Warren A Cheung

List of Publications by Year
in descending order

21 papers	2,111 citations	516710 16 h-index	677142 22 g-index
23 all docs	23 docs citations	23 times ranked	4894 citing authors

#	Article	IF	Citations
1	Genomic answers for children: Dynamic analyses of >1000 pediatric rare disease genomes. Genetics in Medicine, 2022, 24, 1336-1348.	2.4	37
2	Immune cell residency in the nasal mucosa may partially explain respiratory disease severity across the age range. Scientific Reports, 2021, 11, 15927.	3.3	16
3	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. Nature Metabolism, 2020, 2, 97-109.	11.9	272
4	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
5	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. Nature Communications, 2019, 10, 1262.	12.8	215
6	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. Nature Communications, 2019, 10, 1209.	12.8	16
7	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
8	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	12.8	142
9	Inborn Error of Cobalamin Metabolism Associated with the Intracellular Accumulation of Transcobalamin-Bound Cobalamin and Mutations inZNF143, Which Codes for a Transcriptional Activator. Human Mutation, 2016, 37, 976-982.	2.5	30
10	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
11	Risk of re-identification of epigenetic methylation data: a more nuanced response is needed. Clinical Epigenetics, 2015, 7, 45.	4.1	14
12	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	8.8	34
13	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
14	Compensating for literature annotation bias when predicting novel drug-disease relationships through Medical Subject Heading Over-representation Profile (MeSHOP) similarity. BMC Medical Genomics, 2013, 6, S3.	1.5	10
15	The Transcription Factor Encyclopedia. Genome Biology, 2012, 13, R24.	9.6	103
16	Quantitative biomedical annotation using medical subject heading over-representation profiles (MeSHOPs). BMC Bioinformatics, 2012, 13, 249.	2.6	24
17	Inferring novel gene-disease associations using Medical Subject Heading Over-representation Profiles. Genome Medicine, 2012, 4, 75.	8.2	25
18	Optimization of Antibacterial Peptides by Genetic Algorithms and Cheminformatics. Chemical Biology and Drug Design, 2011, 77, 48-56.	3.2	72

#	Article	IF	Citations
19	Identification of Novel Antibacterial Peptides by Chemoinformatics and Machine Learning. Journal of Medicinal Chemistry, 2009, 52, 2006-2015.	6.4	250
20	n-SIFT: n-Dimensional Scale Invariant Feature Transform. IEEE Transactions on Image Processing, 2009, 18, 2012-2021.	9.8	148
21	Gene Characterization Index: Assessing the Depth of Gene Annotation. PLoS ONE, 2008, 3, e1440.	2.5	9