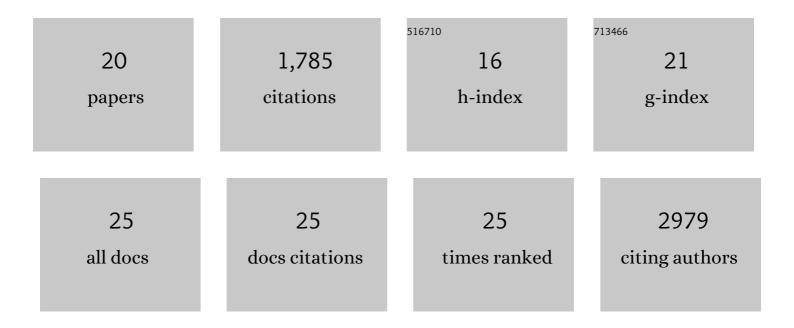
## Nimrod D Rubinstein

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2767945/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Functional circuit architecture underlying parental behaviour. Nature, 2018, 556, 326-331.	27.8	290
2	Computational characterization of B-cell epitopes. Molecular Immunology, 2008, 45, 3477-3489.	2.2	194
3	Genomic insights into the evolutionary origin of Myxozoa within Cnidaria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14912-14917.	7.1	193
4	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
5	Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging. Genome Research, 2019, 29, 2088-2103.	5.5	132
6	A machine-learning approach for predicting B-cell epitopes. Molecular Immunology, 2009, 46, 840-847.	2.2	108
7	Epitope mapping using combinatorial phage-display libraries: a graph-based algorithm. Nucleic Acids Research, 2007, 35, 69-78.	14.5	102
8	New Perspectives on Genomic Imprinting, an Essential and Multifaceted Mode of Epigenetic Control in the Developing and Adult Brain. Annual Review of Neuroscience, 2016, 39, 347-384.	10.7	86
9	Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. Proteins: Structure, Function and Bioinformatics, 2007, 68, 294-304.	2.6	82
10	Single-cell transcriptomics of the naked mole-rat reveals unexpected features of mammalian immunity. PLoS Biology, 2019, 17, e3000528.	5.6	80
11	Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. ELife, 2015, 4, e07860.	6.0	75
12	A window into extreme longevity; the circulating metabolomic signature of the naked mole-rat, a mammal that shows negligible senescence. GeroScience, 2018, 40, 105-121.	4.6	59
13	Deep Sequencing of Mixed Total DNA without Barcodes Allows Efficient Assembly of Highly Plastic Ascidian Mitochondrial Genomes. Genome Biology and Evolution, 2013, 5, 1185-1199.	2.5	56
14	Evolutionary Models Accounting for Layers of Selection in Protein-Coding Genes and their Impact on the Inference of Positive Selection. Molecular Biology and Evolution, 2011, 28, 3297-3308.	8.9	54
15	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. PLoS Computational Biology, 2008, 4, e1000214.	3.2	30
16	The Multipartite Mitochondrial Genome of Enteromyxum leei (Myxozoa): Eight Fast-Evolving Megacircles. Molecular Biology and Evolution, 2017, 34, 1551-1556.	8.9	22
17	Regulation of alternative splicing at the singleâ€cell level. Molecular Systems Biology, 2015, 11, 845.	7.2	17
18	The Operonic Location of Auto-transcriptional Repressors Is Highly Conserved in Bacteria. Molecular Biology and Evolution, 2011, 28, 3309-3318.	8.9	6

#	Article	IF	CITATIONS
19	Transitions in paternal social status predict patterns of offspring growth and metabolic transcription. Molecular Ecology, 2020, 29, 624-638.	3.9	6
20	Benign and tumor parenchyma metabolomic profiles affect compensatory renal growth in renal cell carcinoma surgical patients. PLoS ONE, 2017, 12, e0180350.	2.5	2