

Paulina Jackowiak

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

514
citations

687335

13
h-index

677123

22
g-index

26
all docs

26
docs citations

26
times ranked

944
citing authors

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	1
2	Expression Landscape of circRNAs in Arabidopsis thaliana Seedlings and Adult Tissues. <i>Frontiers in Plant Science</i> , 2020, 11, 576581.	3.6	11
3	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
4	Arabidopsis thaliana cbp80, c2h2, and flk Knockout Mutants Accumulate Increased Amounts of Circular RNAs. <i>Cells</i> , 2020, 9, 1937.	4.1	7
5	Functional characterization of RNA fragments using high-throughput interactome screening. <i>Journal of Proteomics</i> , 2019, 193, 173-183.	2.4	6
6	Effects of G-quadruplex topology on translational inhibition by tRNA fragments in mammalian and plant systems in vitro. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 92, 148-154.	2.8	21
7	Mutations in human AID differentially affect its ability to deaminate cytidine and 5-methylcytidine in ssDNA substrates in vitro. <i>Scientific Reports</i> , 2017, 7, 3873.	3.3	7
8	Small RNA fragments derived from multiple RNA classes – the missing element of multi-omics characteristics of the hepatitis C virus cell culture model. <i>BMC Genomics</i> , 2017, 18, 502.	2.8	17
9	RNA-Seq-based analysis of differential gene expression associated with hepatitis C virus infection in cell culture. <i>Acta Biochimica Polonica</i> , 2017, 63, 789-798.	0.5	5
10	Computational prediction of nonenzymatic RNA degradation patterns. <i>Acta Biochimica Polonica</i> , 2017, 63, 745-751.	0.5	4
11	Copy number variation of genes involved in the hepatitis C virus-human interactome. <i>Scientific Reports</i> , 2016, 6, 31340.	3.3	10
12	Production of an active human AID enzyme in a bacterial system. <i>Biotechnologia</i> , 2016, 3, 235-239.	0.9	0
13	Phylogeny and molecular evolution of the hepatitis C virus. <i>Infection, Genetics and Evolution</i> , 2014, 21, 67-82.	2.3	59
14	Multi-agent model of hepatitis C virus infection. <i>Artificial Intelligence in Medicine</i> , 2014, 60, 123-131.	6.5	17
15	Identification of stable, high copy number, medium-sized RNA degradation intermediates that accumulate in plants under non-stress conditions. <i>Plant Molecular Biology</i> , 2013, 83, 191-204.	3.9	36
16	Evolution of hepatitis C virus hypervariable region 1 in chronically infected children. <i>Virus Research</i> , 2012, 167, 380-384.	2.2	9
17	2D-PAGE as an effective method of RNA degradome analysis. <i>Molecular Biology Reports</i> , 2012, 39, 139-146.	2.3	14
18	Single mutation converts mild pathotype of the Pepino mosaic virus into necrotic one. <i>Virus Research</i> , 2011, 159, 57-61.	2.2	42

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19	RNA degradome--its biogenesis and functions. <i>Nucleic Acids Research</i> , 2011, 39, 7361-7370.	14.5	49
20	Mechanisms Involved in the Development of Chronic Hepatitis C as Potential Targets of Antiviral Therapy. <i>Current Pharmaceutical Biotechnology</i> , 2011, 12, 1774-1780.	1.6	13
21	Pepino Mosaic Virus - A Pathogen of Tomato Crops in Poland: Biology, Evolution and Diagnostics. <i>Journal of Plant Protection Research</i> , 2010, 50, .	1.0	11
22	Hepatitis C virus quasispecies in chronically infected children subjected to interferonâ€“ribavirin therapy. <i>Archives of Virology</i> , 2010, 155, 1977-1987.	2.1	18
23	Quasispecies nature of Pepino mosaic virus and its evolutionary dynamics. <i>Virus Genes</i> , 2010, 41, 260-267.	1.6	18
24	Towards Prediction of HCV Therapy Efficiency. <i>Computational and Mathematical Methods in Medicine</i> , 2010, 11, 185-199.	1.3	9
25	Human- and Virus-Encoded microRNAs as Potential Targets of Antiviral Therapy. <i>Mini-Reviews in Medicinal Chemistry</i> , 2009, 9, 927-937.	2.4	20