Jieming Chen

List of Publications by Year in descending order

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LIEMING CHEN

#	Article	IF	CITATIONS
1	Detecting and Annotating Rare Variants. , 2019, , 388-399.		4
2	Intensification: A Resource for Amplifying Population-Genetic Signals with Protein Repeats. Journal of Molecular Biology, 2017, 429, 435-445.	2.0	2
3	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. Nature Communications, 2016, 7, 11101.	5.8	78
4	Identifying Allosteric Hotspots with Dynamics: Application to Inter- and Intra-species Conservation. Structure, 2016, 24, 826-837.	1.6	55
5	Reads meet rotamers: structural biology in the age of deep sequencing. Current Opinion in Structural Biology, 2015, 35, 125-134.	2.6	6
6	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
7	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
8	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
9	All Repeats Are Not Equal: A Module-Based Approach to Guide Repeat Protein Design. Journal of Molecular Biology, 2013, 425, 1826-1838.	2.0	32
10	Protein–protein interactions: General trends in the relationship between binding affinity and interfacial buried surface area. Protein Science, 2013, 22, 510-515.	3.1	231
11	Interpretation of Genomic Variants Using a Unified Biological Network Approach. PLoS Computational Biology, 2013, 9, e1002886.	1.5	162
12	Natural positive selection and north–south genetic diversity in East Asia. European Journal of Human Genetics, 2012, 20, 102-110.	1.4	42
13	On Sports And Genes. Recent Patents on DNA & Gene Sequences, 2012, 6, 180-188.	0.7	19
14	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
15	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. Nature Biotechnology, 2011, 29, 1132-1144.	9.4	509
16	Interethnic comparisons of important pharmacology genes using SNP databases: potential application to drug regulatory assessments. Pharmacogenomics, 2010, 11, 1077-1094.	0.6	22
17	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. Genome Research, 2009, 19, 2154-2162.	2.4	146
18	Genetic Structure of the Han Chinese Population Revealed by Genome-wide SNP Variation. American Journal of Human Genetics, 2009, 85, 775-785.	2.6	316

#	Article	IF	CITATIONS
19	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	6.0	557