Mauro Petrillo

List of Publications by Year
in descending order

37 papers	1,073 citations	516710 16 h-index	454955 30 g-index
38 all docs	38 docs citations	38 times ranked	1730 citing authors

#	Article	IF	Citations
1	Review of micro- and nanoplastic contamination in the food chain. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2019, 36, 639-673.	2.3	356
2	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.	2.6	65
3	Enterobacterial Repetitive Intergenic Consensus Sequence Repeats in Yersiniae: Genomic Organization and Functional Properties. Journal of Bacteriology, 2005, 187, 7945-7954.	2.2	50
4	Possible genetic events producing colistin resistance gene mcr-1. Lancet Infectious Diseases, The, 2016, 16, 280.	9.1	47
5	Complete sequencing of Novosphingobium sp. PP1Y reveals a biotechnologically meaningful metabolic pattern. BMC Genomics, 2014, 15, 384.	2.8	44
6	The complete 12â€‰Mb genome and transcriptome of Nonomuraea gerenzanensis with new insights into its duplicated â€œmagicâ€•RNA polymerase. Scientific Reports, 2016, 6, 18.	3.3	40
7	Molecular characterization of an unauthorized genetically modified Bacillus subtilis production strain identified in a vitamin B 2 feed additive. Food Chemistry, 2017, 230, 681-689.	8.2	37
8	Development and applicability of a ready-to-use PCR system for GMO screening. Food Chemistry, 2016, 201, 110-119.	8.2	35
9	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. Medicina (Lithuania), 2021, 57, 290.	2.0	34
10	Stem-loop structures in prokaryotic genomes. BMC Genomics, 2006, 7, 170.	2.8	33
11	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459.	1.6	31
12	JRC GMO-Matrix: a web application to support Genetically Modified Organisms detection strategies. BMC Bioinformatics, 2014, 15, 417.	2.6	30
13	Novel nuclear barcode regions for the identification of flatfish species. Food Control, 2017, 79, 297-308.	5.5	29
14	Increase of SARS-CoV-2 RNA load in faecal samples prompts for rethinking of SARS-CoV-2 biology and COVID-19 epidemiology. F1000Research, 2021, 10, 370.	1.6	25
15	Genetically modified animals: Options and issues for traceability and enforcement. Trends in Food Science and Technology, 2015, 44, 159-176.	15.1	24
16	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459.	1.6	24
17	Study of a SARS-CoV-2 Outbreak in a Belgian Military Education and Training Center in Maradi, Niger. Viruses, 2020, 12, 949.	3.3	19
18	Increase of SARS-CoV-2 RNA load in faecal samples prompts for rethinking of SARS-CoV-2 biology and COVID-19 epidemiology. F1000Research, 2021, 10, 370.	1.6	17

#	Article	IF	Citations
19	Toxin-like peptides in plasma,ÂurineÂand faecalÂsamples from COVID-19 patients. F1000Research, 2021, 10, 550.	1.6	16
20	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.	3.0	15
21	Nuclear DNA barcodes for cod identification in mildly-treated and processed food products. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2019, 36, 1-14.	2.3	15
22	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.	5.2	12
23	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.	14.5	11
24	Identification and Characterisation of a Novel Acylpeptide Hydrolase from Sulfolobus Solfataricus: Structural and Functional Insights. PLoS ONE, 2012, 7, e37921.	2.5	11
25	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	1.6	8
26	Towards Plant Species Identification in Complex Samples: A Bioinformatics Pipeline for the Identification of Novel Nuclear Barcode Candidates. PLoS ONE, 2016, 11, e0147692.	2.5	8
27	Systematic identification of stem-loop containing sequence families in bacterial genomes. BMC Genomics, 2008, 9, 20.	2.8	7
28	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. Viruses, 2021, 13, 1359.	3.3	6
29	Evidence of SARS-CoV-2 bacteriophage potential in human gut microbiota. F1000Research, 0, 11, 292.	1.6	6
30	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.	1.6	3
31	The EU one-stop-shop collection of publicly available information on COVID-19 in vitro diagnostic medical devices. F1000Research, 2020, 9, 1296.	1.6	3
32	Toxin-like peptides in plasma,ÂurineÂand faecalÂsamples from COVID-19 patients. F1000Research, 0, 10, 550.	1.6	3
33	SARS-CoV-2: Reinfection after 18 Months of a Previous Case with Multiple Negative Nasopharyngeal Swab Tests and Positive Fecal Molecular Test. Medicina (Lithuania), 2022, 58, 642.	2.0	3
34	The European Union Reference Methods Database and Decision Supporting Tool for the Analysis of Genetically Modified Organisms. , 2016, , 275-288.		1
35	DUGMO: tool for the detection of unknown genetically modified organisms with high-throughput sequencing data for pure bacterial samples. BMC Bioinformatics, 2020, 21, 284.	2.6	1
36	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.	1.6	1

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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.	1.6	0