

# Mariusz Nowacki

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

3,339  
citations

236612

25  
h-index

276539

41  
g-index

50  
all docs

50  
docs citations

50  
times ranked

2914  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early developmental, meiosis-specific proteins Spo11, Msh4-1, and Msh5 Affect subsequent genome reorganization in <i>Paramecium tetraurelia</i> . <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022, 1869, 119239.	1.9	6
2	Identification of novel, functional, long noncoding RNAs involved in programmed, large-scale genome rearrangements. <i>Rna</i> , 2022, 28, 1110-1127.	1.6	1
3	Programmed genome rearrangements in ciliates. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 4615-4629.	2.4	50
4	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , 2020, 17, 481-494.	9.0	97
5	Roles of Noncoding RNAs in Ciliate Genome Architecture. <i>Journal of Molecular Biology</i> , 2020, 432, 4186-4198.	2.0	19
6	Evolutionary origins and impacts of genome architecture in ciliates. <i>Annals of the New York Academy of Sciences</i> , 2019, 1447, 110-118.	1.8	18
7	From Cellular RNA to Smart RNA: Multiple Roles of RNA in Genome Stability and Beyond. <i>Chemical Reviews</i> , 2018, 118, 4365-4403.	23.0	63
8	Dicer-like Enzymes with Sequence Cleavage Preferences. <i>Cell</i> , 2018, 173, 234-247.e7.	13.5	56
9	RNA-mediated transgenerational inheritance in ciliates and plants. <i>Chromosoma</i> , 2018, 127, 19-27.	1.0	14
10	Determination of the presence of 5-methylcytosine in <i>Paramecium tetraurelia</i> . <i>PLoS ONE</i> , 2018, 13, e0206667.	1.1	10
11	A mating-type mutagenesis screen identifies a zinc-finger protein required for specific DNA excision events in <i>Paramecium</i> . <i>Nucleic Acids Research</i> , 2018, 46, 9550-9562.	6.5	8
12	Six domesticated PiggyBac transposases together carry out programmed DNA elimination in <i>Paramecium</i> . <i>ELife</i> , 2018, 7, .	2.8	44
13	Chromosome fusions triggered by noncoding RNA. <i>RNA Biology</i> , 2017, 14, 620-631.	1.5	9
14	Circular Concatemers of Ultra-Short DNA Segments Produce Regulatory RNAs. <i>Cell</i> , 2017, 168, 990-999.e7.	13.5	45
15	Necessity Is the Mother of Invention: Ciliates, Transposons, and Transgenerational Inheritance. <i>Trends in Genetics</i> , 2017, 33, 197-207.	2.9	28
16	The Macronuclear Genome of <i>Stentor coeruleus</i> Reveals Tiny Introns in a Giant Cell. <i>Current Biology</i> , 2017, 27, 569-575.	1.8	105
17	Two Sets of Piwi Proteins Are Involved in Distinct sRNA Pathways Leading to Elimination of Germline-Specific DNA. <i>Cell Reports</i> , 2017, 20, 505-520.	2.9	37
18	Genetic Codes with No Dedicated Stop Codon: Context-Dependent Translation Termination. <i>Cell</i> , 2016, 166, 691-702.	13.5	155

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19	RNA-Guided Genome Editing. , 2016, , 35-50.		0
20	The eukaryotic way to defend and edit genomes by sRNA-targeted DNA deletion. Annals of the New York Academy of Sciences, 2015, 1341, 106-114.	1.8	13
21	Pdsg1 and Pdsg2, Novel Proteins Involved in Developmental Genome Remodelling in Paramecium. PLoS ONE, 2014, 9, e112899.	1.1	13
22	The Draft Assembly of the Radically Organized Stylonychia lemnae Macronuclear Genome. Genome Biology and Evolution, 2014, 6, 1707-1723.	1.1	58
23	Genome-wide analysis of genetic and epigenetic control of programmed DNA deletion. Nucleic Acids Research, 2014, 42, 8970-8983.	6.5	37
24	<i>Paramecium tetraurelia</i> chromatin assembly factor-1-like protein PtCAF-1 is involved in RNA-mediated control of DNA elimination. Nucleic Acids Research, 2014, 42, 11952-11964.	6.5	26
25	Functional Diversification of Dicer-like Proteins and Small RNAs Required for Genome Sculpting. Developmental Cell, 2014, 28, 174-188.	3.1	87
26	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	1.2	24
27	RNA-dependent genome processing during nuclear differentiation: the model systems of stichotrichous ciliates. Epigenomics, 2013, 5, 229-236.	1.0	3
28	The Oxytricha trifallax Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. PLoS Biology, 2013, 11, e1001473.	2.6	198
29	The Paramecium Germline Genome Provides a Niche for Intragenic Parasitic DNA: Evolutionary Dynamics of Internal Eliminated Sequences. PLoS Genetics, 2012, 8, e1002984.	1.5	154
30	The Oxytricha trifallax Mitochondrial Genome. Genome Biology and Evolution, 2012, 4, 136-154.	1.1	52
31	Piwi-Interacting RNAs Protect DNA against Loss during Oxytricha Genome Rearrangement. Cell, 2012, 151, 1243-1255.	13.5	133
32	RNA-Mediated Epigenetic Programming of Genome Rearrangements. Annual Review of Genomics and Human Genetics, 2011, 12, 367-389.	2.5	66
33	RNA-mediated epigenetic regulation of DNA copy number. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22140-22144.	3.3	66
34	Silencing-associated and meiosis-specific small RNA pathways in Paramecium tetraurelia. Nucleic Acids Research, 2009, 37, 903-915.	6.5	120
35	Epigenetic inheritance in ciliates. Current Opinion in Microbiology, 2009, 12, 638-643.	2.3	55
36	A Functional Role for Transposases in a Large Eukaryotic Genome. Science, 2009, 324, 935-938.	6.0	120

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37	RNA-mediated epigenetic programming of a genome-rearrangement pathway. <i>Nature</i> , 2008, 451, 153-158.	13.7	261
38	Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362.	13.7	200
39	Global trends of whole-genome duplications revealed by the ciliate <i>Paramecium tetraurelia</i> . <i>Nature</i> , 2006, 444, 171-178.	13.7	744
40	Nowa1p and Nowa2p: Novel Putative RNA Binding Proteins Involved in trans-Nuclear Crosstalk in <i>Paramecium tetraurelia</i> . <i>Current Biology</i> , 2005, 15, 1616-1628.	1.8	73
41	High Coding Density on the Largest <i>Paramecium tetraurelia</i> Somatic Chromosome. <i>Current Biology</i> , 2004, 14, 1397-1404.	1.8	52
42	Identification and analysis of functional associations among natural eukaryotic genome editing components. <i>F1000Research</i> , 0, 6, 1374.	0.8	16