

Jieming Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8984908/publications.pdf>

Version: 2024-02-01

19
papers

25,743
citations

516561

16
h-index

794469

19
g-index

22
all docs

22
docs citations

22
times ranked

50032
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
3	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
4	Mapping Human Genetic Diversity in Asia. <i>Science</i> , 2009, 326, 1541-1545.	6.0	557
5	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <i>Nature Biotechnology</i> , 2011, 29, 1132-1144.	9.4	509
6	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235-1237.	6.0	341
7	Genetic Structure of the Han Chinese Population Revealed by Genome-wide SNP Variation. <i>American Journal of Human Genetics</i> , 2009, 85, 775-785.	2.6	316
8	Protein-protein interactions: General trends in the relationship between binding affinity and interfacial buried surface area. <i>Protein Science</i> , 2013, 22, 510-515.	3.1	231
9	Interpretation of Genomic Variants Using a Unified Biological Network Approach. <i>PLoS Computational Biology</i> , 2013, 9, e1002886.	1.5	162
10	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. <i>Genome Research</i> , 2009, 19, 2154-2162.	2.4	146
11	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. <i>Nature Communications</i> , 2016, 7, 11101.	5.8	78
12	Identifying Allosteric Hotspots with Dynamics: Application to Inter- and Intra-species Conservation. <i>Structure</i> , 2016, 24, 826-837.	1.6	55
13	Natural positive selection and north-south genetic diversity in East Asia. <i>European Journal of Human Genetics</i> , 2012, 20, 102-110.	1.4	42
14	All Repeats Are Not Equal: A Module-Based Approach to Guide Repeat Protein Design. <i>Journal of Molecular Biology</i> , 2013, 425, 1826-1838.	2.0	32
15	Interethnic comparisons of important pharmacology genes using SNP databases: potential application to drug regulatory assessments. <i>Pharmacogenomics</i> , 2010, 11, 1077-1094.	0.6	22
16	On Sports And Genes. <i>Recent Patents on DNA & Gene Sequences</i> , 2012, 6, 180-188.	0.7	19
17	Reads meet rotamers: structural biology in the age of deep sequencing. <i>Current Opinion in Structural Biology</i> , 2015, 35, 125-134.	2.6	6
18	Detecting and Annotating Rare Variants. , 2019, , 388-399.		4

#	ARTICLE	IF	CITATIONS
19	Intensification: A Resource for Amplifying Population-Genetic Signals with Protein Repeats. Journal of Molecular Biology, 2017, 429, 435-445.	2.0	2