

# Mauro Petrillo

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

1,073  
citations

516215

16  
h-index

454577

30  
g-index

38  
all docs

38  
docs citations

38  
times ranked

1730  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2: Reinfection after 18 Months of a Previous Case with Multiple Negative Nasopharyngeal Swab Tests and Positive Fecal Molecular Test. <i>Medicina (Lithuania)</i> , 2022, 58, 642.	0.8	3
2	SARS-CoV-2 Detection in Fecal Sample from a Patient with Typical Findings of COVID-19 Pneumonia on CT but Negative to Multiple SARS-CoV-2 RT-PCR Tests on Oropharyngeal and Nasopharyngeal Swab Samples. <i>Medicina (Lithuania)</i> , 2021, 57, 290.	0.8	34
3	Increase of SARS-CoV-2 RNA load in faecal samples prompts for rethinking of SARS-CoV-2 biology and COVID-19 epidemiology. <i>F1000Research</i> , 2021, 10, 370.	0.8	25
4	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021, 13, 1359.	1.5	6
5	Toxin-like peptides in plasma, urine and faecal samples from COVID-19 patients. <i>F1000Research</i> , 2021, 10, 550.	0.8	16
6	Increase of SARS-CoV-2 RNA load in faecal samples prompts for rethinking of SARS-CoV-2 biology and COVID-19 epidemiology. <i>F1000Research</i> , 2021, 10, 370.	0.8	17
7	Study of a SARS-CoV-2 Outbreak in a Belgian Military Education and Training Center in Maradi, Niger. <i>Viruses</i> , 2020, 12, 949.	1.5	19
8	DUGMO: tool for the detection of unknown genetically modified organisms with high-throughput sequencing data for pure bacterial samples. <i>BMC Bioinformatics</i> , 2020, 21, 284.	1.2	1
9	The EU one-stop-shop collection of publicly available information on COVID-19 in vitro diagnostic medical devices. <i>F1000Research</i> , 2020, 9, 1296.	0.8	3
10	Nuclear DNA barcodes for cod identification in mildly-treated and processed food products. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2019, 36, 1-14.	1.1	15
11	Review of micro- and nanoplastic contamination in the food chain. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2019, 36, 639-673.	1.1	356
12	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. <i>F1000Research</i> , 2018, 7, 459.	0.8	31
13	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. <i>F1000Research</i> , 2018, 7, 459.	0.8	24
14	Novel nuclear barcode regions for the identification of flatfish species. <i>Food Control</i> , 2017, 79, 297-308.	2.8	29
15	Molecular characterization of an unauthorized genetically modified <i>Bacillus subtilis</i> production strain identified in a vitamin B 2 feed additive. <i>Food Chemistry</i> , 2017, 230, 681-689.	4.2	37
16	The European Union Reference Methods Database and Decision Supporting Tool for the Analysis of Genetically Modified Organisms. , 2016, , 275-288.		1
17	The complete 12.6 Mb genome and transcriptome of <i>Nonomuraea gerenzanensis</i> with new insights into its duplicated $\phi$ mag1c $\phi$ RNA polymerase. <i>Scientific Reports</i> , 2016, 6, 18.	1.6	40
18	Possible genetic events producing colistin resistance gene mcr-1. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 280.	4.6	47

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19	Development and applicability of a ready-to-use PCR system for GMO screening. Food Chemistry, 2016, 201, 110-119.	4.2	35
20	Towards Plant Species Identification in Complex Samples: A Bioinformatics Pipeline for the Identification of Novel Nuclear Barcode Candidates. PLoS ONE, 2016, 11, e0147692.	1.1	8
21	JRC GMO-Amplicons: a collection of nucleic acid sequences related to genetically modified organisms. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav101.	1.4	15
22	Genetically modified animals: Options and issues for traceability and enforcement. Trends in Food Science and Technology, 2015, 44, 159-176.	7.8	24
23	Development, Optimization, and Single Laboratory Validation of an Event-Specific Real-Time PCR Method for the Detection and Quantification of Golden Rice 2 Using a Novel Taxon-Specific Assay. Journal of Agricultural and Food Chemistry, 2015, 63, 1711-1721.	2.4	12
24	JRC GMO-Matrix: a web application to support Genetically Modified Organisms detection strategies. BMC Bioinformatics, 2014, 15, 417.	1.2	30
25	Complete sequencing of <i>Novosphingobium</i> sp. PP1Y reveals a biotechnologically meaningful metabolic pattern. BMC Genomics, 2014, 15, 384.	1.2	44
26	Identification and Characterisation of a Novel Acylpeptide Hydrolase from <i>Sulfolobus Solfataricus</i> : Structural and Functional Insights. PLoS ONE, 2012, 7, e37921.	1.1	11
27	Systematic identification of stem-loop containing sequence families in bacterial genomes. BMC Genomics, 2008, 9, 20.	1.2	7
28	Stem-loop structures in prokaryotic genomes. BMC Genomics, 2006, 7, 170.	1.2	33
29	Systematic analysis of human kinase genes: a large number of genes and alternative splicing events result in functional and structural diversity. BMC Bioinformatics, 2005, 6, S20.	1.2	65
30	Enterobacterial Repetitive Intergenic Consensus Sequence Repeats in <i>Yersinia</i> : Genomic Organization and Functional Properties. Journal of Bacteriology, 2005, 187, 7945-7954.	1.0	50
31	DG-CST (Disease Gene Conserved Sequence Tags), a database of human-mouse conserved elements associated to disease genes. Nucleic Acids Research, 2004, 33, D505-D510.	6.5	11
32	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	0.8	8
33	Increase of SARS-CoV-2 RNA load in faecal samples prompts for rethinking of SARS-CoV-2 biology and COVID-19 epidemiology. F1000Research, 0, 10, 370.	0.8	3
34	Toxin-like peptides in plasma, urine and faecal samples from COVID-19 patients. F1000Research, 0, 10, 550.	0.8	3
35	The first report on detecting SARS-CoV-2 inside human fecal-oral bacteria: A case series on asymptomatic family members and a child with COVID-19. F1000Research, 0, 11, 135.	0.8	1
36	Evidence of SARS-CoV-2 bacteriophage potential in human gut microbiota. F1000Research, 0, 11, 292.	0.8	6

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37	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	0.8	0