

# Haitian Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

127  
papers

5,165  
citations

201674

27  
h-index

114465

63  
g-index

134  
all docs

134  
docs citations

134  
times ranked

7855  
citing authors

#	ARTICLE	IF	CITATIONS
1	Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak. <i>International Journal of Infectious Diseases</i> , 2020, 92, 214-217.	3.3	1,428
2	A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action. <i>International Journal of Infectious Diseases</i> , 2020, 93, 211-216.	3.3	859
3	Estimating the Unreported Number of Novel Coronavirus (2019-nCoV) Cases in China in the First Half of January 2020: A Data-Driven Modelling Analysis of the Early Outbreak. <i>Journal of Clinical Medicine</i> , 2020, 9, 388.	2.4	378
4	The relative transmissibility of asymptomatic COVID-19 infections among close contacts. <i>International Journal of Infectious Diseases</i> , 2020, 94, 145-147.	3.3	199
5	Epigenetic Silencing of miR-490-3p Reactivates the Chromatin Remodeler SMARCD1 to Promote <i>Helicobacter pylori</i> -Induced Gastric Carcinogenesis. <i>Cancer Research</i> , 2015, 75, 754-765.	0.9	115
6	Autophagy in sepsis: Degradation into exhaustion?. <i>Autophagy</i> , 2016, 12, 1073-1082.	9.1	111
7	The involvement of regulatory non-coding RNAs in sepsis: a systematic review. <i>Critical Care</i> , 2016, 20, 383.	5.8	79
8	Estimation of exponential growth rate and basic reproduction number of the coronavirus disease 2019 (COVID-19) in Africa. <i>Infectious Diseases of Poverty</i> , 2020, 9, 96.	3.7	79
9	Quantifying the transmission advantage associated with N501Y substitution of SARS-CoV-2 in the UK: an early data-driven analysis. <i>Journal of Travel Medicine</i> , 2021, 28, .	3.0	79
10	Bacteria pathogens drive host colonic epithelial cell promoter hypermethylation of tumor suppressor genes in colorectal cancer. <i>Microbiome</i> , 2020, 8, 108.	11.1	76
11	Quantifying the association between domestic travel and the exportation of novel coronavirus (2019-nCoV) cases from Wuhan, China in 2020: a correlational analysis. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	71
12	Polygenic Analysis of Late-Onset Alzheimer's Disease from Mainland China. <i>PLoS ONE</i> , 2015, 10, e0144898.	2.5	66
13	Comparative Study of Food Allergies in Children from China, India, and Russia: The EuroPrevall-INCO Surveys. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2020, 8, 1349-1358.e16.	3.8	60
14	Imitation dynamics in the mitigation of the novel coronavirus disease (COVID-19) outbreak in Wuhan, China from 2019 to 2020. <i>Annals of Translational Medicine</i> , 2020, 8, 448-448.	1.7	60
15	Statistical methods for genome-wide association studies. <i>Seminars in Cancer Biology</i> , 2019, 55, 53-60.	9.6	59
16	Estimating the generation interval and inferring the latent period of COVID-19 from the contact tracing data. <i>Epidemics</i> , 2021, 36, 100482.	3.0	55
17	COVID-19 and gender-specific difference: Analysis of public surveillance data in Hong Kong and Shenzhen, China, from January 10 to February 15, 2020. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, 750-751.	1.8	53
18	Genomic and evolutionary comparison between SARS-CoV-2 and other human coronaviruses. <i>Journal of Virological Methods</i> , 2021, 289, 114032.	2.1	46

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19	Dietary intake of manganese and the risk of the metabolic syndrome in a Chinese population. <i>British Journal of Nutrition</i> , 2016, 116, 853-863.	2.3	45
20	Serial interval in determining the estimation of reproduction number of the novel coronavirus disease (COVID-19) during the early outbreak. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	43
21	Interaction-based feature selection and classification for high-dimensional biological data. <i>Bioinformatics</i> , 2012, 28, 2834-2842.	4.1	39
22	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
23	Identifying Meteorological Drivers for the Seasonal Variations of Influenza Infections in a Subtropical City “ Hong Kong. <i>International Journal of Environmental Research and Public Health</i> , 2015, 12, 1560-1576.	2.6	35
24	A re-analysis in exploring the association between temperature and COVID-19 transmissibility: an ecological study with 154 Chinese cities. <i>European Respiratory Journal</i> , 2020, 56, 2001253.	6.7	34
25	Comprehensive molecular profiling of the B7 family of immune-regulatory ligands in breast cancer. <i>Oncolmmunology</i> , 2016, 5, e1207841.	4.6	33
26	Latitudes mediate the association between influenza activity and meteorological factors: A nationwide modelling analysis in 45 Japanese prefectures from 2000 to 2018. <i>Science of the Total Environment</i> , 2020, 703, 134727.	8.0	33
27	Epidemiological Parameters of COVID-19: Case Series Study. <i>Journal of Medical Internet Research</i> , 2020, 22, e19994.	4.3	33
28	Estimating the serial interval of the novel coronavirus disease (COVID-19) based on the public surveillance data in Shenzhen, China, from 19 January to 22 February 2020. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2818-2822.	3.0	29
29	Rapid evaluation of COVID-19 vaccine effectiveness against symptomatic infection with SARS-CoV-2 variants by analysis of genetic distance. <i>Nature Medicine</i> , 2022, 28, 1715-1722.	30.7	29
30	Superspreading and heterogeneity in transmission of SARS, MERS, and COVID-19: A systematic review. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5039-5046.	4.1	28
31	The ambient ozone and COVID-19 transmissibility in China: A data-driven ecological study of 154 cities. <i>Journal of Infection</i> , 2020, 81, e9-e11.	3.3	27
32	MircoRNA-145 promotes activation of hepatic stellate cells via targeting krÄ¼ppel-like factor 4. <i>Scientific Reports</i> , 2017, 7, 40468.	3.3	24
33	The basic reproduction number of novel coronavirus (2019-nCoV) estimation based on exponential growth in the early outbreak in China from 2019 to 2020: A reply to Dhungana. <i>International Journal of Infectious Diseases</i> , 2020, 94, 148-150.	3.3	24
34	Inflated type I error rates when using aggregation methods to analyze rare variants in the 1000 Genomes Project exon sequencing data in unrelated individuals: summary results from Group 7 at Genetic Analysis Workshop 17. <i>Genetic Epidemiology</i> , 2011, 35, S56-60.	1.3	23
35	Positive RT-PCR tests among discharged COVID-19 patients in Shenzhen, China. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, 1110-1112.	1.8	23
36	Inferencing superspreading potential using zero-truncated negative binomial model: exemplification with COVID-19. <i>BMC Medical Research Methodology</i> , 2021, 21, 30.	3.1	23

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37	A fast and powerful <i>W</i> -test for pairwise epistasis testing. <i>Nucleic Acids Research</i> , 2016, 44, e115-e115.	14.5	21
38	Identification of meteorological factors associated with human infection with avian influenza A H7N9 virus in Zhejiang Province, China. <i>Science of the Total Environment</i> , 2018, 644, 696-709.	8.0	21
39	Low dispersion in the infectiousness of COVID-19 cases implies difficulty in control. <i>BMC Public Health</i> , 2020, 20, 1558.	2.9	21
40	Inferring the Association between the Risk of COVID-19 Case Fatality and N501Y Substitution in SARS-CoV-2. <i>Viruses</i> , 2021, 13, 638.	3.3	21
41	Epigenetic silencing of GDF1 disrupts SMAD signaling to reinforce gastric cancer development. <i>Oncogene</i> , 2016, 35, 2133-2144.	5.9	20
42	The prevalence of neck pain and associated risk factors among undergraduate students: A large-scale cross-sectional study. <i>International Journal of Industrial Ergonomics</i> , 2020, 76, 102934.	2.6	19
43	A global analysis of replacement of genetic variants of SARS-CoV-2 in association with containment capacity and changes in disease severity. <i>Clinical Microbiology and Infection</i> , 2021, 27, 750-757.	6.0	19
44	Mathematical modelling of the impact of treating latent tuberculosis infection in the elderly in a city with intermediate tuberculosis burden. <i>Scientific Reports</i> , 2019, 9, 4869.	3.3	18
45	Superspreading potential of COVID-19 outbreak seeded by Omicron variants of SARS-CoV-2 in Hong Kong. <i>Journal of Travel Medicine</i> , 2022, 29, .	3.0	17
46	Real-time estimation of the reproduction number of the novel coronavirus disease (COVID-19) in China in 2020 based on incidence data. <i>Annals of Translational Medicine</i> , 2020, 8, 689-689.	1.7	15
47	Mucosal Antibody Response to SARS-CoV-2 in Paediatric and Adult Patients: A Longitudinal Study. <i>Pathogens</i> , 2022, 11, 397.	2.8	15
48	Interpreting the transmissibility of measles in two different post periods of supplementary immunization activities in Hubei, China. <i>Vaccine</i> , 2017, 35, 1024-1029.	3.8	14
49	Approximate Bayesian algorithm to estimate the basic reproduction number in an influenza pandemic using arrival times of imported cases. <i>Travel Medicine and Infectious Disease</i> , 2018, 23, 80-86.	3.0	14
50	Effects of particulate matter exposure on the transmissibility and case fatality rate of COVID-19: A Nationwide Ecological Study in China. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	13
51	Profiling of SARS-CoV-2 Subgenomic RNAs in Clinical Specimens. <i>Microbiology Spectrum</i> , 2022, 10, e0018222.	3.0	13
52	Monitoring the age-specificity of measles transmissions during 2009-2016 in Southern China. <i>PLoS ONE</i> , 2018, 13, e0205339.	2.5	12
53	Frequent Genetic Mismatch between Vaccine Strains and Circulating Seasonal Influenza Viruses, Hong Kong, China, 1996-2012. <i>Emerging Infectious Diseases</i> , 2018, 24, 1825-1834.	4.3	12
54	Association between meteorological factors, spatiotemporal effects, and prevalence of influenza A subtype H7 in environmental samples in Zhejiang province, China. <i>Science of the Total Environment</i> , 2019, 663, 793-803.	8.0	12

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55	In silico prediction of influenza vaccine effectiveness by sequence analysis. <i>Vaccine</i> , 2021, 39, 1030-1034.	3.8	12
56	Differences in the case fatality risks associated with SARS-CoV-2 Delta and non-Delta variants in relation to vaccine coverage: An early ecological study in the United Kingdom. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105162.	2.3	12
57	Interpreting the transmissibility of the avian influenza A(H7N9) infection from 2013 to 2015 in Zhejiang Province, China. <i>Epidemiology and Infection</i> , 2016, 144, 1584-1591.	2.1	11
58	Targeting Adults for Supplementary Immunization Activities of Measles Control in Central China: A Mathematical Modelling Study. <i>Scientific Reports</i> , 2018, 8, 16124.	3.3	11
59	A statistical method utilizing information of imported cases to estimate the transmissibility for an influenza pandemic. <i>BMC Medical Research Methodology</i> , 2017, 17, 31.	3.1	10
60	A novel susceptibility locus in <i>MST1</i> and gene-gene interaction network for Crohn's disease in the Chinese population. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2368-2377.	3.6	10
61	Quantifying the importance of the key sites on haemagglutinin in determining the selection advantage of influenza virus: Using A/H3N2 as an example. <i>Journal of Infection</i> , 2020, 81, 452-482.	3.3	10
62	Use of a least absolute shrinkage and selection operator (LASSO) model to selected ion flow tube mass spectrometry (SIFT-MS) analysis of exhaled breath to predict the efficacy of dialysis: a pilot study. <i>Journal of Breath Research</i> , 2016, 10, 046004.	3.0	9
63	An increasing trend of rural infections of human influenza A (H7N9) from 2013 to 2017: A retrospective analysis of patient exposure histories in Zhejiang province, China. <i>PLoS ONE</i> , 2018, 13, e0193052.	2.5	9
64	The cost-effectiveness of prostate health index for prostate cancer detection in Chinese men. <i>Prostate Cancer and Prostatic Diseases</i> , 2020, 23, 615-621.	3.9	9
65	Modelling the association between COVID-19 transmissibility and D614G substitution in SARS-CoV-2 spike protein: using the surveillance data in California as an example. <i>Theoretical Biology and Medical Modelling</i> , 2021, 18, 10.	2.1	9
66	Independent association between meteorological factors, PM2.5, and seasonal influenza activity in Hangzhou, Zhejiang province, China. <i>Influenza and Other Respiratory Viruses</i> , 2021, 15, 513-520.	3.4	9
67	Poultry exposure and environmental protection against asthma in rural children. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 2949-2960.	5.7	9
68	Patient Flow Evaluation with System Dynamic Model in an Emergency Department: Data Analytics on Daily Hospital Records. , 2015, , .		8
69	Stratified polygenic risk prediction model with application to CAGI bipolar disorder sequencing data. <i>Human Mutation</i> , 2017, 38, 1235-1239.	2.5	8
70	Determinants for asthma control, quality of life and use of complementary and alternative medicine in asthmatic pediatric patients in four cities. <i>World Journal of Pediatrics</i> , 2018, 14, 482-491.	1.8	8
71	Early Waning of Maternal Measles Antibodies in Infants in Zhejiang Province, China: A Comparison of Two Cross-Sectional Serosurveys. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 4680.	2.6	8
72	wtest: an integrated R package for genetic epistasis testing. <i>BMC Medical Genomics</i> , 2019, 12, 180.	1.5	8

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73	The changing patterns of COVID-19 transmissibility during the social unrest in the United States: A nationwide ecological study with a before-and-after comparison. <i>One Health</i> , 2021, 12, 100201.	3.4	8
74	Oncogenes without a neighboring tumor-suppressor gene are more prone to amplification. <i>Molecular Biology and Evolution</i> , 2017, 34, msW295.	8.9	7
75	Estimation of clinical parameters of chronic kidney disease by exhaled breath full-scan mass spectrometry data and iterative PCA with intensity screening algorithm. <i>Journal of Breath Research</i> , 2017, 11, 036007.	3.0	7
76	Interleukin-27 Is Differentially Associated with HIV Viral Load and CD4+ T Cell Counts in Therapy-Naïve HIV-Mono-Infected and HIV/HCV-Co-Infected Chinese. <i>PLoS ONE</i> , 2014, 9, e96792.	2.5	7
77	Superspreading potential of SARS-CoV-2 Delta variants under intensive disease control measures in China. <i>Journal of Travel Medicine</i> , 2022, 29, .	3.0	7
78	Clinical scores of sleep loss and itch, and antihistamine and topical corticosteroid usage for childhood eczema. <i>British Journal of Dermatology</i> , 2016, 175, 1076-1078.	1.5	6
79	A Wâ€test collapsing method for rareâ€variant association testing in exome sequencing data. <i>Genetic Epidemiology</i> , 2016, 40, 591-596.	1.3	6
80	Initial COVID-19 Transmissibility and Three Gaseous Air Pollutants (NO <sub>2</sub> , SO <sub>2</sub> , and CO): A Nationwide Ecological Study in China. <i>Frontiers in Medicine</i> , 2020, 7, 575839.	2.6	6
81	Predicting the dominant influenza A serotype by quantifying mutation activities. <i>International Journal of Infectious Diseases</i> , 2020, 100, 255-257.	3.3	6
82	Associations between sport participation and knee symptoms: a cross-sectional study involving 3053 undergraduate students. <i>BMC Sports Science, Medicine and Rehabilitation</i> , 2020, 12, 20.	1.7	6
83	Transurethral resection of prostate for acute urinary retention is linked to shorter survival in younger men. <i>Asian Journal of Andrology</i> , 2019, 21, 468.	1.6	6
84	Quantifying the effect of government interventions and virus mutations on transmission advantage during COVID-19 pandemic. <i>Journal of Infection and Public Health</i> , 2022, 15, 338-342.	4.1	6
85	Utilization of Gene Expression Signature for Quality Control of Traditional Chinese Medicine Formula Si-Wu-Tang. <i>AAPS Journal</i> , 2013, 15, 884-892.	4.4	5
86	Genetic evolution of Human Enterovirus A71 subgenotype C4 in Shenzhen, China, 1998â€2013. <i>Journal of Infection</i> , 2016, 72, 731-737.	3.3	5
87	Concurrent epidemics of influenza A/H3N2 and A/H1N1pdm in Southern China: A serial cross-sectional study. <i>Journal of Infection</i> , 2016, 72, 369-376.	3.3	5
88	Genetic Test, Risk Prediction, and Counseling. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1005, 21-46.	1.6	5
89	Quantifying the improvement in confirmation efficiency of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) during the early phase of the outbreak in Hong Kong in 2020. <i>International Journal of Infectious Diseases</i> , 2020, 96, 284-287.	3.3	5
90	An early assessment of a case fatality risk associated with P.1 SARS-CoV-2 lineage in Brazil: an ecological study. <i>Journal of Travel Medicine</i> , 2021, 28, .	3.0	5

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91	The non-pharmaceutical interventions may affect the advantage in transmission of mutated variants during epidemics: A conceptual model for COVID-19. <i>Journal of Theoretical Biology</i> , 2022, 542, 111105.	1.7	5
92	Characterizing superspreading potential of infectious disease: Decomposition of individual transmissibility. <i>PLoS Computational Biology</i> , 2022, 18, e1010281.	3.2	5
93	A Zoom-Focus algorithm (ZFA) to locate the optimal testing region for rare variant association tests. <i>Bioinformatics</i> , 2017, 33, 2330-2336.	4.1	4
94	Incorporating methylation genome information improves prediction accuracy for drug treatment responses. <i>BMC Genetics</i> , 2018, 19, 78.	2.7	4
95	Gene-methylation epistatic analyses via the <i>W</i> -test identifies enriched signals of neuronal genes in patients undergoing lipid-control treatment. <i>BMC Proceedings</i> , 2018, 12, 53.	1.6	4
96	Were infections in migrants associated with the resurgence of measles epidemic during 2013–2014 in southern China? A retrospective data analysis. <i>International Journal of Infectious Diseases</i> , 2020, 90, 77-83.	3.3	4
97	Modelling the Measles Outbreak at Hong Kong International Airport in 2019: A Data-Driven Analysis on the Effects of Timely Reporting and Public Awareness. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1851-1861.	2.7	4
98	Changes in Measles Seroprevalence in China After the Launch of Two Provincial Supplementary Immunization Activities During 2009 to 2013. <i>Pediatric Infectious Disease Journal</i> , 2020, 39, 867-871.	2.0	4
99	Limited role for meteorological factors on the variability in COVID-19 incidence: A retrospective study of 102 Chinese cities. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009056.	3.0	4
100	Differential Influence of Age on the Relationship between Genetic Mismatch and A(H1N1)pdm09 Vaccine Effectiveness. <i>Viruses</i> , 2021, 13, 619.	3.3	4
101	Long-term effectiveness of elderly health care voucher scheme strategies: a system dynamics simulation analysis. <i>BMC Public Health</i> , 2021, 21, 1235.	2.9	4
102	Characterization of key amino acid substitutions and dynamics of the influenza virus H3N2 hemagglutinin. <i>Journal of Infection</i> , 2021, 83, 671-677.	3.3	4
103	The co-circulating transmission dynamics of SARS-CoV-2 Alpha and Eta variants in Nigeria: A retrospective modeling study of COVID-19. <i>Journal of Global Health</i> , 2021, 11, 05028.	2.7	4
104	Identifying influential regions in extremely rare variants using a fixed-bin approach. <i>BMC Proceedings</i> , 2011, 5, S3.	1.6	3
105	Considering interactive effects in the identification of influential regions with extremely rare variants via fixed bin approach. <i>BMC Proceedings</i> , 2014, 8, S7.	1.6	3
106	A partition-based approach to identify gene-environment interactions in genome wide association studies. <i>BMC Proceedings</i> , 2014, 8, S60.	1.6	3
107	Attach importance of the bootstrap test against Student's <i>t</i> -test in clinical epidemiology: a demonstrative comparison using COVID-19 as an example. <i>Epidemiology and Infection</i> , 2021, 149, e107.	2.1	3
108	Temporal-Geographical Dispersion of SARS-CoV-2 Spike Glycoprotein Variant Lineages and Their Functional Prediction Using in Silico Approach. <i>MBio</i> , 2021, 12, e0268721.	4.1	3

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109	Whole-Genome Shotgun Sequencing for Nasopharyngeal Microbiome in Pre-school Children With Recurrent Wheezing. <i>Frontiers in Microbiology</i> , 2021, 12, 792556.	3.5	3
110	Modelling COVID-19 outbreak on the Diamond Princess ship using the public surveillance data. <i>Infectious Disease Modelling</i> , 2022, 7, 189-195.	1.9	3
111	Two Screening Methods for Genetic Association Study with Application to Psoriasis Microarray Data Sets. , 2015, , .		2
112	A clustering approach to identify rare variants associated with hypertension. <i>BMC Proceedings</i> , 2016, 10, 153-157.	1.6	2
113	Epidemiological changes in measles infections in southern China between 2009 and 2016: a retrospective database analysis. <i>BMC Infectious Diseases</i> , 2020, 20, 197.	2.9	2
114	A Bayesian method for synthesizing multiple diagnostic outcomes of COVID-19 tests. <i>Royal Society Open Science</i> , 2021, 8, 201867.	2.4	2
115	Cross Sectional Survey of Influenza Antibodies before and during the 2009 Pandemic in Shenzhen, China. <i>PLoS ONE</i> , 2013, 8, e53847.	2.5	2
116	Real-time quantification of the transmission advantage associated with a single mutation in pathogen genomes: a case study on the D614G substitution of SARS-CoV-2. <i>BMC Infectious Diseases</i> , 2021, 21, 1039.	2.9	2
117	A tentative assessment of the changes in transmissibility and fatality risk associated with Beta SARS-CoV-2 variants in South Africa: an ecological study. <i>Pathogens and Global Health</i> , 2021, , 1-3.	2.3	2
118	New insights into old methods for identifying causal rare variants. <i>BMC Proceedings</i> , 2011, 5, S50.	1.6	1
119	Discovering pure gene-environment interactions in blood pressure genome-wide association studies data: a two-step approach incorporating new statistics. <i>BMC Proceedings</i> , 2014, 8, S62.	1.6	1
120	Detecting responses to treatment with fenofibrate in pedigrees. <i>BMC Genetics</i> , 2018, 19, 64.	2.7	1
121	Persistence of Pneumococcal Serotype 3 in Adult Pneumococcal Disease in Hong Kong. <i>Vaccines</i> , 2021, 9, 756.	4.4	1
122	Shrinkage in serial intervals across transmission generations of COVID-19. <i>Journal of Theoretical Biology</i> , 2021, 529, 110861.	1.7	1
123	Temporal Patterns in the Evolutionary Genetic Distance of SARS-CoV-2 during the COVID-19 Pandemic. <i>Public Health Genomics</i> , 2022, 25, 108-111.	1.0	1
124	Risk-Adjusted Monitoring Method for Surgical Data: Methodology for Data Analytics (Work in Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142		
125	Response to 'Mortality, length-of-stay, bloodstream and respiratory viral infections in a pediatric intensivecare unit: comment on data sparsity. <i>Journal of Critical Care</i> , 2017, 41, 334.	2.2	0
126	W-Test for Genetic Epistasis Testing. <i>Methods in Molecular Biology</i> , 2021, 2212, 45-53.	0.9	0

#	ARTICLE	IF	CITATIONS
127	Abstract LB-254: Thymidylate synthase gene polymorphisms is negatively associated with gastric cancer survival. , 2017, , .		0