

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

516215

16
h-index

713013

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.	2.0	6
2	Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging. <i>Genome Research</i> , 2019, 29, 2088-2103.	2.4	132
3	Single-cell transcriptomics of the naked mole-rat reveals unexpected features of mammalian immunity. <i>PLoS Biology</i> , 2019, 17, e3000528.	2.6	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.	2.1	59
5	Functional circuit architecture underlying parental behaviour. <i>Nature</i> , 2018, 556, 326-331.	13.7	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.	3.5	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.	1.1	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.	5.0	86
9	Regulation of alternative splicing at the single-cell level. <i>Molecular Systems Biology</i> , 2015, 11, 845.	3.2	17
10	Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. <i>ELife</i> , 2015, 4, e07860.	2.8	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.	3.3	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.	1.1	56
13	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	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.	3.5	54
15	The Operonic Location of Auto-transcriptional Repressors Is Highly Conserved in Bacteria. <i>Molecular Biology and Evolution</i> , 2011, 28, 3309-3318.	3.5	6
16	A machine-learning approach for predicting B-cell epitopes. <i>Molecular Immunology</i> , 2009, 46, 840-847.	1.0	108
17	Computational characterization of B-cell epitopes. <i>Molecular Immunology</i> , 2008, 45, 3477-3489.	1.0	194
18	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. <i>PLoS Computational Biology</i> , 2008, 4, e1000214.	1.5	30

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19	Epitope mapping using combinatorial phage-display libraries: a graph-based algorithm. <i>Nucleic Acids Research</i> , 2007, 35, 69-78.	6.5	102
20	Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 294-304.	1.5	82