

# Nir Atias

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10500813/publications.pdf>

Version: 2024-02-01

12  
papers

612  
citations

840585

11  
h-index

1199470

12  
g-index

12  
all docs

12  
docs citations

12  
times ranked

1082  
citing authors

#	ARTICLE	IF	CITATIONS
1	An Algorithmic Framework for Predicting Side Effects of Drugs. <i>Journal of Computational Biology</i> , 2011, 18, 207-218.	0.8	122
2	Alternative Splicing Regulates Biogenesis of miRNAs Located across Exon-Intron Junctions. <i>Molecular Cell</i> , 2013, 50, 869-881.	4.5	83
3	Metabolic Network Prediction of Drug Side Effects. <i>Cell Systems</i> , 2016, 2, 209-213.	2.9	81
4	ANAT: A Tool for Constructing and Analyzing Functional Protein Networks. <i>Science Signaling</i> , 2011, 4, p11.	1.6	78
5	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020, 32, 108050.	2.9	64
6	A network-based analysis of colon cancer splicing changes reveals a tumorigenesis-favoring regulatory pathway emanating from ELK1. <i>Genome Research</i> , 2016, 26, 541-553.	2.4	45
7	iPoint: an integer programming based algorithm for inferring protein subnetworks. <i>Molecular BioSystems</i> , 2013, 9, 1662.	2.9	43
8	Regulation of Sec16 levels and dynamics links proliferation and secretion. <i>Journal of Cell Science</i> , 2015, 128, 670-82.	1.2	39
9	Systematic identification and correction of annotation errors in the genetic interaction map of <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2016, 44, e50-e50.	6.5	19
10	Pathway-based analysis of genomic variation data. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 622-626.	1.5	16
11	ANAT 2.0: reconstructing functional protein subnetworks. <i>BMC Bioinformatics</i> , 2017, 18, 495.	1.2	12
12	Experimental design schemes for learning Boolean network models. <i>Bioinformatics</i> , 2014, 30, i445-i452.	1.8	10