

# Magdalena Zarowiecki

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

1,549  
citations

623734  
14  
h-index

752698  
20  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2940  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	27.8	603
2	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014, 15, R43.	9.6	212
3	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , 2014, 46, 693-700.	21.4	139
4	OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163.	5.5	111
5	Making the most of mitochondrial genomes – Markers for phylogeny, molecular ecology and barcodes in <i>Schistosoma</i> (Platyhelminthes: Digenea). <i>International Journal for Parasitology</i> , 2007, 37, 1401-1418.	3.1	78
6	What helminth genomes have taught us about parasite evolution. <i>Parasitology</i> , 2015, 142, S85-S97.	1.5	75
7	Rapid Evolution of Yeast Centromeres in the Absence of Drive. <i>Genetics</i> , 2008, 178, 2161-2167.	2.9	57
8	Ca <sup>2+</sup> channels and praziquantel: A view from the free world. <i>Parasitology International</i> , 2013, 62, 619-628.	1.3	55
9	microRNA profiling in the zoonotic parasite <i>Echinococcus canadensis</i> using a high-throughput approach. <i>Parasites and Vectors</i> , 2015, 8, 83.	2.5	52
10	Genome-wide transcriptome profiling and spatial expression analyses identify signals and switches of development in tapeworms. <i>EvoDevo</i> , 2018, 9, 21.	3.2	30
11	Genome-wide identification of microRNA targets in the neglected disease pathogens of the genus <i>Echinococcus</i> . <i>Molecular and Biochemical Parasitology</i> , 2017, 214, 91-100.	1.1	22
12	Transcriptional memory of cells of origin overrides $\beta$ -catenin requirement of MLL cancer stem cells. <i>EMBO Journal</i> , 2017, 36, 3139-3155.	7.8	22
13	A Novel Terminal-Repeat Retrotransposon in Miniature (TRIM) Is Massively Expressed in <i>Echinococcus multilocularis</i> Stem Cells. <i>Genome Biology and Evolution</i> , 2015, 7, 2136-2153.	2.5	20
14	Utilizing the planarian voltage-gated ion channel transcriptome to resolve a role for a Ca <sup>2+</sup> channel in neuromuscular function and regeneration. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1036-1045.	4.1	17
15	Functional reconstruction of human AML reveals stem cell origin and vulnerability of treatment-resistant MLL-rearranged leukemia. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	15
16	Dataset for a <i>Dugesia japonica</i> de novo transcriptome assembly, utilized for defining the voltage-gated like ion channel superfamily. <i>Data in Brief</i> , 2016, 9, 1044-1047.	1.0	12
17	Pleistocene genetic connectivity in a widespread, open-habitat-adapted mosquito in the Indo-Oriental region. <i>Journal of Biogeography</i> , 2011, 38, 1422-1432.	3.0	10
18	Towards a new role for vector systematics in parasite control. <i>Parasitology</i> , 2011, 138, 1723-1729.	1.5	6

#	ARTICLE	IF	CITATIONS
19	Repeated landmass reformation limits diversification in the widespread littoral zone mosquito <i>Aopuheles sundaicus</i> sensu lato in the Indo-Oriental Region. Molecular Ecology, 2014, 23, 2573-2589.	3.9	6
20	Metagenomics with guts. Nature Reviews Microbiology, 2012, 10, 674-674.	28.6	4
21	Animals learn new tricks from microorganisms. Nature Reviews Microbiology, 2011, 9, 836-836.	28.6	0