

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 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | Profiling of SARS-CoV-2 Subgenomic RNAs in Clinical Specimens. <i>Microbiology Spectrum</i> , 2022, 10, e0018222. | 3.0 | 13 |
| 6 | Mucosal Antibody Response to SARS-CoV-2 in Paediatric and Adult Patients: A Longitudinal Study. <i>Pathogens</i> , 2022, 11, 397. | 2.8 | 15 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | Characterizing superspreading potential of infectious disease: Decomposition of individual transmissibility. <i>PLoS Computational Biology</i> , 2022, 18, e1010281. | 3.2 | 5 |
| 13 | Genomic and evolutionary comparison between SARS-CoV-2 and other human coronaviruses. <i>Journal of Virological Methods</i> , 2021, 289, 114032. | 2.1 | 46 |
| 14 | 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 |
| 15 | W-Test for Genetic Epistasis Testing. <i>Methods in Molecular Biology</i> , 2021, 2212, 45-53. | 0.9 | 0 |
| 16 | Attach importance of the bootstrap test against Student's test in clinical epidemiology: a demonstrative comparison using COVID-19 as an example. <i>Epidemiology and Infection</i> , 2021, 149, e107. | 2.1 | 3 |
| 17 | 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 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | In silico prediction of influenza vaccine effectiveness by sequence analysis. <i>Vaccine</i> , 2021, 39, 1030-1034. | 3.8 | 12 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Persistence of Pneumococcal Serotype 3 in Adult Pneumococcal Disease in Hong Kong. <i>Vaccines</i> , 2021, 9, 756. | 4.4 | 1 |
| 29 | A Bayesian method for synthesizing multiple diagnostic outcomes of COVID-19 tests. <i>Royal Society Open Science</i> , 2021, 8, 201867. | 2.4 | 2 |
| 30 | 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 |
| 31 | Shrinkage in serial intervals across transmission generations of COVID-19. <i>Journal of Theoretical Biology</i> , 2021, 529, 110861. | 1.7 | 1 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | Were infections in migrants associated with the resurgence of measles epidemic during 2013â€“2014 in southern China? A retrospective data analysis. <i>International Journal of Infectious Diseases</i> , 2020, 90, 77-83. | 3.3 | 4 |
| 40 | 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 |
| 41 | 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 |
| 42 | Low dispersion in the infectiousness of COVID-19 cases implies difficulty in control. <i>BMC Public Health</i> , 2020, 20, 1558. | 2.9 | 21 |
| 43 | Initial COVID-19 Transmissibility and Three Gaseous Air Pollutants (NO ₂ , SO ₂ , and CO): A Nationwide Ecological Study in China. <i>Frontiers in Medicine</i> , 2020, 7, 575839. | 2.6 | 6 |
| 44 | 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 |
| 45 | 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 |
| 46 | <p>Modelling the Measles Outbreak at Hong Kong International Airport in 2019: A Data-Driven Analysis on the Effects of Timely Reporting and Public Awareness</p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1851-1861. | 2.7 | 4 |
| 47 | 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 |
| 48 | 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 |
| 49 | Predicting the dominant influenza A serotype by quantifying mutation activities. <i>International Journal of Infectious Diseases</i> , 2020, 100, 255-257. | 3.3 | 6 |
| 50 | 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 |
| 51 | 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 |
| 52 | Estimating the serial interval of the novel coronavirus disease (COVIDâ€“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 |
| 53 | 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 |
| 54 | 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 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | 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 |
| 62 | 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 |
| 63 | 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 |
| 64 | 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 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | 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 |
| 70 | Epidemiological Parameters of COVID-19: Case Series Study. <i>Journal of Medical Internet Research</i> , 2020, 22, e19994. | 4.3 | 33 |
| 71 | 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 |
| 72 | 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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|----|---|-----|-----------|
| 73 | 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 |
| 74 | wtest: an integrated R package for genetic epistasis testing. <i>BMC Medical Genomics</i> , 2019, 12, 180. | 1.5 | 8 |
| 75 | Statistical methods for genome-wide association studies. <i>Seminars in Cancer Biology</i> , 2019, 55, 53-60. | 9.6 | 59 |
| 76 | 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 |
| 77 | 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 |
| 78 | 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 |
| 79 | Incorporating methylation genome information improves prediction accuracy for drug treatment responses. <i>BMC Genetics</i> , 2018, 19, 78. | 2.7 | 4 |
| 80 | 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 |
| 81 | Detecting responses to treatment with fenofibrate in pedigrees. <i>BMC Genetics</i> , 2018, 19, 64. | 2.7 | 1 |
| 82 | Monitoring the age-specificity of measles transmissions during 2009-2016 in Southern China. <i>PLoS ONE</i> , 2018, 13, e0205339. | 2.5 | 12 |
| 83 | Gene-methylation epistatic analyses via the W-test identifies enriched signals of neuronal genes in patients undergoing lipid-control treatment. <i>BMC Proceedings</i> , 2018, 12, 53. | 1.6 | 4 |
| 84 | 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 |
| 85 | 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 |
| 86 | 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 |
| 87 | 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 |
| 88 | MircoRNA-145 promotes activation of hepatic stellate cells via targeting Krppel-like factor 4. <i>Scientific Reports</i> , 2017, 7, 40468. | 3.3 | 24 |
| 89 | Oncogenes without a neighboring tumor-suppressor gene are more prone to amplification. <i>Molecular Biology and Evolution</i> , 2017, 34, msw295. | 8.9 | 7 |
| 90 | Stratified polygenic risk prediction model with application to CAGI bipolar disorder sequencing data. <i>Human Mutation</i> , 2017, 38, 1235-1239. | 2.5 | 8 |

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|-----|---|-----|-----------|
| 91 | 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 |
| 92 | 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 |
| 93 | Genetic Test, Risk Prediction, and Counseling. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1005, 21-46. | 1.6 | 5 |
| 94 | 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 |
| 95 | 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 |
| 96 | 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 |
| 97 | 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 |
| 98 | Abstract LB-254: Thymidylate synthase gene polymorphisms is negatively associated with gastric cancer survival. , 2017, , . | | 0 |
| 99 | Comprehensive molecular profiling of the B7 family of immune-regulatory ligands in breast cancer. <i>Oncolmmunology</i> , 2016, 5, e1207841. | 4.6 | 33 |
| 100 | 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 |
| 101 | A clustering approach to identify rare variants associated with hypertension. <i>BMC Proceedings</i> , 2016, 10, 153-157. | 1.6 | 2 |
| 102 | The involvement of regulatory non-coding RNAs in sepsis: a systematic review. <i>Critical Care</i> , 2016, 20, 383. | 5.8 | 79 |
| 103 | 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 |
| 104 | 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 |
| 105 | Autophagy in sepsis: Degradation into exhaustion?. <i>Autophagy</i> , 2016, 12, 1073-1082. | 9.1 | 111 |
| 106 | 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 |
| 107 | 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 |
| 108 | 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 |

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|-----|--|------|-----------|
| 109 | A fast and powerful <i>W</i> -test for pairwise epistasis testing. <i>Nucleic Acids Research</i> , 2016, 44, e115-e115. | 14.5 | 21 |
| 110 | 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 |
| 111 | Epigenetic silencing of GDF1 disrupts SMAD signaling to reinforce gastric cancer development. <i>Oncogene</i> , 2016, 35, 2133-2144. | 5.9 | 20 |
| 112 | Polygenic Analysis of Late-Onset Alzheimer's Disease from Mainland China. <i>PLoS ONE</i> , 2015, 10, e0144898. | 2.5 | 66 |
| 113 | Risk-Adjusted Monitoring Method for Surgical Data: Methodology for Data Analytics (Work in Progress). <i>ETQq1 1 0.784314 rgBT /Overlock 10</i> | | |
| 114 | Identifying Meteorological Drivers for the Seasonal Variations of Influenza Infections in a Subtropical City of Hong Kong. <i>International Journal of Environmental Research and Public Health</i> , 2015, 12, 1560-1576. | 2.6 | 35 |
| 115 | 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 |
| 116 | Two Screening Methods for Genetic Association Study with Application to Psoriasis Microarray Data Sets. , 2015, , . | | 2 |
| 117 | Patient Flow Evaluation with System Dynamic Model in an Emergency Department: Data Analytics on Daily Hospital Records. , 2015, , . | | 8 |
| 118 | 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 |
| 119 | A partition-based approach to identify gene-environment interactions in genome wide association studies. <i>BMC Proceedings</i> , 2014, 8, S60. | 1.6 | 3 |
| 120 | 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 |
| 121 | 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 |
| 122 | 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 |
| 123 | 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 |
| 124 | Interaction-based feature selection and classification for high-dimensional biological data. <i>Bioinformatics</i> , 2012, 28, 2834-2842. | 4.1 | 39 |
| 125 | Identifying influential regions in extremely rare variants using a fixed-bin approach. <i>BMC Proceedings</i> , 2011, 5, S3. | 1.6 | 3 |
| 126 | New insights into old methods for identifying causal rare variants. <i>BMC Proceedings</i> , 2011, 5, S50. | 1.6 | 1 |

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|-----|--|-----|-----------|
| 127 | 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 |