

Erfan Sayyari

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11488340/publications.pdf>

Version: 2024-02-01

12
papers

2,947
citations

840776

11
h-index

1199594

12
g-index

13
all docs

13
docs citations

13
times ranked

4192
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. BMC Bioinformatics, 2018, 19, 153. | 2.6 | 1,451 |
| 2 | Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. Molecular Biology and Evolution, 2016, 33, 1654-1668. | 8.9 | 650 |
| 3 | Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477. | 12.8 | 197 |
| 4 | ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. Lecture Notes in Computer Science, 2017, , 53-75. | 1.3 | 129 |
| 5 | Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. Genes, 2018, 9, 132. | 2.4 | 107 |
| 6 | DiscoVista: Interpretable visualizations of gene tree discordance. Molecular Phylogenetics and Evolution, 2018, 122, 110-115. | 2.7 | 106 |
| 7 | Multi-allele species reconstruction using ASTRAL. Molecular Phylogenetics and Evolution, 2019, 130, 286-296. | 2.7 | 106 |
| 8 | Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. Molecular Biology and Evolution, 2017, 34, 3279-3291. | 8.9 | 73 |
| 9 | Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. PLoS ONE, 2017, 12, e0182238. | 2.5 | 71 |
| 10 | Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. BMC Genomics, 2016, 17, 783. | 2.8 | 24 |
| 11 | More is neededâ€”Thousands of loci are required to elucidate the relationships of the â€˜flowers of the seaâ€™™ (Sabellida, Annelida). Molecular Phylogenetics and Evolution, 2020, 151, 106892. | 2.7 | 24 |
| 12 | TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. Bioinformatics, 2019, 35, i31-i40. | 4.1 | 9 |