

# Nimrod D Rubinstein

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2767945/publications.pdf>

Version: 2024-02-01

20  
papers

1,785  
citations

516710

16  
h-index

713466

21  
g-index

25  
all docs

25  
docs citations

25  
times ranked

2979  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Transitions in paternal social status predict patterns of offspring growth and metabolic transcription. <i>Molecular Ecology</i> , 2020, 29, 624-638.   | 3.9  | 6         |
| 2  | Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging. <i>Genome Research</i> , 2019, 29, 2088-2103.  | 5.5  | 132       |
| 3  | Single-cell transcriptomics of the naked mole-rat reveals unexpected features of mammalian immunity. <i>PLoS Biology</i> , 2019, 17, e3000528.  | 5.6  | 80        |
| 4  | A window into extreme longevity; the circulating metabolomic signature of the naked mole-rat, a mammal that shows negligible senescence. <i>GeroScience</i> , 2018, 40, 105-121.                      | 4.6  | 59        |
| 5  | Functional circuit architecture underlying parental behaviour. <i>Nature</i> , 2018, 556, 326-331.  | 27.8 | 290       |
| 6  | The Multipartite Mitochondrial Genome of <i>Enteromyxum leei</i> (Myxozoa): Eight Fast-Evolving Megacircles. <i>Molecular Biology and Evolution</i> , 2017, 34, 1551-1556.                            | 8.9  | 22        |
| 7  | Benign and tumor parenchyma metabolomic profiles affect compensatory renal growth in renal cell carcinoma surgical patients. <i>PLoS ONE</i> , 2017, 12, e0180350.                                    | 2.5  | 2         |
| 8  | New Perspectives on Genomic Imprinting, an Essential and Multifaceted Mode of Epigenetic Control in the Developing and Adult Brain. <i>Annual Review of Neuroscience</i> , 2016, 39, 347-384.         | 10.7 | 86        |
| 9  | Regulation of alternative splicing at the single-cell level. <i>Molecular Systems Biology</i> , 2015, 11, 845.  | 7.2  | 17        |
| 10 | Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. <i>ELife</i> , 2015, 4, e07860.   | 6.0  | 75        |
| 11 | Genomic insights into the evolutionary origin of Myxozoa within Cnidaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14912-14917.            | 7.1  | 193       |
| 12 | Deep Sequencing of Mixed Total DNA without Barcodes Allows Efficient Assembly of Highly Plastic Ascidian Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 1185-1199.             | 2.5  | 56        |
| 13 | The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.  | 7.6  | 188       |
| 14 | Evolutionary Models Accounting for Layers of Selection in Protein-Coding Genes and their Impact on the Inference of Positive Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3297-3308. | 8.9  | 54        |
| 15 | The Operonic Location of Auto-transcriptional Repressors Is Highly Conserved in Bacteria. <i>Molecular Biology and Evolution</i> , 2011, 28, 3309-3318.   | 8.9  | 6         |
| 16 | A machine-learning approach for predicting B-cell epitopes. <i>Molecular Immunology</i> , 2009, 46, 840-847.  | 2.2  | 108       |
| 17 | Computational characterization of B-cell epitopes. <i>Molecular Immunology</i> , 2008, 45, 3477-3489.   | 2.2  | 194       |
| 18 | Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. <i>PLoS Computational Biology</i> , 2008, 4, e1000214.   | 3.2  | 30        |

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|----|--|------|-----------|
| 19 | Epitope mapping using combinatorial phage-display libraries: a graph-based algorithm. Nucleic Acids Research, 2007, 35, 69-78.   | 14.5 | 102       |
| 20 | Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. Proteins: Structure, Function and Bioinformatics, 2007, 68, 294-304. | 2.6  | 82        |