

# Tandy Warnow

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

124  
papers

7,936  
citations

38  
h-index

88  
g-index

157  
ext. papers

10,330  
ext. citations

5.7  
avg, IF

6.43  
L-index

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 124 | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , <b>2014</b> , 346, 1320-31   | 33.3 | 1182      |
| 123 | Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E4859-68 | 11.5 | 835       |
| 122 | ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. <i>Bioinformatics</i> , <b>2015</b> , 31, i44-52   | 7.2  | 593       |
| 121 | Chemical phylogenetics of histone deacetylases. <i>Nature Chemical Biology</i> , <b>2010</b> , 6, 238-243   | 11.7 | 564       |
| 120 | Rapid and accurate large-scale coestimation of sequence alignments and phylogenetic trees. <i>Science</i> , <b>2009</b> , 324, 1561-4   | 33.3 | 417       |
| 119 | Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , <b>2014</b> , 3, 17  | 7.6  | 403       |
| 118 | PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. <i>Journal of Computational Biology</i> , <b>2015</b> , 22, 377-86  | 1.7  | 237       |
| 117 | Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , <b>2014</b> , 346, 1250463  | 33.3 | 166       |
| 116 | Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , <b>2021</b> , 592, 737-746   | 46.4 | 161       |
| 115 | Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. <i>Systematic Biology</i> , <b>2016</b> , 65, 366-80                                     | 8.4  | 156       |
| 114 | The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 330-44   | 3.9  | 130       |
| 113 | RAXML and FastTree: comparing two methods for large-scale maximum likelihood phylogeny estimation. <i>PLoS ONE</i> , <b>2011</b> , 6, e27731  | 3.7  | 124       |
| 112 | Phylogenetic networks: modeling, reconstructibility, and accuracy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2004</b> , 1, 13-23                                      | 3    | 121       |
| 111 | ASTRID: Accurate Species TRees from Internode Distances. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 10, S3  | 4.5  | 112       |
| 110 | Naive binning improves phylogenomic analyses. <i>Bioinformatics</i> , <b>2013</b> , 29, 2277-84   | 7.2  | 111       |
| 109 | To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. <i>Systematic Biology</i> , <b>2018</b> , 67, 285-303  | 8.4  | 105       |
| 108 | On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. <i>Systematic Biology</i> , <b>2015</b> , 64, 663-76  | 8.4  | 103       |

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| 107 | A comparative study of SVDquartets and other coalescent-based species tree estimation methods. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 10, S2   | 4.5  | 95 |
| 106 | Kaikoura tree theorems: Computing the maximum agreement subtree. <i>Information Processing Letters</i> , <b>1993</b> , 48, 77-82   | 0.8  | 85 |
| 105 | Steps toward accurate reconstructions of phylogenies from gene-order data. <i>Journal of Computer and System Sciences</i> , <b>2002</b> , 65, 508-525  | 1    | 79 |
| 104 | Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. <i>PLoS ONE</i> , <b>2015</b> , 10, e0129183   | 3.7  | 76 |
| 103 | Ultra-large alignments using phylogeny-aware profiles. <i>Genome Biology</i> , <b>2015</b> , 16, 124   | 18.3 | 73 |
| 102 | Computational Phylogenetics: An Introduction to Designing Methods for Phylogeny Estimation <b>2017</b> ,   |      | 67 |
| 101 | TIPP: taxonomic identification and phylogenetic profiling. <i>Bioinformatics</i> , <b>2014</b> , 30, 3548-55   | 7.2  | 59 |
| 100 | Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , <b>2015</b> , 4, 4   | 7.6  | 54 |
| 99  | Algorithms for MDC-based multi-locus phylogeny inference: beyond rooted binary gene trees on single alleles. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 1543-59                           | 1.7  | 54 |
| 98  | Taking the first steps towards a standard for reporting on phylogenies: Minimum Information About a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 231-7 | 3.8  | 54 |
| 97  | A new implementation and detailed study of breakpoint analysis. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2001</b> , 583-94  | 1.3  | 54 |
| 96  | MRL and SuperFine+MRL: new supertree methods. <i>Algorithms for Molecular Biology</i> , <b>2012</b> , 7, 3   | 1.8  | 52 |
| 95  | The impact of multiple protein sequence alignment on phylogenetic estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2011</b> , 8, 1108-19                          | 3    | 51 |
| 94  | A Fast Algorithm for the Computation and Enumeration of Perfect Phylogenies. <i>SIAM Journal on Computing</i> , <b>1997</b> , 26, 1749-1763  | 1.1  | 49 |
| 93  | Tutorial on Computational Linguistic Phylogeny. <i>Language and Linguistics Compass</i> , <b>2008</b> , 2, 760-820   | 2    | 47 |
| 92  | A comparison of phylogenetic reconstruction methods on an Indo-European dataset. <i>Transactions of the Philological Society</i> , <b>2005</b> , 103, 171-192  | 0.3  | 46 |
| 91  | Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 10, S1                                       | 4.5  | 44 |
| 90  | Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. <i>Systematic Biology</i> , <b>2019</b> , 68, 281-297                       | 8.4  | 43 |

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| 89 | SuperFine: fast and accurate supertree estimation. <i>Systematic Biology</i> , <b>2012</b> , 61, 214-27  | 8.4  | 42 |
| 88 | Towards complete and error-free genome assemblies of all vertebrate species  |      | 38 |
| 87 | Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , <b>2015</b> , 349, 1460                                  | 33.3 | 37 |
| 86 | PASTA: Ultra-Large Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 177-191   | 0.9  | 37 |
| 85 | Multiple sequence alignment: a major challenge to large-scale phylogenetics. <i>PLOS Currents</i> , <b>2010</b> , 2, RRN1198   |      | 37 |
| 84 | The development and application of bioinformatics core competencies to improve bioinformatics training and education. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005772 | 5    | 37 |
| 83 | Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. <i>Bioinformatics</i> , <b>2019</b> , 35, 1613-1614                                       | 7.2  | 37 |
| 82 | FastSP: linear time calculation of alignment accuracy. <i>Bioinformatics</i> , <b>2011</b> , 27, 3250-8  | 7.2  | 36 |
| 81 | Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , <b>2017</b> , 66, 786-798   | 8.4  | 35 |
| 80 | The performance of coalescent-based species tree estimation methods under models of missing data. <i>BMC Genomics</i> , <b>2018</b> , 19, 286  | 4.5  | 33 |
| 79 | Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1743-1757                  | 8.3  | 31 |
| 78 | DACTAL: divide-and-conquer trees (almost) without alignments. <i>Bioinformatics</i> , <b>2012</b> , 28, i274-82  | 7.2  | 31 |
| 77 | BBCA: Improving the scalability of *BEAST using random binning. <i>BMC Genomics</i> , <b>2014</b> , 15 Suppl 6, S11  | 4.5  | 30 |
| 76 | Distance-based genome rearrangement phylogeny. <i>Journal of Molecular Evolution</i> , <b>2006</b> , 63, 473-83  | 3.1  | 30 |
| 75 | A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , <b>2018</b> , 105, 614-622   | 2.7  | 29 |
| 74 | An experimental study of Quartets MaxCut and other supertree methods. <i>Algorithms for Molecular Biology</i> , <b>2011</b> , 6, 7   | 1.8  | 28 |
| 73 | Fast and accurate methods for phylogenomic analyses. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 9, S4  | 3.6  | 28 |
| 72 | A simulation study comparing supertree and combined analysis methods using SMIDGen. <i>Algorithms for Molecular Biology</i> , <b>2010</b> , 5, 8                                     | 1.8  | 27 |

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|----|---|-----|----|
| 71 | An experimental study comparing linguistic phylogenetic reconstruction methods. <i>Diachronica</i> , <b>2013</b> , 30, 143-170  | 0.9 | 25 |
| 70 | Estimating optimal species trees from incomplete gene trees under deep coalescence. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 591-605   | 1.7 | 25 |
| 69 | Short quartet puzzling: a new quartet-based phylogeny reconstruction algorithm. <i>Journal of Computational Biology</i> , <b>2008</b> , 15, 91-103  | 1.7 | 25 |
| 68 | Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining. <i>Journal of Algorithms</i> , <b>2003</b> , 48, 173-193  |     | 24 |
| 67 | SVDquest: Improving SVDquartets species tree estimation using exact optimization within a constrained search space. <i>Molecular Phylogenetics and Evolution</i> , <b>2018</b> , 124, 122-136                           | 4.1 | 22 |
| 66 | Concatenation Analyses in the Presence of Incomplete Lineage Sorting. <i>PLOS Currents</i> , <b>2015</b> , 7,   |     | 22 |
| 65 | Disk covering methods improve phylogenomic analyses. <i>BMC Genomics</i> , <b>2014</b> , 15 Suppl 6, S7   | 4.5 | 21 |
| 64 | Pattern identification in biogeography. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2006</b> , 3, 334-46  | 3   | 20 |
| 63 | Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , <b>2018</b> , 14,  | 3.6 | 19 |
| 62 | Advances in phylogeny reconstruction from gene order and content data. <i>Methods in Enzymology</i> , <b>2005</b> , 395, 673-700  | 1.7 | 18 |
| 61 | Minimizing phylogenetic number to find good evolutionary trees. <i>Discrete Applied Mathematics</i> , <b>1996</b> , 71, 111-136   | 1   | 18 |
| 60 | Phylogenomics using Target-Restricted Assembly Resolves Intrageneric Relationships of Parasitic Lice (Phthiraptera: Columbicola). <i>Systematic Biology</i> , <b>2017</b> , 66, 896-911                                 | 8.4 | 17 |
| 59 | Better methods for solving parsimony and compatibility. <i>Journal of Computational Biology</i> , <b>1998</b> , 5, 391-407  | 1.7 | 17 |
| 58 | Computing the Local Consensus of Trees. <i>SIAM Journal on Computing</i> , <b>1998</b> , 27, 1695-1724  | 1.1 | 16 |
| 57 | HenQ teeth and whaleQ feet: generalized characters and their compatibility. <i>Journal of Computational Biology</i> , <b>1995</b> , 2, 515-25   | 1.7 | 16 |
| 56 | Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum Task Force of ISCBQ Education Committee). <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004943 <sup>5</sup> |     | 15 |
| 55 | FastMulRFS: fast and accurate species tree estimation under generic gene duplication and loss models. <i>Bioinformatics</i> , <b>2020</b> , 36, i57-i65   | 7.2 | 14 |
| 54 | FastRFS: fast and accurate Robinson-Foulds Supertrees using constrained exact optimization. <i>Bioinformatics</i> , <b>2017</b> , 33, 631-639   | 7.2 | 14 |

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|----|--|------|----|
| 53 | Gene tree parsimony for incomplete gene trees: addressing true biological loss. <i>Algorithms for Molecular Biology</i> , <b>2018</b> , 13, 1  | 1.8  | 13 |
| 52 | Evaluating Statistical Multiple Sequence Alignment in Comparison to Other Alignment Methods on Protein Data Sets. <i>Systematic Biology</i> , <b>2019</b> , 68, 396-411                                | 8.4  | 13 |
| 51 | High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , <b>2016</b> , 5, e90   | 18.9 | 12 |
| 50 | Large-scale multiple sequence alignment and tree estimation using SAT. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1079, 219-44  | 1.4  | 12 |
| 49 | Response to Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , <b>2015</b> , 350, 171  | 33.3 | 11 |
| 48 | MAGUS: Multiple sequence Alignment using Graph clUstering. <i>Bioinformatics</i> , <b>2021</b> , 37, 1666-1672   | 7.2  | 11 |
| 47 | Phylogeny Estimation Given Sequence Length Heterogeneity. <i>Systematic Biology</i> , <b>2021</b> , 70, 268-282  | 8.4  | 11 |
| 46 | Scaling statistical multiple sequence alignment to large datasets. <i>BMC Genomics</i> , <b>2016</b> , 17, 764   | 4.5  | 9  |
| 45 | Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. <i>Algorithms for Molecular Biology</i> , <b>2019</b> , 14, 14   | 1.8  | 9  |
| 44 | HIPPI: highly accurate protein family classification with ensembles of HMMs. <i>BMC Genomics</i> , <b>2016</b> , 17, 765   | 4.5  | 9  |
| 43 | TreeMerge: a new method for improving the scalability of species tree estimation methods. <i>Bioinformatics</i> , <b>2019</b> , 35, i417-i426  | 7.2  | 8  |
| 42 | Unidentifiable divergence times in rates-across-sites models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2004</b> , 1, 130-4  | 3    | 8  |
| 41 | Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Journal of Computational Biology</i> , <b>2021</b> , 28, 452-468   | 1.7  | 8  |
| 40 | Constrained incremental tree building: new absolute fast converging phylogeny estimation methods with improved scalability and accuracy. <i>Algorithms for Molecular Biology</i> , <b>2019</b> , 14, 2 | 1.8  | 7  |
| 39 | Analyzing the Order of Items in Manuscripts of The Canterbury Tales. <i>Computers and the Humanities</i> , <b>2003</b> , 37, 97-109  |      | 7  |
| 38 | TIPP2: metagenomic taxonomic profiling using phylogenetic markers. <i>Bioinformatics</i> , <b>2021</b> ,   | 7.2  | 7  |
| 37 | NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees. <i>Lecture Notes in Computer Science</i> , <b>2018</b> , 260-276                           | 0.9  | 7  |
| 36 | OCTAL: Optimal Completion of gene trees in polynomial time. <i>Algorithms for Molecular Biology</i> , <b>2018</b> , 13, 6  | 1.8  | 6  |

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|----|---|------|---|
| 35 | Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,                 | 11.5 | 6 |
| 34 | Divide-and-Conquer Tree Estimation: Opportunities and Challenges. <i>Computational Biology</i> , <b>2019</b> , 121-150                                    |      | 5 |
| 33 | Treelength optimization for phylogeny estimation. <i>PLoS ONE</i> , <b>2012</b> , 7, e33104   | 3.7  | 5 |
| 32 | Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 120-135 | 0.9  | 5 |
| 31 | Using INC Within Divide-and-Conquer Phylogeny Estimation. <i>Lecture Notes in Computer Science</i> , <b>2019</b> , 167-178                                | 0.9  | 4 |
| 30 | Co-citations in context: Disciplinary heterogeneity is relevant. <i>Quantitative Science Studies</i> , <b>2020</b> , 1, 264-276                           | 3.75 | 4 |
| 29 | PASTA for proteins. <i>Bioinformatics</i> , <b>2018</b> , 34, 3939-3941   | 7.2  | 4 |
| 28 | MAGUS+eHMMs: Improved Multiple Sequence Alignment Accuracy for Fragmentary Sequences. <i>Bioinformatics</i> , <b>2021</b> ,                               | 7.2  | 4 |
| 27 | FastMulRFS: Fast and accurate species tree estimation under generic gene duplication and loss models  |      | 4 |
| 26 | Constructing Evolutionary Trees in the Presence of Polymorphic Characters. <i>SIAM Journal on Computing</i> , <b>1999</b> , 29, 103-131                   | 1.1  | 3 |
| 25 | Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge  |      | 3 |
| 24 | Non-parametric correction of estimated gene trees using TRACTION. <i>Algorithms for Molecular Biology</i> , <b>2020</b> , 15, 1                           | 1.8  | 3 |
| 23 | Viewing Computer Science through Citation Analysis: Salton and Bergmark Redux. <i>Scientometrics</i> , <b>2020</b> , 125, 271-287                         | 3    | 3 |
| 22 | Unblended disjoint tree merging using GTM improves species tree estimation. <i>BMC Genomics</i> , <b>2020</b> , 21, 235                                   | 4.5  | 3 |
| 21 | Finding scientific communities in citation graphs: Articles and authors. <i>Quantitative Science Studies</i> , <b>2021</b> , 2, 184-203                   | 3.8  | 3 |
| 20 | SIESTA: enhancing searches for optimal supertrees and species trees. <i>BMC Genomics</i> , <b>2018</b> , 19, 252  | 4.5  | 2 |
| 19 | Re-evaluating Deep Neural Networks for Phylogeny Estimation: The Issue of Taxon Sampling.. <i>Journal of Computational Biology</i> , <b>2022</b> ,        | 1.7  | 2 |
| 18 | Polynomial-Time Statistical Estimation of Species Trees under Gene Duplication and Loss   |      | 2 |

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|----|--|------|---|
| 17 | Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , <b>2021</b> , 52,                             | 13.5 | 2 |
| 16 | Scalable and Accurate Phylogenetic Placement Using pplacer-XR. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 94-105   | 0.9  | 2 |
| 15 | An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 417  | 3.6  | 1 |
| 14 | Frequently cocited publications: Features and kinetics. <i>Quantitative Science Studies</i> , <b>2020</b> , 1, 1223-1241   | 3.8  | 1 |
| 13 | Advancing Divide-and-Conquer Phylogeny Estimation using Robinson-Foulds Supertrees   |      | 1 |
| 12 | Using Constrained-INC for Large-Scale Gene Tree and Species Tree Estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2-15 | 3    | 1 |
| 11 | Disjoint Tree Mergers for Large-Scale Maximum Likelihood Tree Estimation. <i>Algorithms</i> , <b>2021</b> , 14, 148  | 1.8  | 1 |
| 10 | Multiple Sequence Alignment for Large Heterogeneous Datasets Using SAT[PASTA, and UPP. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2231, 99-119                        | 1.4  | 1 |
| 9  | Profile Hidden Markov Models Are Not Identifiable. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 162-172                        | 3    | 1 |
| 8  | FASTRAL: Improving scalability of phylogenomic analysis. <i>Bioinformatics</i> , <b>2021</b> ,   | 7.2  | 1 |
| 7  | Revisiting Evaluation of Multiple Sequence Alignment Methods. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2231, 299-317  | 1.4  | 1 |
| 6  | Center-periphery structure in research communities. <i>Quantitative Science Studies</i> , 1-26   | 3.8  | 1 |
| 5  | Reconstructing Chromosomal Evolution. <i>SIAM Journal on Computing</i> , <b>2006</b> , 36, 99-131  | 1.1  | 0 |
| 4  | The Maximum Weight Trace Alignment Merging Problem. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 159-171   | 1.1  | 0 |
| 3  | Comparing Methods for Species Tree Estimation with Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 106-117                                 | 0.9  | 0 |
| 2  | New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation. <i>Lecture Notes in Computer Science</i> , <b>2019</b> , 3-21                                       | 0.9  |   |
| 1  | Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. <i>Algorithms for Molecular Biology</i> , <b>2021</b> , 16, 12                                    | 1.8  |   |