

# Xian Yang

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

608  
citations

1162889

8  
h-index

794469

19  
g-index

31  
all docs

31  
docs citations

31  
times ranked

1194  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayesian data assimilation for estimating instantaneous reproduction numbers during epidemics: Applications to COVID-19. PLoS Computational Biology, 2022, 18, e1009807.	1.5	0
2	Distinct Regimes of O3 Response to COVID-19 Lockdown in China. Atmosphere, 2021, 12, 184.	1.0	8
3	Nonlinear modulation of COVID-19 transmission by climate conditions. Meteorological Applications, 2021, 28, e1985.	0.9	8
4	COVID-19 Rehabilitation With Herbal Medicine and Cardiorespiratory Exercise: Protocol for a Clinical Study. JMIR Research Protocols, 2021, 10, e25556.	0.5	4
5	Effective low capacity status prediction for cloud systems. , 2021, , .		1
6	A Bayesian Updating Scheme for Pandemics: Estimating the Infection Dynamics of COVID-19. IEEE Computational Intelligence Magazine, 2020, 15, 23-33.	3.4	12
7	An epidemiological modelling approach for COVID-19 via data assimilation. European Journal of Epidemiology, 2020, 35, 749-761.	2.5	37
8	Identifying linked incidents in large-scale online service systems. , 2020, , .		19
9	IL-17 <sup>hi</sup> high asthma with features of a psoriasis immunophenotype. Journal of Allergy and Clinical Immunology, 2019, 144, 1198-1213.	1.5	80
10	Outage Prediction and Diagnosis for Cloud Service Systems. , 2019, , .		43
11	Epithelial dysregulation in obese severe asthmatics with gastro-oesophageal reflux. European Respiratory Journal, 2019, 53, 1900453.	3.1	15
12	Integrated Multi-omics Analysis Using Variational Autoencoders: Application to Pan-cancer Classification. , 2019, , .		41
13	Unsupervised Annotation of Phenotypic Abnormalities via Semantic Latent Representations on Electronic Health Records. , 2019, , .		3
14	Lipid phenotyping of lung epithelial lining fluid in healthy human volunteers. Metabolomics, 2018, 14, 123.	1.4	17
15	Data Science for Asthma Study. Translational Bioinformatics, 2018, , 277-301.	0.0	1
16	A computational framework for complex disease stratification from multiple large-scale datasets. BMC Systems Biology, 2018, 12, 60.	3.0	43
17	Deep Unfolded IRLS-ADMM Network for Classification and Sparse Feature Selection. International Journal of Machine Learning and Computing, 2018, 8, 241-251.	0.8	1
18	Inferring functional connectivity in fMRI using minimum partial correlation. International Journal of Automation and Computing, 2017, 14, 371-385.	4.5	5

#	ARTICLE	IF	CITATIONS
19	U-BIOPRED clinical adult asthma clusters linked to a subset of sputum omics. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1797-1807.	1.5	236
20	Sparse Bayesian classification and feature selection for biological expression data with high correlations. <i>PLoS ONE</i> , 2017, 12, e0189541.	1.1	5
21	The critical regularization value: Incorporating spatial smoothness to enhance signal detection in highly noisy fMRI data. , 2015, , .		0
22	Minimum Partial Correlation: An Accurate and Parameter-Free Measure of Functional Connectivity in fMRI. <i>Lecture Notes in Computer Science</i> , 2015, , 125-134.	1.0	6
23	Inferring Cell-Scale Signalling Networks via Compressive Sensing. <i>PLoS ONE</i> , 2014, 9, e95326.	1.1	2
24	Integration of sparse Bayesian learning and random subspace for fMRI Multivariate Pattern Analysis. , 2014, 2014, 1035-8.		0
25	Balancing the Stability and Predictive Performance for Multivariate Voxel Selection in fMRI Study. <i>Lecture Notes in Computer Science</i> , 2014, , 90-99.	1.0	3
26	An iterative parameter estimation method for biological systems and its parallel implementation. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 1249-1267.	1.4	4
27	An iterative parameter estimation method for biological systems. , 2012, , .		0
28	Developing a novel integrated model of p38 MAPK and glucocorticoid signalling pathways. , 2012, , .		1
29	System Biology Approach to Study Cancer Related Pathways. , 2012, , 39-67.		0
30	Modelling and performance analysis of clinical pathways using the stochastic process algebra PEPA. <i>BMC Bioinformatics</i> , 2012, 13, S4.	1.2	13