

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	Global trends of whole-genome duplications revealed by the ciliate <i>Paramecium tetraurelia</i> . <i>Nature</i> , 2006, 444, 171-178.	13.7	744
2	RNA-mediated epigenetic programming of a genome-rearrangement pathway. <i>Nature</i> , 2008, 451, 153-158.	13.7	261
3	Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362.	13.7	200
4	The <i>Oxytricha trifallax</i> Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. <i>PLoS Biology</i> , 2013, 11, e1001473.	2.6	198
5	Genetic Codes with No Dedicated Stop Codon: Context-Dependent Translation Termination. <i>Cell</i> , 2016, 166, 691-702.	13.5	155
6	The <i>Paramecium</i> Germline Genome Provides a Niche for Intragenic Parasitic DNA: Evolutionary Dynamics of Internal Eliminated Sequences. <i>PLoS Genetics</i> , 2012, 8, e1002984.	1.5	154
7	Piwi-Interacting RNAs Protect DNA against Loss during <i>Oxytricha</i> Genome Rearrangement. <i>Cell</i> , 2012, 151, 1243-1255.	13.5	133
8	Silencing-associated and meiosis-specific small RNA pathways in <i>Paramecium tetraurelia</i> . <i>Nucleic Acids Research</i> , 2009, 37, 903-915.	6.5	120
9	A Functional Role for Transposases in a Large Eukaryotic Genome. <i>Science</i> , 2009, 324, 935-938.	6.0	120
10	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
11	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , 2020, 17, 481-494.	9.0	97
12	Functional Diversification of Dicer-like Proteins and Small RNAs Required for Genome Sculpting. <i>Developmental Cell</i> , 2014, 28, 174-188.	3.1	87
13	<i>Nowa1p</i> and <i>Nowa2p</i> : 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
14	RNA-mediated epigenetic regulation of DNA copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22140-22144.	3.3	66
15	RNA-Mediated Epigenetic Programming of Genome Rearrangements. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 367-389.	2.5	66
16	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
17	The Draft Assembly of the Radically Organized <i>Stylonychia lemnae</i> Macronuclear Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 1707-1723.	1.1	58
18	Dicer-like Enzymes with Sequence Cleavage Preferences. <i>Cell</i> , 2018, 173, 234-247.e7.	13.5	56

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19	Epigenetic inheritance in ciliates. <i>Current Opinion in Microbiology</i> , 2009, 12, 638-643.	2.3	55
20	High Coding Density on the Largest <i>Paramecium tetraurelia</i> Somatic Chromosome. <i>Current Biology</i> , 2004, 14, 1397-1404.	1.8	52
21	The <i>Oxytricha trifallax</i> Mitochondrial Genome. <i>Genome Biology and Evolution</i> , 2012, 4, 136-154.	1.1	52
22	Programmed genome rearrangements in ciliates. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 4615-4629.	2.4	50
23	Circular Concatemers of Ultra-Short DNA Segments Produce Regulatory RNAs. <i>Cell</i> , 2017, 168, 990-999.e7.	13.5	45
24	Six domesticated PiggyBac transposases together carry out programmed DNA elimination in <i>Paramecium</i> . <i>ELife</i> , 2018, 7, .	2.8	44
25	Genome-wide analysis of genetic and epigenetic control of programmed DNA deletion. <i>Nucleic Acids Research</i> , 2014, 42, 8970-8983.	6.5	37
26	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
27	Necessity Is the Mother of Invention: Ciliates, Transposons, and Transgenerational Inheritance. <i>Trends in Genetics</i> , 2017, 33, 197-207.	2.9	28
28	<i>Paramecium tetraurelia</i> chromatin assembly factor-1-like protein PtCAF-1 is involved in RNA-mediated control of DNA elimination. <i>Nucleic Acids Research</i> , 2014, 42, 11952-11964.	6.5	26
29	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	1.2	24
30	Roles of Noncoding RNAs in Ciliate Genome Architecture. <i>Journal of Molecular Biology</i> , 2020, 432, 4186-4198.	2.0	19
31	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
32	Identification and analysis of functional associations among natural eukaryotic genome editing components. <i>F1000Research</i> , 0, 6, 1374.	0.8	16
33	RNA-mediated transgenerational inheritance in ciliates and plants. <i>Chromosoma</i> , 2018, 127, 19-27.	1.0	14
34	Pdsg1 and Pdsg2, Novel Proteins Involved in Developmental Genome Remodelling in <i>Paramecium</i> . <i>PLoS ONE</i> , 2014, 9, e112899.	1.1	13
35	The eukaryotic way to defend and edit genomes by sRNA-targeted DNA deletion. <i>Annals of the New York Academy of Sciences</i> , 2015, 1341, 106-114.	1.8	13
36	Determination of the presence of 5-methylcytosine in <i>Paramecium tetraurelia</i> . <i>PLoS ONE</i> , 2018, 13, e0206667.	1.1	10

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37	Chromosome fusions triggered by noncoding RNA. <i>RNA Biology</i> , 2017, 14, 620-631.	1.5	9
38	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
39	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
40	RNA-dependent genome processing during nuclear differentiation: the model systems of stichotrichous ciliates. <i>Epigenomics</i> , 2013, 5, 229-236.	1.0	3
41	Identification of novel, functional, long noncoding RNAs involved in programmed, large-scale genome rearrangements. <i>Rna</i> , 2022, 28, 1110-1127.	1.6	1
42	RNA-Guided Genome Editing. , 2016, , 35-50.		0