

Cesare CammÀ

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

1,741
citations

257101

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315357

38
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all docs

82
docs citations

82
times ranked

2784
citing authors

#	ARTICLE	IF	CITATIONS
1	In vitro and in silico parameters for precise cgMLST typing of <i>Listeria monocytogenes</i> . BMC Genomics, 2022, 23, 235.	1.2	7
2	SARS-CoV-2 Delta VOC in a Paucisymptomatic Dog, Italy. Pathogens, 2022, 11, 514.	1.2	5
3	Validation of AmpliSeq NGS Panel for BRCA1 and BRCA2 Variant Detection in Canine Formalin-Fixed Paraffin-Embedded Mammary Tumors. Life, 2022, 12, 851.	1.1	4
4	Full Genome Characterization of Respiratory Syncytial Virus Causing a Fatal Infection in an Immunocompromised Patient in Tunisia. Pathogens, 2022, 11, 758.	1.2	0
5	Hypo- and Hyper-Virulent <i>Listeria monocytogenes</i> Clones Persisting in Two Different Food Processing Plants of Central Italy. Microorganisms, 2021, 9, 376.	1.6	25
6	Characterization and In Vitro Efficacy against <i>Listeria monocytogenes</i> of a Newly Isolated Bacteriophage, ÎZSAM-1. Microorganisms, 2021, 9, 731.	1.6	4
7	A large food-borne outbreak of campylobacteriosis in kindergartens and primary schools in Pescara, Italy, May-June 2018. Journal of Medical Microbiology, 2021, 70, .	0.7	7
8	Emergence and Spread of SARS-CoV-2 Lineages B.1.1.7 and P.1 in Italy. Viruses, 2021, 13, 794.	1.5	32
9	<i>Campylobacter jejuni</i> in Different Canine Populations: Characteristics and Zoonotic Potential. Microorganisms, 2021, 9, 2231.	1.6	10
10	SARS-CoV-2 surveillance in Italy through phylogenomic inferences based on Hamming distances derived from pan-SNPs, -MNP and -InDels. BMC Genomics, 2021, 22, 782.	1.2	12
11	Whole Genome Sequencing Characterization of HEV3-e and HEV3-f Subtypes among the Wild Boar Population in the Abruzzo Region, Italy: First Report. Microorganisms, 2020, 8, 1393.	1.6	11
12	Genome Sequencing of a Camelpox Vaccine Reveals Close Similarity to Modified Vaccinia virus Ankara (MVA). Viruses, 2020, 12, 786.	1.5	3
13	Genomic Epidemiology of the First Wave of SARS-CoV-2 in Italy. Viruses, 2020, 12, 1438.	1.5	39
14	Electrospun PLGA Fiber Diameter and Alignment of Tendon Biomimetic Fleece Potentiate Tenogenic Differentiation and Immunomodulatory Function of Amniotic Epithelial Stem Cells. Cells, 2020, 9, 1207.	1.8	35
15	Detection of Astrovirus in a Cow with Neurological Signs by Nanopore Technology, Italy. Viruses, 2020, 12, 530.	1.5	7
16	A Real-Time PCR Screening Assay for Rapid Detection of <i>Listeria Monocytogenes</i> Outbreak Strains. Foods, 2020, 9, 67.	1.9	10
17	Whole Genome Sequencing for Studying <i>Bacillus anthracis</i> from an Outbreak in the Abruzzo Region of Italy. Microorganisms, 2020, 8, 87.	1.6	8
18	Pro-Inflammatory Response of Bovine Polymorphonuclear Cells Induced by <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> . Frontiers in Veterinary Science, 2020, 7, 142.	0.9	1

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19	A "One-Health" approach for diagnosis and molecular characterization of SARS-CoV-2 in Italy. <i>One Health</i> , 2020, 10, 100135.	1.5	46
20	Metagenomic and volatile profiles of ripened cheese obtained from dairy ewes fed a dietary hemp seed supplementation. <i>Journal of Dairy Science</i> , 2020, 103, 5882-5892.	1.4	11
21	Assessing the role of migratory birds in the introduction of ticks and tick-borne pathogens from African countries: An Italian experience. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 101272.	1.1	35
22	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated In Silico High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	34
23	Molecular typing of Bluetongue virus using the nCounter [®] analysis system platform. <i>Journal of Virological Methods</i> , 2019, 269, 64-69.	1.0	4
24	Diagnosis and characterization of canine distemper virus through sequencing by MinION nanopore technology. <i>Scientific Reports</i> , 2019, 9, 1714.	1.6	21
25	Diversity of Rickettsia in Ticks Collected in Abruzzi and Molise Regions (Central Italy). <i>Microorganisms</i> , 2019, 7, 696.	1.6	10
26	A study in the Abruzzo region on the presence of Paenibacillus larvae spores in honeys indicated underestimation of American foulbrood prevalence in Italy. <i>Journal of Apicultural Research</i> , 2019, 58, 416-419.	0.7	4
27	Bifidobacterium jacchi sp. nov., isolated from the faeces of a baby common marmoset (Callithrix Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	23
28	Whole-Genome Sequence of Listeria monocytogenes Serovar 1/2a Strain IZSAM_Lm_15_17439_A144, Representative of a Human Outbreak in 2008. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
29	Complete Genome Sequencing of 10 Brucella abortus Biovar 3 Strains Isolated from Water Buffalo. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
30	One after the other: A novel Bluetongue virus strain related to Toggenburg virus detected in the Piedmont region (North-western Italy), extends the panel of novel atypical BTV strains. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 370-374.	1.3	57
31	Complete Genome Sequencing of Eight Brucella abortus Biovar 1 Strains Isolated from Water Buffalo. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
32	Whole-Genome Sequence of a Reemerging Listeria monocytogenes Serovar 1/2a Strain in Central Italy. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	8
33	Whole-Genome Sequences of Two Listeria monocytogenes Serovar 1/2a Strains Responsible for a Severe Listeriosis Outbreak in Central Italy. <i>Genome Announcements</i> , 2018, 6, .	0.8	12
34	Campylobacter infection occurrence in canine population in Italy. <i>International Journal of Infectious Diseases</i> , 2018, 73, 146.	1.5	1
35	The Italian information system for the collection and analysis of complete genome sequence of pathogens isolated from animal, food and environment. <i>International Journal of Infectious Diseases</i> , 2018, 73, 296-297.	1.5	22
36	A new fast real-time PCR method for the identification of three sibling Apodemus species (A. sylvaticus, A. flavicollis, and A. alpicola) in Italy. <i>Ecology and Evolution</i> , 2018, 8, 4807-4814.	0.8	2

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37	Core Genome Multilocus Sequence Typing and Single Nucleotide Polymorphism Analysis in the Epidemiology of <i>Brucella melitensis</i> Infections. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	58
38	Identification and genetic characterization of bovine enterovirus by combination of two next generation sequencing platforms. <i>Journal of Virological Methods</i> , 2018, 260, 21-25.	1.0	13
39	Genetic diversity of <i>Coxiella burnetii</i> in domestic ruminants in central Italy. <i>BMC Veterinary Research</i> , 2018, 14, 171.	0.7	11
40	A severe outbreak of listeriosis in central Italy with a rare pulsotype associated with processed pork products. <i>Journal of Medical Microbiology</i> , 2018, 67, 1351-1360.	0.7	43
41	<i>Aphanomyces astaci</i> genotypes involved in recent crayfish plague outbreaks in central Italy. <i>Diseases of Aquatic Organisms</i> , 2018, 130, 209-219.	0.5	11
42	Complete sequence of human mitochondrial DNA obtained by combining multiple displacement amplification and next-generation sequencing on a single oocyte. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 180-181.	0.7	7
43	Novel putative Bluetongue virus in healthy goats from Sardinia, Italy. <i>Infection, Genetics and Evolution</i> , 2017, 51, 108-117.	1.0	89
44	Origins and global context of <i>Brucella abortus</i> in Italy. <i>BMC Microbiology</i> , 2017, 17, 28.	1.3	28
45	Validation of a fast real-time PCR method to detect fraud and mislabeling in milk and dairy products. <i>Journal of Dairy Science</i> , 2017, 100, 106-112.	1.4	63
46	Mitochondrial heteroplasmy profiling in single human oocytes by next-generation sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 542-543.	0.2	3
47	Bluetongue virus serotype 3 in Western Sicily, November 2017. <i>Veterinaria Italiana</i> , 2017, 53, 273-275.	0.5	20
48	Occurrence of <i>Coxiella burnetii</i> in goat and ewe unpasteurized cheeses: Screening and genotyping. <i>International Journal of Food Microbiology</i> , 2016, 237, 47-54.	2.1	26
49	Amniotic epithelial stem cell biocompatibility for electrospun poly(lactide-co-glycolide), poly(μ -caprolactone), poly(lactic acid) scaffolds. <i>Materials Science and Engineering C</i> , 2016, 69, 321-329.	3.8	27
50	Detection of <i>Anaplasma phagocytophilum</i> genotypes that are potentially virulent for human in wild ruminants and <i>Ixodes ricinus</i> in Central Italy. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 782-787.	1.1	24
51	Coinfection by <i>Ureaplasma</i> spp., <i>Photobacterium damsela</i> and an <i>Actinomyces</i> -like microorganism in a bottlenose dolphin (<i>Tursiops truncatus</i>) with pleuropneumonia stranded along the Adriatic coast of Italy. <i>Research in Veterinary Science</i> , 2016, 105, 111-114.	0.9	12
52	Monomorphic genotypes within a generalist lineage of <i>Campylobacter jejuni</i> show signs of global dispersion. <i>Microbial Genomics</i> , 2016, 2, e000088.	1.0	31
53	Outbreak of unusual <i>Salmonella enterica</i> serovar Typhimurium monophasic variant 1,4 [5],12:i:-, Italy, June 2013 to September 2014. <i>Eurosurveillance</i> , 2016, 21, .	3.9	22
54	Genome Sequences of 11 <i>Brucella abortus</i> Isolates from Persistently Infected Italian Regions. <i>Genome Announcements</i> , 2015, 3, .	0.8	6

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55	Whole-Genome Sequencing of <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> Italian Strain 57/13, the Causative Agent of Contagious Bovine Pleuropneumonia. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
56	Draft Genome Sequences of 19 <i>Salmonella enterica</i> Serovar Typhimurium [4,5:i:â™] Strains Resistant to Nalidixic Acid from a Long-Term Outbreak in Italy. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
57	A new member of the Pteropine Orthoreovirus species isolated from fruit bats imported to Italy. <i>Infection, Genetics and Evolution</i> , 2015, 30, 55-58.	1.0	31
58	Detection of Lyme Disease and Q Fever Agents in Wild Rodents in Central Italy. <i>Vector-Borne and Zoonotic Diseases</i> , 2015, 15, 404-411.	0.6	35
59	Choice of Next-Generation Sequencing Pipelines. <i>Methods in Molecular Biology</i> , 2015, 1231, 31-47.	0.4	13
60	Genetic characterization of <i>Brucella melitensis</i> and <i>Brucella abortus</i> geographical clusters in Italy. <i>Veterinaria Italiana</i> , 2015, 51, 225-33.	0.5	0
61	Complete Genome Sequence of a <i>Brucella ceti</i> ST26 Strain Isolated from a Striped Dolphin (<i>Stenella Tj ETQq1</i> 1 0.784314 rgBT /Ov	0.8	10
62	Complete Genome Sequence of Bluetongue Virus Serotype 1 Circulating in Italy, Obtained through a Fast Next-Generation Sequencing Protocol. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
63	<i>Coxiella burnetii</i> in Central Italy: Novel Genotypes Are Circulating in Cattle and Goats. <i>Vector-Borne and Zoonotic Diseases</i> , 2014, 14, 710-715.	0.6	17
64	Whole genome sequence analysis of the arctic-lineage strain responsible for distemper in Italian wolves and dogs through a fast and robust next generation sequencing protocol. <i>Journal of Virological Methods</i> , 2014, 202, 64-68.	1.0	14
65	Molecular epidemiology of bluetongue virus serotype 1 circulating in Italy and its connection with northern Africa. <i>Infection, Genetics and Evolution</i> , 2014, 28, 144-149.	1.0	19
66	Investigating genetic diversity of <i>Brucella abortus</i> and <i>Brucella melitensis</i> in Italy with MLVA-16. <i>Infection, Genetics and Evolution</i> , 2013, 19, 59-70.	1.0	53
67	Diagnosis of dourine in outbreaks in Italy. <i>Veterinary Parasitology</i> , 2013, 193, 30-38.	0.7	40
68	Self-limiting outbreak of crayfish plague in an <i>Austropotamobius pallipes</i> population of a river basin in the Abruzzi region (central Italy). <i>Diseases of Aquatic Organisms</i> , 2013, 103, 149-156.	0.5	14
69	Complete Genome Sequence Analysis of a Reassortant Strain of Bluetongue Virus Serotype 16 from Italy. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
70	Development and validation of fast Real-Time PCR assays for species identification in raw and cooked meat mixtures. <i>Food Control</i> , 2012, 23, 400-404.	2.8	100
71	Survey of Ixodid Ticks and Two Tick-Borne Pathogens in African Buffaloes, <i>Syncerus caffer</i> , from the Caprivi Strip, Namibia. <i>Journal of Zoo and Wildlife Medicine</i> , 2011, 42, 634-640.	0.3	9
72	Confirmation of crayfish plague in Italy: detection of <i>Aphanomyces astaci</i> in white clawed crayfish. <i>Diseases of Aquatic Organisms</i> , 2010, 89, 265-268.	0.5	22

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73	First evidence of bluetongue virus serotype 16 in Croatia. <i>Veterinary Microbiology</i> , 2009, 138, 92-97.	0.8	14
74	Differentiation between field and vaccine strain of bluetongue virus serotype 16. <i>Veterinary Microbiology</i> , 2006, 116, 45-52.	0.8	51
75	Molecular Detection of <i>Anaplasma Platys</i> in Dogs Using Polymerase Chain Reaction and Reverse Line Blot Hybridization. <i>Journal of Veterinary Diagnostic Investigation</i> , 2003, 15, 527-534.	0.5	45
76	The β -tubulin gene of <i>Babesia</i> and <i>Theileria</i> parasites is an informative marker for species discrimination. <i>International Journal for Parasitology</i> , 2000, 30, 1181-1185.	1.3	80
77	Molecular detection of <i>Babesia equi</i> and <i>Babesia caballi</i> in horse blood by PCR amplification of part of the 16S rRNA gene. <i>Veterinary Parasitology</i> , 1999, 84, 75-83.	0.7	104
78	Epidemiologic Surveillance of Visceral Leishmaniasis in Sicily, Italy. <i>American Journal of Tropical Medicine and Hygiene</i> , 1997, 57, 75-78.	0.6	38