

Shay Zakov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11162189/publications.pdf>

Version: 2024-02-01

10
papers

235
citations

1478280

6
h-index

1372474

10
g-index

11
all docs

11
docs citations

11
times ranked

452
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. PLoS Genetics, 2015, 11, e1005527. | 1.5 | 19 |
| 2 | Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Journal of Computational Biology, 2015, 22, 577-594. | 0.8 | 10 |
| 3 | Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Lecture Notes in Computer Science, 2014, , 400-417. | 1.0 | 1 |
| 4 | Unrooted unordered homeomorphic subtree alignment of RNA trees. Algorithms for Molecular Biology, 2013, 8, 13. | 0.3 | 6 |
| 5 | An algorithmic approach for breakage-fusion-bridge detection in tumor genomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5546-5551. | 3.3 | 53 |
| 6 | Efficient edit distance with duplications and contractions. Algorithms for Molecular Biology, 2013, 8, 27. | 0.3 | 6 |
| 7 | Have your spaghetti and eat it too: evolutionary algorithmics and post-evolutionary analysis. Genetic Programming and Evolvable Machines, 2011, 12, 121-160. | 1.5 | 2 |
| 8 | Reducing the worst case running times of a family of RNA and CFG problems, using Valiant's approach. Algorithms for Molecular Biology, 2011, 6, 20. | 0.3 | 13 |
| 9 | Sparse RNA folding: Time and space efficient algorithms. Journal of Discrete Algorithms, 2011, 9, 12-31. | 0.7 | 45 |
| 10 | Rich Parameterization Improves RNA Structure Prediction. Journal of Computational Biology, 2011, 18, 1525-1542. | 0.8 | 80 |