

Mandev S Gill

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1349727/publications.pdf>

Version: 2024-02-01

15
papers

1,418
citations

840776

11
h-index

996975

15
g-index

17
all docs

17
docs citations

17
times ranked

3337
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260. | 12.6 | 454 |
| 2 | Improving Bayesian Population Dynamics Inference: A Coalescent-Based Model for Multiple Loci. <i>Molecular Biology and Evolution</i> , 2013, 30, 713-724. | 8.9 | 449 |
| 3 | Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717. | 27.8 | 133 |
| 4 | A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 1608-1613. | 8.9 | 79 |
| 5 | Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. <i>Systematic Biology</i> , 2016, 65, 1041-1056. | 5.6 | 60 |
| 6 | Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392. | 4.7 | 35 |
| 7 | Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620. | 12.8 | 35 |
| 8 | Relax, Keep Walking – A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493. | 8.9 | 31 |
| 9 | A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017, 66, syw093. | 5.6 | 25 |
| 10 | Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020, 37, 1832-1842. | 8.9 | 25 |
| 11 | Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. <i>PLoS Pathogens</i> , 2021, 17, e1009571. | 4.7 | 24 |
| 12 | Hamiltonian Monte Carlo sampling to estimate past population dynamics using the skygrid coalescent model in a Bayesian phylogenetics framework. <i>Wellcome Open Research</i> , 2020, 5, 53. | 1.8 | 15 |
| 13 | Markov-Modulated Continuous-Time Markov Chains to Identify Site- and Branch-Specific Evolutionary Variation in BEAST. <i>Systematic Biology</i> , 2021, 70, 181-189. | 5.6 | 11 |
| 14 | On the Use of Phylogeographic Inference to Infer the Dispersal History of Rabies Virus: A Review Study. <i>Viruses</i> , 2021, 13, 1628. | 3.3 | 9 |
| 15 | YMrCA: Improving Y-chromosomal ancestor time estimation for DNA kinship research. <i>Human Mutation</i> , 2021, 42, 1307-1320. | 2.5 | 5 |