

Tony Kwan

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,175
citations

430874

18
h-index

526287

27
g-index

28
all docs

28
docs citations

28
times ranked

9391
citing authors

#	ARTICLE	IF	CITATIONS
1	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	28.9	1,052
2	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	28.9	573
3	The relationship between DNA methylation, genetic and expression inter-individual variation in untransformed human fibroblasts. <i>Genome Biology</i> , 2014, 15, R37.	9.6	384
4	Genome-wide analysis of transcript isoform variation in humans. <i>Nature Genetics</i> , 2008, 40, 225-231.	21.4	283
5	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	12.8	142
6	Heritability of alternative splicing in the human genome. <i>Genome Research</i> , 2007, 17, 1210-1218.	5.5	101
7	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. <i>Genome Biology</i> , 2015, 16, 290.	8.8	90
8	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. <i>Nature Communications</i> , 2015, 6, 7211.	12.8	84
9	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	8.8	71
10	Tissue Effect on Genetic Control of Transcript Isoform Variation. <i>PLoS Genetics</i> , 2009, 5, e1000608.	3.5	50
11	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. <i>BMC Genomics</i> , 2017, 18, 214.	2.8	40
12	High-resolution analyses of human sperm dynamic methylome reveal thousands of novel age-related epigenetic alterations. <i>Clinical Epigenetics</i> , 2020, 12, 192.	4.1	29
13	Personalized and graph genomes reveal missing signal in epigenomic data. <i>Genome Biology</i> , 2020, 21, 124.	8.8	29
14	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. <i>BMC Medical Genomics</i> , 2016, 9, 59.	1.5	26
15	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. <i>Cell Reports</i> , 2021, 36, 109418.	6.4	25
16	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. <i>Nature Communications</i> , 2021, 12, 1132.	12.8	24
17	Allelic expression mapping across cellular lineages to establish impact of non-coding <sc>SNP</sc>s. <i>Molecular Systems Biology</i> , 2014, 10, 754.	7.2	21
18	Computational Analysis of HLA-presentation of Non-synonymous Recipient Mismatches Indicates Effect on the Risk of Chronic Graft-vs.-Host Disease After Allogeneic HSCT. <i>Frontiers in Immunology</i> , 2019, 10, 1625.	4.8	20

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19	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. <i>Nature Communications</i> , 2019, 10, 1209.	12.8	16
20	Exploring rare and low-frequency variants in the Saguenayâ€“Lac-Saint-Jean population identified genes associated with asthma and allergy traits. <i>European Journal of Human Genetics</i> , 2019, 27, 90-101.	2.8	15
21	Eosinophil microRNAs Play a Regulatory Role in Allergic Diseases Included in the Atopic March. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9011.	4.1	15
22	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. <i>Scientific Data</i> , 2020, 7, 376.	5.3	15
23	Hidden genomic MHC disparity between HLA-matched sibling pairs in hematopoietic stem cell transplantation. <i>Scientific Reports</i> , 2018, 8, 5396.	3.3	11
24	Interrogation of allelic chromatin states in human cells by high-density ChIP-genotyping. <i>Epigenetics</i> , 2014, 9, 1238-1251.	2.7	9
25	Asthma-associated polymorphisms in 17q12-21 locus modulate methylation and gene expression of GSDMA in naÃ“ve CD4+ T cells. <i>Journal of Genetics and Genomics</i> , 2020, 47, 171-174.	3.9	9
26	Differentially methylated CpGs in response to growth hormone administration in children with idiopathic short stature. <i>Clinical Epigenetics</i> , 2022, 14, 65.	4.1	1