

# Andre J Aberer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10731830/publications.pdf>

Version: 2024-02-01

12  
papers

4,949  
citations

1040056

9  
h-index

1372567

10  
g-index

12  
all docs

12  
docs citations

12  
times ranked

7622  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.  | 12.6 | 2,096     |
| 2  | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.   | 12.6 | 1,583     |
| 3  | ExaBayes: Massively Parallel Bayesian Tree Inference for the Whole-Genome Era. <i>Molecular Biology and Evolution</i> , 2014, 31, 2553-2556.   | 8.9  | 423       |
| 4  | Pruning Rogue Taxa Improves Phylogenetic Accuracy: An Efficient Algorithm and Webservice. <i>Systematic Biology</i> , 2013, 62, 162-166.   | 5.6  | 327       |
| 5  | ExaML version 3: a tool for phylogenomic analyses on supercomputers. <i>Bioinformatics</i> , 2015, 31, 2577-2579.  | 4.1  | 209       |
| 6  | Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. <i>Molecular Biology and Evolution</i> , 2014, 31, 239-249. | 8.9  | 127       |
| 7  | Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.  | 6.4  | 72        |
| 8  | Uncovering Hidden Phylogenetic Consensus in Large Data Sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 902-911.                              | 3.0  | 32        |
| 9  | A Simple and Accurate Method for Rogue Taxon Identification. , 2011, , .   |      | 29        |
| 10 | Novel Parallelization Schemes for Large-Scale Likelihood-based Phylogenetic Inference. , 2013, , .   |      | 29        |
| 11 | Parallelized phylogenetic post-analysis on multi-core architectures. <i>Journal of Computational Science</i> , 2010, 1, 107-114.   | 2.9  | 11        |
| 12 | An Efficient Independence Sampler for Updating Branches in Bayesian Markov chain Monte Carlo Sampling of Phylogenetic Trees. <i>Systematic Biology</i> , 2016, 65, 161-176.            | 5.6  | 11        |