Tony Kwan

List of Publications by Year in descending order

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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	Differentially methylated CpGs in response to growth hormone administration in children with idiopathic short stature. Clinical Epigenetics, 2022, 14, 65.	4.1	1
2	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. Nature Communications, 2021, 12, 1132.	12.8	24
3	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. Cell Reports, 2021, 36, 109418.	6.4	25
4	Eosinophil microRNAs Play a Regulatory Role in Allergic Diseases Included in the Atopic March. International Journal of Molecular Sciences, 2020, 21, 9011.	4.1	15
5	High-resolution analyses of human sperm dynamic methylome reveal thousands of novel age-related epigenetic alterations. Clinical Epigenetics, 2020, 12, 192.	4.1	29
6	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. Scientific Data, 2020, 7, 376.	5.3	15
7	Asthma-associated polymorphisms in 17q12-21 locus modulate methylation and gene expression of GSDMA in naÃ¯ve CD4+ T cells. Journal of Genetics and Genomics, 2020, 47, 171-174.	3.9	9
8	Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biology, 2020, 21, 124.	8.8	29
9	Computational Analysis of HLA-presentation of Non-synonymous Recipient Mismatches Indicates Effect on the Risk of Chronic Graft-vs.-Host Disease After Allogeneic HSCT. Frontiers in Immunology, 2019, 10, 1625.	4.8	20
10	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. Nature Communications, 2019, 10, 1209.	12.8	16
11	Exploring rare and low-frequency variants in the Saguenayâ€“Lac-Saint-Jean population identified genes associated with asthma and allergy traits. European Journal of Human Genetics, 2019, 27, 90-101.	2.8	15
12	Hidden genomic MHC disparity between HLA-matched sibling pairs in hematopoietic stem cell transplantation. Scientific Reports, 2018, 8, 5396.	3.3	11
13	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	8.8	71
14	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. BMC Genomics, 2017, 18, 214.	2.8	40
15	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	12.8	142
16	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
17	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
18	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. BMC Medical Genomics, 2016, 9, 59.	1.5	26

#	Article	IF	Citations
19	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology, 2015, 16, 290.	8.8	90
20	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. Nature Communications, 2015, 6, 7211.	12.8	84
21	Interrogation of allelic chromatin states in human cells by high-density ChIP-genotyping. Epigenetics, 2014, 9, 1238-1251.	2.7	9
22	Allelic expression mapping across cellular lineages to establish impact of nonâ€coding <scp>SNP</scp>s. Molecular Systems Biology, 2014, 10, 754.	7.2	21
23	The relationship between DNA methylation, genetic and expression inter-individual variation in untransformed human fibroblasts. Genome Biology, 2014, 15, R37.	9.6	384
24	Tissue Effect on Genetic Control of Transcript Isoform Variation. PLoS Genetics, 2009, 5, e1000608.	3.5	50
25	Genome-wide analysis of transcript isoform variation in humans. Nature Genetics, 2008, 40, 225-231.	21.4	283
26	Heritability of alternative splicing in the human genome. Genome Research, 2007, 17, 1210-1218.	5.5	101