

Warren A Cheung

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7308682/publications.pdf>

Version: 2024-02-01

21
papers

2,111
citations

516215

16
h-index

676716

22
g-index

23
all docs

23
docs citations

23
times ranked

4894
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
2	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. <i>Nature Metabolism</i> , 2020, 2, 97-109.	5.1	272
3	Identification of Novel Antibacterial Peptides by Chemoinformatics and Machine Learning. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 2006-2015.	2.9	250
4	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. <i>Nature Communications</i> , 2019, 10, 1262.	5.8	215
5	SIFT: Dimensional Scale Invariant Feature Transform. <i>IEEE Transactions on Image Processing</i> , 2009, 18, 2012-2021.	6.0	148
6	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142
7	The Transcription Factor Encyclopedia. <i>Genome Biology</i> , 2012, 13, R24.	13.9	103
8	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.	3.8	90
9	Optimization of Antibacterial Peptides by Genetic Algorithms and Cheminformatics. <i>Chemical Biology and Drug Design</i> , 2011, 77, 48-56.	1.5	72
10	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.	3.8	71
11	Genomic answers for children: Dynamic analyses of >1000 pediatric rare disease genomes. <i>Genetics in Medicine</i> , 2022, 24, 1336-1348.	1.1	37
12	Epigenome data release: a participant-centered approach to privacy protection. <i>Genome Biology</i> , 2015, 16, 142.	3.8	34
13	Inborn Error of Cobalamin Metabolism Associated with the Intracellular Accumulation of Transcobalamin-Bound Cobalamin and Mutations in <i>ZNF143</i> , Which Codes for a Transcriptional Activator. <i>Human Mutation</i> , 2016, 37, 976-982.	1.1	30
14	Inferring novel gene-disease associations using Medical Subject Heading Over-representation Profiles. <i>Genome Medicine</i> , 2012, 4, 75.	3.6	25
15	Quantitative biomedical annotation using medical subject heading over-representation profiles (MeSHOPs). <i>BMC Bioinformatics</i> , 2012, 13, 249.	1.2	24
16	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. <i>Nature Communications</i> , 2019, 10, 1209.	5.8	16
17	Immune cell residency in the nasal mucosa may partially explain respiratory disease severity across the age range. <i>Scientific Reports</i> , 2021, 11, 15927.	1.6	16
18	Risk of re-identification of epigenetic methylation data: a more nuanced response is needed. <i>Clinical Epigenetics</i> , 2015, 7, 45.	1.8	14

#	ARTICLE	IF	CITATIONS
19	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.	0.7	10
20	Gene Characterization Index: Assessing the Depth of Gene Annotation. PLoS ONE, 2008, 3, e1440.	1.1	9
21	Asthma-associated polymorphisms in 17q12-21 locus modulate methylation and gene expression of GSDMA in naïve CD4+ T cells. Journal of Genetics and Genomics, 2020, 47, 171-174.	1.7	9