

# Dominik Schrempf

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1852371/publications.pdf>

Version: 2024-02-01

11  
papers

6,393  
citations

1163117

8  
h-index

1372567

10  
g-index

19  
all docs

19  
docs citations

19  
times ranked

8353  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Relative Time Constraints Improve Molecular Dating. <i>Systematic Biology</i> , 2022, 71, 797-809.  | 5.6  | 9         |
| 2  | Distinguishing excess mutations and increased cell death based on variant allele frequencies. <i>PLoS Computational Biology</i> , 2022, 18, e1010048.   | 3.2  | 0         |
| 3  | Inferring the Deep Past from Molecular Data. <i>Genome Biology and Evolution</i> , 2021, 13, .  | 2.5  | 19        |
| 4  | Scalable Empirical Mixture Models That Account for Across-Site Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2020, 37, 3616-3631.   | 8.9  | 32        |
| 5  | IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.  | 8.9  | 5,960     |
| 6  | The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.   | 10.3 | 115       |
| 7  | Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. <i>Molecular Biology and Evolution</i> , 2019, 36, 1294-1301.  | 8.9  | 27        |
| 8  | Inference in population genetics using forward and backward, discrete and continuous time processes. <i>Journal of Theoretical Biology</i> , 2018, 439, 166-180.  | 1.7  | 5         |
| 9  | An alternative derivation of the stationary distribution of the multivariate neutral Wright-Fisher model for low mutation rates with a view to mutation rate estimation from site frequency data. <i>Theoretical Population Biology</i> , 2017, 114, 88-94. | 1.1  | 17        |
| 10 | Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016, 407, 362-370.  | 1.7  | 70        |
| 11 | PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. <i>Systematic Biology</i> , 2015, 64, 1018-1031.  | 5.6  | 66        |