

# Layla Oesper

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/502493/publications.pdf>

Version: 2024-02-01

14  
papers

856  
citations

1307594

7  
h-index

1372567

10  
g-index

14  
all docs

14  
docs citations

14  
times ranked

1413  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | GraPhyC: Using Consensus to Infer Tumor Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 465-478.      | 3.0 | 5         |
| 2  | Emerging Topics in Cancer Evolution. , 2021, , .  |     | 2         |
| 3  | Distance measures for tumor evolutionary trees. Bioinformatics, 2020, 36, 2090-2097.  | 4.1 | 26        |
| 4  | Parameter, noise, and tree topology effects in tumor phylogeny inference. BMC Medical Genomics, 2019, 12, 184.                                | 1.5 | 2         |
| 5  | Identifying simultaneous rearrangements in cancer genomes. Bioinformatics, 2018, 34, 346-352.   | 4.1 | 4         |
| 6  | Examining Tumor Phylogeny Inference in Noisy Sequencing Data. , 2018, , .   |     | 2         |
| 7  | A Consensus Approach to Infer Tumor Evolutionary Histories. , 2018, , .   |     | 24        |
| 8  | Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. Cell Systems, 2016, 3, 43-53.                       | 6.2 | 140       |
| 9  | Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. Bioinformatics, 2015, 31, i62-i70.                    | 4.1 | 194       |
| 10 | Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. Genome Medicine, 2014, 6, 5. | 8.2 | 186       |
| 11 | Quantifying tumor heterogeneity in whole-genome and whole-exome sequencing data. Bioinformatics, 2014, 30, 3532-3540.                         | 4.1 | 115       |
| 12 | Workshop: Reconstructing the organization of cancer genomes. , 2013, , .  |     | 0         |
| 13 | Reconstructing cancer genomes from paired-end sequencing data. BMC Bioinformatics, 2012, 13, S10.   | 2.6 | 36        |
| 14 | WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. Source Code for Biology and Medicine, 2011, 6, 7.              | 1.7 | 120       |