## Shay Zakov

## List of Publications by Year in descending order

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

Version: 2024-02-01

|          |                | 1478505      | 1372567        |  |
|----------|----------------|--------------|----------------|--|
| 10       | 235            | 6            | 10             |  |
| papers   | citations      | h-index      | g-index        |  |
|          |                |              |                |  |
|          |                |              |                |  |
|          |                |              |                |  |
| 11       | 11             | 11           | 452            |  |
| all docs | docs citations | times ranked | citing authors |  |
|          |                |              |                |  |

| #  | Article                                                                                                                                                                               | IF  | CITATIONS |
|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 1  | Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. PLoS Genetics, 2015, 11, e1005527.                                                           | 3.5 | 19        |
| 2  | Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Journal of Computational Biology, 2015, 22, 577-594.                                                    | 1.6 | 10        |
| 3  | Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Lecture Notes in Computer Science, 2014, , 400-417.                                                     | 1.3 | 1         |
| 4  | Unrooted unordered homeomorphic subtree alignment of RNA trees. Algorithms for Molecular Biology, 2013, 8, 13.                                                                        | 1.2 | 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. | 7.1 | 53        |
| 6  | Efficient edit distance with duplications and contractions. Algorithms for Molecular Biology, 2013, 8, 27.                                                                            | 1.2 | 6         |
| 7  | Have your spaghetti and eat it too: evolutionary algorithmics and post-evolutionary analysis. Genetic Programming and Evolvable Machines, 2011, 12, 121-160.                          | 2.2 | 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.                                   | 1.2 | 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.                                                                       | 1.6 | 80        |