

# Damian Wã³jtowicz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4442373/publications.pdf>

Version: 2024-02-01

32  
papers

1,457  
citations

623574

14  
h-index

477173

29  
g-index

39  
all docs

39  
docs citations

39  
times ranked

2396  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription-dependent dynamic supercoiling is a short-range genomic force. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 396-403.	3.6	270
2	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	13.5	211
3	Permanganate/S1 Nuclease Footprinting Reveals Non-B DNA Structures with Regulatory Potential across a Mammalian Genome. <i>Cell Systems</i> , 2017, 4, 344-356.e7.	2.9	169
4	Global Regulation of Promoter Melting in Naive Lymphocytes. <i>Cell</i> , 2013, 153, 988-999.	13.5	145
5	Structural and Functional Characterization of the LPS Transporter LptDE from Gram-Negative Pathogens. <i>Structure</i> , 2016, 24, 965-976.	1.6	110
6	Detecting presence of mutational signatures in cancer with confidence. <i>Bioinformatics</i> , 2018, 34, 330-337.	1.8	86
7	Crystal Structures of the Outer Membrane Domain of Intimin and Invasin from Enterohemorrhagic <i>E. coli</i> and Enteropathogenic <i>Y. pseudotuberculosis</i> . <i>Structure</i> , 2012, 20, 1233-1243.	1.6	82
8	DNA Break Mapping Reveals Topoisomerase II Activity Genome-Wide. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13111-13122.	1.8	70
9	The genome-wide distribution of non-B DNA motifs is shaped by operon structure and suggests the transcriptional importance of non-B DNA structures in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2013, 41, 5965-5977.	6.5	55
10	Potential non-B DNA regions in the human genome are associated with higher rates of nucleotide mutation and expression variation. <i>Nucleic Acids Research</i> , 2014, 42, 12367-12379.	6.5	45
11	BeWith: A Between-Within method to discover relationships between cancer modules via integrated analysis of mutual exclusivity, co-occurrence and functional interactions. <i>PLoS Computational Biology</i> , 2017, 13, e1005695.	1.5	38
12	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. <i>Genome Medicine</i> , 2019, 11, 49.	3.6	22
13	Teasing Apart Translational and Transcriptional Components of Stochastic Variations in Eukaryotic Gene Expression. <i>PLoS Computational Biology</i> , 2012, 8, e1002644.	1.5	21
14	Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. <i>Genome Medicine</i> , 2020, 12, 52.	3.6	20
15	Mutational Signatures: From Methods to Mechanisms. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 189-206.	2.8	19
16	A DISCRETE MODEL OF EVOLUTION OF SMALL PARALOG FAMILIES. <i>Mathematical Models and Methods in Applied Sciences</i> , 2007, 17, 933-955.	1.7	12
17	In Vivo Chemical Probing for G-Quadruplex Formation. <i>Methods in Molecular Biology</i> , 2019, 2035, 369-382.	0.4	12
18	A model for the evolution of paralog families in genomes. <i>Journal of Mathematical Biology</i> , 2006, 53, 759-770.	0.8	11

#	ARTICLE	IF	CITATIONS
19	Dosage-Dependent Expression Variation Suppressed on the <i>Drosophila</i> Male X Chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 587-598.	0.8	9
20	Evolution of Gene Families Based on Gene Duplication, Loss, Accumulated Change, and Innovation. <i>Journal of Computational Biology</i> , 2007, 14, 479-495.	0.8	8
21	Mapping DNA Breaks by Next-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1672, 155-166.	0.4	6
22	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. <i>Cell Systems</i> , 2021, 12, 994-1003.e4.	2.9	6
23	A Case Study of Genome Evolution: From Continuous to Discrete Time Model. <i>Lecture Notes in Computer Science</i> , 2004, , 1-24.	1.0	5
24	Identifying Drug Sensitivity Subnetworks with NETPHIX. <i>IScience</i> , 2020, 23, 101619.	1.9	5
25	A Sticky Multinomial Mixture Model of Strand-Coordinated Mutational Processes in Cancer. <i>IScience</i> , 2020, 23, 100900.	1.9	5
26	On Genome Evolution with Innovation. <i>Lecture Notes in Computer Science</i> , 2006, , 801-811.	1.0	3
27	Ups and Downs of Poised RNA Polymerase II in B-Cells. <i>PLoS Computational Biology</i> , 2016, 12, e1004821.	1.5	2
28	DNA Repair Footprint Uncovers Contribution of DNA Repair Mechanism to Mutational Signatures. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 262-273.	0.7	2
29	MODELING CELL HETEROGENEITY: FROM SINGLE-CELL VARIATIONS TO MIXED CELLS. , 2012, , .		1
30	Correlated rigid modes in protein families. <i>Physical Biology</i> , 2016, 13, 025003.	0.8	1
31	Almost FPRAS for Lattice Models of Protein Folding. <i>Lecture Notes in Computer Science</i> , 2005, , 534-544.	1.0	0
32	A Sticky Multinomial Mixture Model of Strand-Coordinated Mutational Processes in Cancer. <i>Lecture Notes in Computer Science</i> , 2019, , 243-255.	1.0	0