

Jason E Shoemaker

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,140
citations

516710

16
h-index

414414

32
g-index

44
all docs

44
docs citations

44
times ranked

2468
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Mathematical Modeling Finds Disparate Interferon Production Rates Drive Strain-Specific Immunodynamics during Deadly Influenza Infection. <i>Viruses</i> , 2022, 14, 906. | 3.3 | 2 |
| 2 | Agent-based modeling reveals benefits of heterogeneous and stochastic cell populations during cGAS-mediated IFN β production. <i>Bioinformatics</i> , 2021, 37, 1428-1434. | 4.1 | 9 |
| 3 | DeltaNeTS+: elucidating the mechanism of drugs and diseases using gene expression and transcriptional regulatory networks. <i>BMC Bioinformatics</i> , 2021, 22, 108. | 2.6 | 0 |
| 4 | Multicellular spatial model of RNA virus replication and interferon responses reveals factors controlling plaque growth dynamics. <i>PLoS Computational Biology</i> , 2021, 17, e1008874. | 3.2 | 8 |
| 5 | COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387. | 7.2 | 53 |
| 6 | Network Controllability-Based Prioritization of Candidates for SARS-CoV-2 Drug Repositioning. <i>Viruses</i> , 2020, 12, 1087. | 3.3 | 3 |
| 7 | Pathogenesis of Influenza A(H7N9) Virus in Aged Nonhuman Primates. <i>Journal of Infectious Diseases</i> , 2020, 222, 1155-1164. | 4.0 | 8 |
| 8 | Mathematical Modeling of RNA Virus Sensing Pathways Reveals Paracrine Signaling as the Primary Factor Regulating Excessive Cytokine Production. <i>Processes</i> , 2020, 8, 719. | 2.8 | 8 |
| 9 | Repurposing the psoriasis drug Oxarol to an ointment adjuvant for the influenza vaccine. <i>International Immunology</i> , 2020, 32, 499-507. | 4.0 | 7 |
| 10 | TREAP: A New Topological Approach to Drug Target Inference. <i>Biophysical Journal</i> , 2020, 119, 2290-2298. | 0.5 | 1 |
| 11 | Predicting Host Immune Cell Dynamics and Key Disease-Associated Genes Using Tissue Transcriptional Profiles. <i>Processes</i> , 2019, 7, 301. | 2.8 | 0 |
| 12 | A dual controllability analysis of influenza virus-host protein-protein interaction networks for antiviral drug target discovery. <i>BMC Bioinformatics</i> , 2019, 20, 297. | 2.6 | 7 |
| 13 | Strain-Specific Immune Response to Influenza Virus Infection. <i>IFAC-PapersOnLine</i> , 2019, 52, 101-106. | 0.9 | 0 |
| 14 | Mathematical modeling of the cGAS pathway reveals robustness of DNA sensing to TREX1 feedback. <i>Journal of Theoretical Biology</i> , 2019, 462, 148-157. | 1.7 | 13 |
| 15 | Chemical hazard prediction and hypothesis testing using quantitative adverse outcome pathways. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2019, 36, 91-102. | 1.5 | 29 |
| 16 | Network perturbation analysis of gene transcriptional profiles reveals protein targets and mechanism of action of drugs and influenza A viral infection. <i>Nucleic Acids Research</i> , 2018, 46, e34-e34. | 14.5 | 33 |
| 17 | Network-Guided Discovery of Influenza Virus Replication Host Factors. <i>MBio</i> , 2018, 9, . | 4.1 | 24 |
| 18 | Predicting host immune cell dynamics using tissue gene expression. <i>IFAC-PapersOnLine</i> , 2018, 51, 5-6. | 0.9 | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Examining Dynamic Emergent Properties of the DNA Sensing Pathway. IFAC-PapersOnLine, 2018, 51, 112-113. | 0.9 | 5 |
| 20 | A Systems and Treatment Perspective of Models of Influenza Virus-Induced Host Responses. Processes, 2018, 6, 138. | 2.8 | 6 |
| 21 | C646, a Novel p300/CREB-Binding Protein-Specific Inhibitor of Histone Acetyltransferase, Attenuates Influenza A Virus Infection. Antimicrobial Agents and Chemotherapy, 2016, 60, 1902-1906. | 3.2 | 25 |
| 22 | An Ultrasensitive Mechanism Regulates Influenza Virus-Induced Inflammation. PLoS Pathogens, 2015, 11, e1004856. | 4.7 | 32 |
| 23 | Identifying problematic drugs based on the characteristics of their targets. Frontiers in Pharmacology, 2015, 6, 186. | 3.5 | 11 |
| 24 | Multi-spectral fluorescent reporter influenza viruses (Color-flu) as powerful tools for in vivo studies. Nature Communications, 2015, 6, 6600. | 12.8 | 98 |
| 25 | Influenza Virus-Host Interactome Screen as a Platform for Antiviral Drug Development. Cell Host and Microbe, 2014, 16, 795-805. | 11.0 | 239 |
| 26 | Disease Severity Is Associated with Differential Gene Expression at the Early and Late Phases of Infection in Nonhuman Primates Infected with Different H5N1 Highly Pathogenic Avian Influenza Viruses. Journal of Virology, 2014, 88, 8981-8997. | 3.4 | 45 |
| 27 | A comprehensive map of the influenza A virus replication cycle. BMC Systems Biology, 2013, 7, 97. | 3.0 | 97 |
| 28 | Adding Protein Context to the Human Protein-Protein Interaction Network to Reveal Meaningful Interactions. PLoS Computational Biology, 2013, 9, e1002860. | 3.2 | 70 |
| 29 | CTen: a web-based platform for identifying enriched cell types from heterogeneous microarray data. BMC Genomics, 2012, 13, 460. | 2.8 | 113 |
| 30 | Integrated network analysis reveals a novel role for the cell cycle in 2009 pandemic influenza virus-induced inflammation in macaque lungs. BMC Systems Biology, 2012, 6, 117. | 3.0 | 22 |
| 31 | Tissue-specific subnetworks and characteristics of publicly available human protein interaction databases. Bioinformatics, 2011, 27, 2414-2421. | 4.1 | 46 |
| 32 | Confidence from uncertainty - A multi-target drug screening method from robust control theory. BMC Systems Biology, 2010, 4, 161. | 3.0 | 13 |
| 33 | Fathead minnow steroidogenesis: in silico analyses reveals tradeoffs between nominal target efficacy and robustness to cross-talk. BMC Systems Biology, 2010, 4, 89. | 3.0 | 18 |
| 34 | Automatic Control in Systems Biology. , 2009, , 1335-1360. | | 2 |
| 35 | Identifying Fragilities in Biochemical Networks: Robust Performance Analysis of Fas Signaling-Induced Apoptosis. Biophysical Journal, 2008, 95, 2610-2623. | 0.5 | 24 |
| 36 | The dynamics of single-substrate continuous cultures: the role of transport enzymes. Journal of Theoretical Biology, 2003, 222, 307-322. | 1.7 | 12 |