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	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
2	Association of CNVs with methylation variation. Npj Genomic Medicine, 2020, 5, 41.	3.8	17
3	A parallelized strategy for epistasis analysis based on Empirical Bayesian Elastic Net models. Bioinformatics, 2020, 36, 3803-3810.	4.1	4
4	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
5	Sparse Convolutional Denoising Autoencoders for Genotype Imputation. Genes, 2019, 10, 652.	2.4	28
6	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
7	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
8	Bayesian Hyperparameter Optimization for Machine Learning Based eQTL Analysis. , 2017, , .		4
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	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
12	A deep auto-encoder model for gene expression prediction. BMC Genomics, 2017, 18, 845.	2.8	79
13	A predictive model of gene expression using a deep learning framework. , 2016, , .		5
14	Infringement of Individual Privacy via Mining Differentially Private GWAS Statistics. Lecture Notes in Computer Science, 2016, , 355-366.	1.3	3
15	An integrated network of microRNA and gene expression in ovarian cancer. BMC Bioinformatics, 2015, 16, S5.	2.6	24
16	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
17	A Graph Community Approach for Constructing microRNA Networks. Lecture Notes in Computer Science, 2015, , 283-293.	1.3	0
18	Methods for population-based eQTL analysis in human genetics. Tsinghua Science and Technology, 2014, 19, 624-634.	6.1	13

#	Article	IF	Citations
19	CNVnet. , 2014, , .		1
20	Finding Alternative Expression Quantitative Trait Loci by Exploring Sparse Model Space. Journal of Computational Biology, 2014, 21, 385-393.	1.6	5
21	Using aggregate human genome data for individual identification. , 2013, , .		11
22	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
23	Refinement of primate copy number variationhotspots identifies candidate genomic regions evolving under positive selection. Genome Biology, 2011, 12, R52.	8.8	58
24	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
25	Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants. Nature Biotechnology, 2011, 29, 512-520.	17.5	384
26	Capacity of data collection in randomly-deployed wireless sensor networks. Wireless Networks, 2011, 17, 305-318.	3.0	11
27	802.11 User Anonymization. , 2010, , .		0