

# Daniel E Carlin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/36389/publications.pdf>

Version: 2024-02-01

13  
papers

870  
citations

1040056

9  
h-index

1372567

10  
g-index

13  
all docs

13  
docs citations

13  
times ranked

1907  
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic Evaluation of Molecular Networks for Discovery of Disease Genes. <i>Cell Systems</i> , 2018, 6, 484-495.e5.	6.2	215
2	Phosphoproteome Integration Reveals Patient-Specific Networks in Prostate Cancer. <i>Cell</i> , 2016, 166, 1041-1054.	28.9	206
3	Discovering causal pathways linking genomic events to transcriptional states using Tied Diffusion Through Interacting Events (TieDIE). <i>Bioinformatics</i> , 2013, 29, 2757-2764.	4.1	189
4	Network propagation in the cytoscape cyberinfrastructure. <i>PLoS Computational Biology</i> , 2017, 13, e1005598.	3.2	73
5	The Emerging Potential for Network Analysis to Inform Precision Cancer Medicine. <i>Journal of Molecular Biology</i> , 2018, 430, 2875-2899.	4.2	72
6	Unveiling Complexity and Multipotentiality of Early Heart Fields. <i>Circulation Research</i> , 2021, 129, 474-487.	4.5	50
7	A Fast and Flexible Framework for Network-Assisted Genomic Association. <i>IScience</i> , 2019, 16, 155-161.	4.1	31
8	pyNBS: a Python implementation for network-based stratification of tumor mutations. <i>Bioinformatics</i> , 2018, 34, 2859-2861.	4.1	19
9	Prophetic Granger Causality to infer gene regulatory networks. <i>PLoS ONE</i> , 2017, 12, e0170340.	2.5	10
10	Strategies for Network GWAS Evaluated Using Classroom Crowd Science. <i>Cell Systems</i> , 2019, 8, 275-280.	6.2	5
11	A multi-tool recipe to identify regions of protein-DNA binding and their influence on associated gene expression. <i>F1000Research</i> , 2017, 6, 784.	1.6	0
12	A multi-tool recipe to identify regions of protein-DNA binding and their influence on associated gene expression. <i>F1000Research</i> , 2017, 6, 784.	1.6	0
13	A unified GenomeSpace recipe to identify essential genes and associated subnetworks from Genome-Scale CRISPR-Cas9 knockout screens. <i>F1000Research</i> , 0, 7, 1636.	1.6	0