

Ruowang Li

List of Publications by Year in descending order

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

Version: 2024-02-01

15
papers

1,064
citations

1307594

7
h-index

1372567

10
g-index

17
all docs

17
docs citations

17
times ranked

2495
citing authors

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