

Francesco Cerutti

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

966
citations

471509

17
h-index

454955

30
g-index

43
all docs

43
docs citations

43
times ranked

1994
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 microfluidic antigen point-of-care testing in Emergency Room patients during COVID-19 pandemic. <i>Journal of Virological Methods</i> , 2022, 299, 114337.	2.1	10
2	Feline morbillivirus in northwestern Italy: first detection of genotype 1-B. <i>Journal of Feline Medicine and Surgery</i> , 2021, 23, 584-591.	1.6	4
3	Diagnostic SARS-CoV-2 Cycle Threshold Value Predicts Disease Severity, Survival, and Six-Month Sequelae in COVID-19 Symptomatic Patients. <i>Viruses</i> , 2021, 13, 281.	3.3	51
4	On the SARS-CoV-2 "Variolation Hypothesis": No Association Between Viral Load of Index Cases and COVID-19 Severity of Secondary Cases. <i>Frontiers in Microbiology</i> , 2021, 12, 646679.	3.5	17
5	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. <i>Nature Communications</i> , 2021, 12, 3903.	12.8	14
6	Draft Genome Sequence of <i>Rhodococcus qingshengii</i> Strain PN_19, Isolated from a Moribund Individual of <i>Pinna nobilis</i> in Sardinia, Italy. <i>Microbiology Resource Announcements</i> , 2021, 10, e0035621.	0.6	6
7	Exploring the botanical composition of polyfloral and monofloral honeys through DNA metabarcoding. <i>Food Control</i> , 2021, 128, 108175.	5.5	11
8	Urgent need of rapid tests for SARS CoV-2 antigen detection: Evaluation of the SD-Biosensor antigen test for SARS-CoV-2. <i>Journal of Clinical Virology</i> , 2020, 132, 104654.	3.1	178
9	Specific capture and whole-genome phylogeography of Dolphin morbillivirus. <i>Scientific Reports</i> , 2020, 10, 20831.	3.3	9
10	Multiple Non-Species-Specific Pathogens Possibly Triggered the Mass Mortality in <i>Pinna nobilis</i> . <i>Life</i> , 2020, 10, 238.	2.4	25
11	Genome Sequence of <i>Oenococcus oeni</i> OE37, an Autochthonous Strain Isolated from an Italian White Wine. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
12	First identification of porcine parvovirus 3 in a wild boar in Italy by viral metagenomics " Short communication. <i>Acta Veterinaria Hungarica</i> , 2019, 67, 135-139.	0.5	2
13	Evaluation of DNA isolation procedures from meat-based foods and development of a DNA quality score. <i>LWT - Food Science and Technology</i> , 2019, 106, 64-71.	5.2	3
14	The genome of Border disease virus genotype 8 from chamois by next generation sequencing. <i>Veterinaria Italiana</i> , 2019, 55, 103-105.	0.5	2
15	Impact of DNA purification method and primer selection on 16S rRNA gene metabarcoding on wine. <i>Oeno One</i> , 2019, 53, .	1.4	2
16	Efficient isolation on Vero.DogSLAMtag cells and full genome characterization of Dolphin Morbillivirus (DMV) by next generation sequencing. <i>Scientific Reports</i> , 2018, 8, 860.	3.3	11
17	Highlighting priority areas for bovine viral diarrhea control in Italy: A phylogeographic approach. <i>Infection, Genetics and Evolution</i> , 2018, 58, 258-268.	2.3	10
18	The microbiota of hematophagous ectoparasites collected from migratory birds. <i>PLoS ONE</i> , 2018, 13, e0202270.	2.5	20

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19	Isolation and molecular characterisation of <i>Halicephalobus gingivalis</i> in the brain of a horse in Piedmont, Italy. <i>Parasites and Vectors</i> , 2017, 10, 135.	2.5	9
20	Evidence of circulation of the novel border disease virus genotype 8 in chamois. <i>Archives of Virology</i> , 2017, 162, 511-515.	2.1	13
21	Characterization of the upper and lower respiratory tract microbiota in Piedmontese calves. <i>Microbiome</i> , 2017, 5, 152.	11.1	52
22	Phylogeography, phylodynamics and transmission chains of bovine viral diarrhea virus subtype 1f in Northern Italy. <i>Infection, Genetics and Evolution</i> , 2016, 45, 262-267.	2.3	18
23	A new genotype of border disease virus with implications for molecular diagnostics. <i>Archives of Virology</i> , 2016, 161, 471-477.	2.1	26
24	Combination of conventional blood cultures and the SeptiFast molecular test in patients with suspected sepsis for the identification of bloodstream pathogens. <i>Diagnostic Microbiology and Infectious Disease</i> , 2014, 79, 287-292.	1.8	24
25	Aujeszky's Disease in Red Fox (<i>Vulpes vulpes</i>): Phylogenetic Analysis Unravels an Unexpected Epidemiologic Link. <i>Journal of Wildlife Diseases</i> , 2014, 50, 707.	0.8	13
26	Molecular characterization of flaviviruses from field-collected mosquitoes in northwestern Italy, 2011-2012. <i>Parasites and Vectors</i> , 2014, 7, 395.	2.5	28
27	Recent outbreak of aseptic meningitis in Italy due to Echovirus 30 and phylogenetic relationship with other European circulating strains. <i>Journal of Clinical Virology</i> , 2013, 58, 579-583.	3.1	37
28	A<sc>H</sc>1<sc>N</sc>1pdm09 hemagglutinin <sc>D</sc>222<sc>G</sc> and <sc>D</sc>222<sc>N</sc> variants are frequently harbored by patients requiring extracorporeal membrane oxygenation and advanced respiratory assistance for severe <sc>A</sc>(<sc>H</sc>1<sc>N</sc>1)pdm09 infection. <i>Influenza and Other Respiratory Viruses</i> , 2013, 7, 1416-1426.	3.4	20
29	Ranking viruses: measures of positional importance within networks define core viruses for rational polyvalent vaccine development. <i>Bioinformatics</i> , 2012, 28, 1624-1632.	4.1	20
30	Evidence of mosquito-transmitted flavivirus circulation in Piedmont, north-western Italy. <i>Parasites and Vectors</i> , 2012, 5, 99.	2.5	15
31	<i>Culex</i> Flavivirus and West Nile Virus Mosquito Coinfection and Positive Ecological Association in Chicago, United States. <i>Vector-Borne and Zoonotic Diseases</i> , 2011, 11, 1099-1105.	1.5	106
32	Differentiation of Mesenchymal Stem Cells Derived from Pancreatic Islets and Bone Marrow into Islet-Like Cell Phenotype. <i>PLoS ONE</i> , 2011, 6, e28175.	2.5	59
33	Analysis of different medulloblastoma histotypes by two-dimensional gel and MALDI-TOF. <i>Child's Nervous System</i> , 2011, 27, 2077-2085.	1.1	13
34	Taxon ordering in phylogenetic trees by means of evolutionary algorithms. <i>BioData Mining</i> , 2011, 4, 20.	4.0	2
35	Taxon ordering in phylogenetic trees: a workbench test. <i>BMC Bioinformatics</i> , 2011, 12, 58.	2.6	4
36	Adding Vertical Meaning to Phylogenetic Trees by Artificial Evolution. <i>Lecture Notes in Computer Science</i> , 2011, , 329-336.	1.3	0

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37	Investigating Populational Evolutionary Algorithms to Add Vertical Meaning in Phylogenetic Trees. Lecture Notes in Computer Science, 2010, , 240-247.	1.3	0
38	Clinical evaluation of the COBAS Ampliprep [®] , [®] /COBAS TaqMan [®] , [®] for HCV RNA quantitation in comparison with the branched [®] DNA assay. Journal of Medical Virology, 2008, 80, 254-260.	5.0	43
39	Evaluation of a novel real-time PCR system for cytomegalovirus DNA quantitation on whole blood and correlation with pp65-antigen test in guiding pre-emptive antiviral treatment. Journal of Virological Methods, 2008, 148, 9-16.	2.1	31
40	COBAS AmpliPrep-COBAS TaqMan Hepatitis B Virus (HBV) Test: a Novel Automated Real-Time PCR Assay for Quantification of HBV DNA in Plasma. Journal of Clinical Microbiology, 2007, 45, 828-834.	3.9	55
41	Real-time PCR per HBV DNA: valutazione del nuovo sistema automatizzato COBAS AMPLIPREP [®] , [®] /COBAS TAQMAN [®] , [®] HBV. Microbiologia Medica, 2007, 22, .	0.1	0