Ruowang Li

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6181086/publications.pdf

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15	1,064	1307594 7	1372567 10
papers	citations	h-index	g-index

17	17	17	2495
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Methods of integrating data to uncover genotypeâ€“phenotype interactions. Nature Reviews Genetics, 2015, 16, 85-97.	16.3	803
2	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	16.3	78
3	Using knowledge-driven genomic interactions for multi-omics data analysis: metadimensional models for predicting clinical outcomes in ovarian carcinoma. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 577-587.	4.4	41
4	Predicting censored survival data based on the interactions between meta-dimensional omics data in breast cancer. Journal of Biomedical Informatics, 2015, 56, 220-228.	4.3	32
5	BINNING SOMATIC MUTATIONS BASED ON BIOLOGICAL KNOWLEDGE FOR PREDICTING SURVIVAL: AN APPLICATION IN RENAL CELL CARCINOMA. , 2014, , .		24
6	Collective feature selection to identify crucial epistatic variants. BioData Mining, 2018, 11, 5.	4.0	22
7	Knowledge-driven genomic interactions: an application in ovarian cancer. BioData Mining, 2014, 7, 20.	4.0	21
8	Integration of genetic and clinical information to improve imputation of data missing from electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1056-1063.	4.4	17
9	A regression framework to uncover pleiotropy in large-scale electronic health record data. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1083-1090.	4.4	9
10	Identification of genetic interaction networks via an evolutionary algorithm evolved Bayesian network. BioData Mining, 2016, 9, 18.	4.0	8
11	Robust-ODAL: Learning from heterogeneous health systems without sharing patient-level data. , 2019, , .		5
12	Lossless integration of multiple electronic health records for identifying pleiotropy using summary statistics. Nature Communications, 2021, 12, 168.	12.8	2
13	Evaluation of Phenotyping Errors on Polygenic Risk Score Predictions. , 2020, , .		1
14	Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. Pharmacogenomics Journal, 2019, 19, 178-190.	2.0	0
15	Statistical Impact of Sample Size and Imbalance on Multivariate Analysis and A Case Study in the UK Biobank. AMIA ... Annual Symposium proceedings, 2020, 2020, 1383-1391.	0.2	0