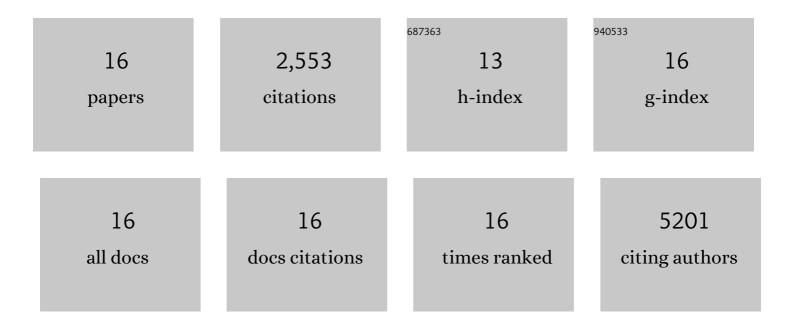
Kim Wong

List of Publications by Year in descending order

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KIM WONC

#	Article	IF	CITATIONS
1	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	27.8	1,461
2	Sequence-based characterization of structural variation in the mouse genome. Nature, 2011, 477, 326-329.	27.8	299
3	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
4	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	21.4	169
5	Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. Nature Communications, 2019, 10, 353.	12.8	99
6	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
7	The fine-scale architecture of structural variants in 17 mouse genomes. Genome Biology, 2012, 13, R18.	9.6	47
8	<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
9	Association of the <i>POT1</i> Germline Missense Variant p.178T With Familial Melanoma. JAMA Dermatology, 2019, 155, 604.	4.1	34
10	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease–Associated Colorectal Cancers. Clinical Cancer Research, 2018, 24, 5133-5142.	7.0	26
11	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature Communications, 2020, 11, 4306.	12.8	26
12	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
13	The clinicopathologic spectrum and genomic landscape of de-/trans-differentiated melanoma. Modern Pathology, 2021, 34, 2009-2019.	5.5	18
14	Cut-like homeobox 1 (CUX1) tumor suppressor gene haploinsufficiency induces apoptosis evasion to sustain myeloid leukemia. Nature Communications, 2021, 12, 2482.	12.8	14
15	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. Nature Communications, 2020, 11, 1407.	12.8	13
16	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