Xinghua Shi

List of Publications by Year
in descending order

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27 papers	4,907 citations	759233 12 h-index	713466 21 g-index
31 all docs	31 docs citations	31 times ranked	10345 citing authors

#	Article	IF	Citations
1	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
2	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
3	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
4	Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants. Nature Biotechnology, 2011, 29, 512-520.	17.5	384
5	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
6	Extensive genetic diversity and substructuring among zebrafish strains revealed through copy number variant analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 529-534.	7.1	102
7	A deep auto-encoder model for gene expression prediction. BMC Genomics, 2017, 18, 845.	2.8	79
8	Refinement of primate copy number variationhotspots identifies candidate genomic regions evolving under positive selection. Genome Biology, 2011, 12, R52.	8.8	58
9	Effects of short indels on protein structure and function in human genomes. Scientific Reports, 2017, 7, 9313.	3.3	58
10	An overview of human genetic privacy. Annals of the New York Academy of Sciences, 2017, 1387, 61-72.	3.8	54
11	Sparse Convolutional Denoising Autoencoders for Genotype Imputation. Genes, 2019, 10, 652.	2.4	28
12	An integrated network of microRNA and gene expression in ovarian cancer. BMC Bioinformatics, 2015, 16, S5.	2.6	24
13	Association of CNVs with methylation variation. Npj Genomic Medicine, 2020, 5, 41.	3.8	17
14	Methods for population-based eQTL analysis in human genetics. Tsinghua Science and Technology, 2014, 19, 624-634.	6.1	13
15	Capacity of data collection in randomly-deployed wireless sensor networks. Wireless Networks, 2011, 17, 305-318.	3.0	11
16	Using aggregate human genome data for individual identification. , 2013, , .		11
17	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
18	Finding Alternative Expression Quantitative Trait Loci by Exploring Sparse Model Space. Journal of Computational Biology, 2014, 21, 385-393.	1.6	5

#	Article	IF	Citations
19	A predictive model of gene expression using a deep learning framework. , 2016, , .		5
20	Bayesian Hyperparameter Optimization for Machine Learning Based eQTL Analysis. , 2017, , .		4
21	Epistasis analysis of microRNAs on pathological stages in colon cancer based on anÂEmpirical Bayesian Elastic Net method. BMC Genomics, 2017, 18, 756.	2.8	4
22	A parallelized strategy for epistasis analysis based on Empirical Bayesian Elastic Net models. Bioinformatics, 2020, 36, 3803-3810.	4.1	4
23	Infringement of Individual Privacy via Mining Differentially Private GWAS Statistics. Lecture Notes in Computer Science, 2016, , 355-366.	1.3	3
24	A Sparse Learning Framework for Joint Effect Analysis of Copy Number Variants. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1013-1027.	3.0	2
25	CNVnet. , 2014, , .		1
26	802.11 User Anonymization. , 2010, , .		0
27	A Graph Community Approach for Constructing microRNA Networks. Lecture Notes in Computer Science, 2015, , 283-293.	1.3	0