

Jakub Barylski

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,365
citations

516710

16
h-index

526287

27
g-index

29
all docs

29
docs citations

29
times ranked

2065
citing authors

#	ARTICLE	IF	CITATIONS
1	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	5.9	53
2	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021, 166, 3239-3244.	2.1	24
3	Characterization and expression of a novel thaumatin-like protein (CcTLP1) from papaveraceous plant <i>Corydalis cava</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 189, 678-689.	7.5	2
4	Taxonomy-aware, sequence similarity ranking reliably predicts phage-host relationships. <i>BMC Biology</i> , 2021, 19, 223.	3.8	16
5	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	5.6	89
6	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	2.1	144
7	ICTV Virus Taxonomy Profile: Herelleviridae. <i>Journal of General Virology</i> , 2020, 101, 362-363.	2.9	37
8	Correlation between specific groups of heterotrophic bacteria and microcystin biodegradation in freshwater bodies of central Europe. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	18
9	Bacteriophages are more virulent to bacteria with human cells than they are in bacterial culture; insights from HT-29 cells. <i>Scientific Reports</i> , 2018, 8, 5091.	3.3	79
10	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	2.1	172
11	Two novel temperate bacteriophages infecting <i>Streptococcus pyogenes</i> : Their genomes, morphology and stability. <i>PLoS ONE</i> , 2018, 13, e0205995.	2.5	15
12	Complete genome sequences of two novel autographiviruses infecting a bacterium from the <i>Pseudomonas fluorescens</i> group. <i>Archives of Virology</i> , 2017, 162, 2907-2911.	2.1	7
13	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	2.1	57
14	Characterization of the complete chloroplast genome of <i>Pinus uliginosa</i> (Neumann) from the <i>Pinus mugo</i> complex. <i>Conservation Genetics Resources</i> , 2017, 9, 209-212.	0.8	10
15	Cylindrospermopsin Biodegradation Abilities of <i>Aeromonas</i> sp. Isolated from RusaÅka Lake. <i>Toxins</i> , 2016, 8, 55.	3.4	24
16	Two Novel Myoviruses from the North of Iraq Reveal Insights into <i>Clostridium difficile</i> Phage Diversity and Biology. <i>Viruses</i> , 2016, 8, 310.	3.3	31
17	Combination of transcriptomic and proteomic approaches helps to unravel the protein composition of <i>Chelidonium majus</i> L. milky sap. <i>Planta</i> , 2016, 244, 1055-1064.	3.2	22
18	Uncoupling proteins of invertebrates: A review. <i>IUBMB Life</i> , 2016, 68, 691-699.	3.4	22

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19	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. Archives of Virology, 2016, 161, 1095-1099.	2.1	83
20	Effect of temperature on the pathogenesis, accumulation of viral and satellite RNAs and on plant proteome in peanut stunt virus and satellite RNA-infected plants. Frontiers in Plant Science, 2015, 6, 903.	3.6	40
21	Viral and Other Cell-Penetrating Peptides as Vectors of Therapeutic Agents in Medicine. Journal of Pharmacology and Experimental Therapeutics, 2015, 354, 32-42.	2.5	62
22	Molecular, morphological, and ecological differences between the terrestrial and aquatic forms of <i>Oxyrrhynchium speciosum</i> (Brid.) Warnst. (Brachytheciaceae). Journal of Bryology, 2014, 36, 180-190.	1.2	1
23	Complete Genome Sequence of <i>Lelliottia</i> Podophage phD2B. Genome Announcements, 2014, 2, .	0.8	3
24	Plant antimicrobial peptides. Folia Microbiologica, 2014, 59, 181-196.	2.3	305
25	The Discovery of phiAGATE, A Novel Phage Infecting <i>Bacillus pumilus</i> , Leads to New Insights into the Phylogeny of the Subfamily Spounavirinae. PLoS ONE, 2014, 9, e86632.	2.5	29
26	Incorrectly annotated keratin derived peptide sequences lead to misleading MS/MS data interpretation. Journal of Proteomics, 2013, 91, 270-273.	2.4	7