

# Mark D M Leiserson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2890340/publications.pdf>

Version: 2024-02-01

24  
papers

5,737  
citations

623574

14  
h-index

610775

24  
g-index

26  
all docs

26  
docs citations

26  
times ranked

12908  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | <scp>ScalpelSig</scp> Designs Targeted Genomic Panels from Data to Detect Activity of Mutational Signatures. <i>Journal of Computational Biology</i> , 2022, 29, 56-73.   | 0.8 | 1         |
| 2  | SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. <i>Cell Genomics</i> , 2022, 2, 100099.                  | 3.0 | 2         |
| 3  | Mutational Signatures: From Methods to Mechanisms. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 189-206.  | 2.8 | 19        |
| 4  | A data-driven approach for constructing mutation categories for mutational signature analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1009542.                    | 1.5 | 1         |
| 5  | A mixture model for signature discovery from sparse mutation data. <i>Genome Medicine</i> , 2021, 13, 173.  | 3.6 | 8         |
| 6  | A systematic genome-wide mapping of oncogenic mutation selection during CRISPR-Cas9 genome editing. <i>Nature Communications</i> , 2021, 12, 6512.                        | 5.8 | 24        |
| 7  | Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. <i>Genome Medicine</i> , 2020, 12, 52.                           | 3.6 | 20        |
| 8  | A Sticky Multinomial Mixture Model of Strand-Coordinated Mutational Processes in Cancer. <i>IScience</i> , 2020, 23, 100900.  | 1.9 | 5         |
| 9  | Matrix (factorization) reloaded: flexible methods for imputing genetic interactions with cross-species and side information. <i>Bioinformatics</i> , 2020, 36, i866-i874. | 1.8 | 1         |
| 10 | Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. <i>Genome Medicine</i> , 2019, 11, 49.                                      | 3.6 | 22        |
| 11 | Modeling clinical and molecular covariates of mutational process activity in cancer. <i>Bioinformatics</i> , 2019, 35, i492-i500.   | 1.8 | 15        |
| 12 | Functional protein representations from biological networks enable diverse cross-species inference. <i>Nucleic Acids Research</i> , 2019, 47, e51-e51.                    | 6.5 | 23        |
| 13 | Criticality in tumor evolution and clinical outcome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11101-E11110.   | 3.3 | 23        |
| 14 | A multifactorial model of T cell expansion and durable clinical benefit in response to a PD-L1 inhibitor. <i>PLoS ONE</i> , 2018, 13, e0208422.                           | 1.1 | 14        |
| 15 | Hierarchical HotNet: identifying hierarchies of altered subnetworks. <i>Bioinformatics</i> , 2018, 34, i972-i980.   | 1.8 | 102       |
| 16 | Precision Oncology: The Road Ahead. <i>Trends in Molecular Medicine</i> , 2017, 23, 874-898.  | 3.5 | 131       |
| 17 | Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. <i>Nature Genetics</i> , 2016, 48, 106-108.   | 9.4 | 2         |
| 18 | CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. <i>Genome Biology</i> , 2015, 16, 160.                                | 3.8 | 182       |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 19 | MAGI: visualization and collaborative annotation of genomic aberrations. Nature Methods, 2015, 12, 483-484.  | 9.0  | 25        |
| 20 | Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.                            | 5.8  | 243       |
| 21 | Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114. | 9.4  | 830       |
| 22 | Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.  | 5.8  | 253       |
| 23 | Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.  | 13.7 | 3,695     |
| 24 | Network analysis of GWAS data. Current Opinion in Genetics and Development, 2013, 23, 602-610.   | 1.5  | 95        |