

# Piotr Wojciech Dabrowski

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

1,434  
citations

471509

17  
h-index

345221

36  
g-index

42  
all docs

42  
docs citations

42  
times ranked

2459  
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigating the zoonotic origin of the West African Ebola epidemic. <i>EMBO Molecular Medicine</i> , 2015, 7, 17-23.	6.9	347
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
3	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	4.3	100
4	Fatal Monkeypox in Wild-Living Sooty Mangabey, Côte d'Ivoire, 2012. <i>Emerging Infectious Diseases</i> , 2014, 20, 1009-1011.	4.3	100
5	Protocol for Metagenomic Virus Detection in Clinical Specimens. <i>Emerging Infectious Diseases</i> , 2015, 21, 48-57.	4.3	90
6	Genome Analysis of Bat Adenovirus 2: Indications of Interspecies Transmission. <i>Journal of Virology</i> , 2012, 86, 1888-1892.	3.4	74
7	What caused the outbreak of ESBL-producing <i>Klebsiella pneumoniae</i> in a neonatal intensive care unit, Germany 2009 to 2012? Reconstructing transmission with epidemiological analysis and whole-genome sequencing. <i>BMJ Open</i> , 2015, 5, e007397-e007397.	1.9	62
8	Genome-Wide Comparison of Cowpox Viruses Reveals a New Clade Related to Variola Virus. <i>PLoS ONE</i> , 2013, 8, e79953.	2.5	55
9	Comparison of host cell gene expression in cowpox, monkeypox or vaccinia virus-infected cells reveals virus-specific regulation of immune response genes. <i>Virology Journal</i> , 2013, 10, 61.	3.4	43
10	Pipasic: similarity and expression correction for strain-level identification and quantification in metaproteomics. <i>Bioinformatics</i> , 2014, 30, i149-i156.	4.1	32
11	Rapid characterisation of <i>Klebsiella oxytoca</i> isolates from contaminated liquid hand soap using mass spectrometry, FTIR and Raman spectroscopy. <i>Faraday Discussions</i> , 2016, 187, 353-375.	3.2	29
12	PAIPline: pathogen identification in metagenomic and clinical next generation sequencing samples. <i>Bioinformatics</i> , 2018, 34, i715-i721.	4.1	27
13	seq-seq-pan: building a computational pan-genome data structure on whole genome alignment. <i>BMC Genomics</i> , 2018, 19, 47.	2.8	25
14	Comparing Viral Metagenomic Extraction Methods. <i>Current Issues in Molecular Biology</i> , 2017, 24, 59-70.	2.4	25
15	Zwiesel bat banyangvirus, a potentially zoonotic Huaiyangshan banyangvirus (Formerly known as) Tj ETQq1 1 0.784314 rgBT/Overlook	3.3	24
16	A novel Coltivirus-related virus isolated from free-tailed bats from Côte d'Ivoire is able to infect human cells in vitro. <i>Virology Journal</i> , 2017, 14, 181.	3.4	21
17	The virome of German bats: comparing virus discovery approaches. <i>Scientific Reports</i> , 2021, 11, 7430.	3.3	21
18	An environment for sustainable research software in Germany and beyond: current state, open challenges, and call for action. <i>F1000Research</i> , 2020, 9, 295.	1.6	21

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19	HiLive: real-time mapping of illumina reads while sequencing. <i>Bioinformatics</i> , 2017, 33, 917-319.	4.1	18
20	RAMBO-K: Rapid and Sensitive Removal of Background Sequences from Next Generation Sequencing Data. <i>PLoS ONE</i> , 2015, 10, e0137896.	2.5	18
21	Complete Genome Sequence of the Porcine Isolate <i>Enterococcus faecalis</i> D32. <i>Journal of Bacteriology</i> , 2012, 194, 5490-5491.	2.2	16
22	An environment for sustainable research software in Germany and beyond: current state, open challenges, and call for action. <i>F1000Research</i> , 2020, 9, 295.	1.6	16
23	Seasonal recurrence of cowpox virus outbreaks in captive cheetahs ( <i>Acinonyx jubatus</i> ). <i>PLoS ONE</i> , 2017, 12, e0187089.	2.5	15
24	Comparative Genomic Analysis of Two Novel Sporadic Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4 Strains Isolated 2011 in Germany. <i>PLoS ONE</i> , 2015, 10, e0122074.	2.5	14
25	SuRankCo: supervised ranking of contigs in de novo assemblies. <i>BMC Bioinformatics</i> , 2015, 16, 240.	2.6	13
26	First detection of bat-borne Issyk-Kul virus in Europe. <i>Scientific Reports</i> , 2020, 10, 22384.	3.3	13
27	Infection of human airway epithelial cells by different subtypes of Dobrava-Belgrade virus reveals gene expression patterns corresponding to their virulence potential. <i>Virology</i> , 2016, 493, 189-201.	2.4	11
28	Fostering global data sharing: highlighting the recommendations of the Research Data Alliance COVID-19 working group. <i>Wellcome Open Research</i> , 2020, 5, 267.	1.8	11
29	Rapid detection of anti-Vaccinia virus neutralizing antibodies. <i>Virology Journal</i> , 2011, 8, 139.	3.4	9
30	Berlin Squirrelpox Virus, a New Poxvirus in Red Squirrels, Berlin, Germany. <i>Emerging Infectious Diseases</i> , 2017, 23, 1726-1729.	4.3	9
31	Antigenic and immunosuppressive properties of a trimeric recombinant transmembrane envelope protein gp41 of HIV-1. <i>PLoS ONE</i> , 2017, 12, e0173454.	2.5	7
32	mPSQed: A Software for the Design of Multiplex Pyrosequencing Assays. <i>PLoS ONE</i> , 2012, 7, e38140.	2.5	6
33	Fostering global data sharing: highlighting the recommendations of the Research Data Alliance COVID-19 working group. <i>Wellcome Open Research</i> , 2020, 5, 267.	1.8	6
34	Comparison of 454 Ultra-Deep Sequencing and Allele-Specific Real-Time PCR with Regard to the Detection of Emerging Drug-Resistant Minor HIV-1 Variants after Antiretroviral Prophylaxis for Vertical Transmission. <i>PLoS ONE</i> , 2015, 10, e0140809.	2.5	5
35	Identification and characterization of episomal forms of integrative genomic islands in the genus <i>Francisella</i> . <i>International Journal of Medical Microbiology</i> , 2015, 305, 874-880.	3.6	5
36	PriLive: privacy-preserving real-time filtering for next-generation sequencing. <i>Bioinformatics</i> , 2018, 34, 2376-2383.	4.1	5

#	ARTICLE	IF	CITATIONS
37	MultiPSQ: A Software Solution for the Analysis of Diagnostic n-Plexed Pyrosequencing Reactions. PLoS ONE, 2013, 8, e60055.	2.5	4
38	Multiplex Pyrosequencing <sup>Â</sup> : Simultaneous Genotyping Based on SNPs from Distant Genomic Regions. Methods in Molecular Biology, 2015, 1315, 337-347.	0.9	0
39	Comparing Viral Metagenomic Extraction Methods. , 2017, , .		0
40	NGS read classification using AI. PLoS ONE, 2021, 16, e0261548.	2.5	0