Marta Canuti

List of Publications by Year in descending order

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315357 361045 1,700 54 20 38 citations h-index g-index papers 58 58 58 2293 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Coâ€circulation of five species of dog parvoviruses and canine adenovirus type 1 among gray wolves () Tj ETQq1	1 0.78431 1.3	14 _g gBT/Over
2	Waiting for the truth: is reluctance in accepting an early origin hypothesis for SARS-CoV-2 delaying our understanding of viral emergence?. BMJ Global Health, 2022, 7, e008386.	2.0	10
3	Natural disease and evolution of an <i>Amdoparvovirus</i> endemic in striped skunks (<i>Mephitis) Tj ETQq1 1 (</i>	0.784314 1.3	rgBT /Over <mark>l</mark> or
4	Characterization of Vaccine Breakthrough Cases during Measles Outbreaks in Milan and Surrounding Areas, Italy, 2017–2021. Viruses, 2022, 14, 1068.	1.5	9
5	A new perspective on the evolution and diversity of the genus <i>Amdoparvovirus </i> (family) Tj ETQq1 1 0.7843 phylogenetics. Virus Evolution, 2022, 8, .	14 rgBT /0 2.2	Overlock 101 4
6	Distribution and diversity of dog parvoviruses in wild, freeâ€roaming and domestic canids of Newfoundland and Labrador, Canada. Transboundary and Emerging Diseases, 2022, 69, .	1.3	13
7	Evidence of SARS-CoV-2 RNA in an Oropharyngeal Swab Specimen, Milan, Italy, Early December 2019. Emerging Infectious Diseases, 2021, 27, 648-650.	2.0	64
8	Detection and Molecular Characterization of Two Gammaherpesviruses from Pantesco Breed Donkeys during an Outbreak of Mild Respiratory Disease. Viruses, 2021, 13, 1527.	1.5	1
9	Investigating the Diversity and Host Range of Novel Parvoviruses from North American Ducks Using Epidemiology, Phylogenetics, Genome Structure, and Codon Usage Analysis. Viruses, 2021, 13, 193.	1.5	11
10	Dried Blood Spot as an Alternative to Plasma/Serum for SARS-CoV-2 IgG Detection, an Opportunity to Be Sized to Facilitate COVID-19 Surveillance Among Schoolchildren. Pediatric Infectious Disease Journal, 2021, 40, e46-e47.	1.1	20
11	Newlavirus, a Novel, Highly Prevalent, and Highly Diverse Protoparvovirus of Foxes (Vulpes spp.). Viruses, 2021, 13, 1969.	1.5	6
12	Multi-host dispersal of known and novel carnivore amdoparvoviruses. Virus Evolution, 2020, 6, .	2.2	15
13	Reorganizing the family Parvoviridae: a revised taxonomy independent of the canonical approach based on host association. Archives of Virology, 2020, 165, 2133-2146.	0.9	154
14	A Two-Component System Acquired by Horizontal Gene Transfer Modulates Gene Transfer and Motility via Cyclic Dimeric GMP. Journal of Molecular Biology, 2020, 432, 4840-4855.	2.0	8
15	Molecular Epidemiology of B3 and D8 Measles Viruses through Hemagglutinin Phylogenetic History. International Journal of Molecular Sciences, 2020, 21, 4435.	1.8	12
16	Ecology and Infection Dynamics of Multi-Host Amdoparvoviral and Protoparvoviral Carnivore Pathogens. Pathogens, 2020, 9, 124.	1.2	25
17	Discovery and Characterization of Novel RNA Viruses in Aquatic North American Wild Birds. Viruses, 2019, 11, 768.	1.5	41
18	New Insight Into Avian Papillomavirus Ecology and Evolution From Characterization of Novel Wild Bird Papillomaviruses. Frontiers in Microbiology, 2019, 10, 701.	1.5	22

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19	Identification of a Novel Gammaherpesvirus in Canada lynx (Lynx canadensis). Viruses, 2019, 11, 363.	1.5	6
20	Molecular Characterization and Evolutionary Analyses of Carnivore Protoparvovirus 1 NS1 Gene. Viruses, 2019, 11 , 308 .	1.5	31
21	Virus discovery reveals frequent infection by diverse novel members of the Flaviviridae in wild lemurs. Archives of Virology, 2019, 164, 509-522.	0.9	11
22	ICTV Virus Taxonomy Profile: Parvoviridae. Journal of General Virology, 2019, 100, 367-368.	1.3	312
23	ViDiT–CACTUS: an inexpensive and versatile library preparation and sequence analysis method for virus discovery and other microbiology applications. Canadian Journal of Microbiology, 2018, 64, 761-773.	0.8	12
24	Measles re-emergence in Northern Italy: Pathways of measles virus genotype D8, 2013–2014. Infection, Genetics and Evolution, 2017, 48, 120-126.	1.0	10
25	Introduction of canine parvovirus 2 into wildlife on the Island of Newfoundland, Canada. Infection, Genetics and Evolution, 2017, 55, 205-208.	1.0	18
26	Epidemiology and molecular characterization of protoparvoviruses infecting wild raccoons (Procyon lotor) in British Columbia, Canada. Virus Research, 2017, 242, 85-89.	1.1	13
27	Full genetic characterization and epidemiology of a novel amdoparvovirus in striped skunk (Mephitis) Tj ETQq1	1 0.78431	4 rgBT /Overl
28	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. Virus Evolution, 2016, 2, vew005.	2.2	26
29	Analysis of the structure, evolution, and expression of CD24, an important regulator of cell fate. Gene, 2016, 590, 324-337.	1.0	21
30	Driving forces behind the evolution of the Aleutian mink disease parvovirus in the context of intensive farming. Virus Evolution, 2016, 2, vew004.	2.2	40
31	Amdoparvoviruses in small mammals: expanding our understanding of parvovirus diversity, distribution, and pathology. Frontiers in Microbiology, 2015, 6, 1119.	1.5	45
32	Reduced maternal levels of common viruses during pregnancy predict offspring psychosis: Potential role of enhanced maternal immune activity?. Schizophrenia Research, 2015, 166, 248-254.	1.1	13
33	Identification of a Novel Human Rhinovirus C Type by Antibody Capture VIDISCA-454. Viruses, 2015, 7, 239-251.	1.5	2
34	Viral metagenomics in drug-na \tilde{A} -ve, first-onset schizophrenia patients with prominent negative symptoms. Psychiatry Research, 2015, 229, 678-684.	1.7	2
35	A novel genus in the order Picornavirales detected in human stool. Journal of General Virology, 2015, 96, 3440-3443.	1.3	23
36	Influenza and Other Respiratory Viruses Involved in Severe Acute Respiratory Disease in Northern Italy during the Pandemic and Postpandemic Period (2009–2011). BioMed Research International, 2014, 2014, 1-5.	0.9	25

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37	Metagenomic analysis of a sample from a patient with respiratory tract infection reveals the presence of a $\tilde{A}\tilde{Z}\hat{A}^3$ -papillomavirus. Frontiers in Microbiology, 2014, 5, 347.	1.5	15
38	Persistent viremia by a novel parvovirus in a slow loris (Nycticebus coucang) with diffuse histiocytic sarcoma. Frontiers in Microbiology, 2014, 5, 655.	1.5	14
39	Unexplained diarrhoea in HIV-1 infected individuals. BMC Infectious Diseases, 2014, 14, 22.	1.3	48
40	Identification and characterization of unrecognized viruses in stool samples of non-polio acute flaccid paralysis children by simplified VIDISCA. Virology Journal, 2014, 11, 146.	1.4	18
41	Virus discovery: are we scientists or genome collectors?. Trends in Microbiology, 2014, 22, 229-231.	3.5	17
42	Limited geographic distribution of the novel cyclovirus CyCV-VN. Scientific Reports, 2014, 4, 3967.	1.6	11
43	Full Genome Virus Detection in Fecal Samples Using Sensitive Nucleic Acid Preparation, Deep Sequencing, and a Novel Iterative Sequence Classification Algorithm. PLoS ONE, 2014, 9, e93269.	1.1	71
44	Identification of a new genotype of Torque Teno Mini virus. Virology Journal, 2013, 10, 323.	1.4	17
45	Identification of a New Cyclovirus in Cerebrospinal Fluid of Patients with Acute Central Nervous System Infections. MBio, 2013, 4, e00231-13.	1.8	109
46	Autologous Antibody Capture to Enrich Immunogenic Viruses for Viral Discovery. PLoS ONE, 2013, 8, e78454.	1.1	16
47	Performance of VIDISCA-454 in Feces-Suspensions and Serum. Viruses, 2012, 4, 1328-1334.	1.5	37
48	Hepatitis E in Italy: A long-term prospective study. Journal of Hepatology, 2011, 54, 34-40.	1.8	77
49	Two Novel Parvoviruses in Frugivorous New and Old World Bats. PLoS ONE, 2011, 6, e29140.	1.1	62
50	Coâ€circulation of genetically distinct human metapneumovirus and human bocavirus strains in young children with respiratory tract infections in Italy. Journal of Medical Virology, 2011, 83, 156-164.	2.5	21
51	A Sensitive Assay for Virus Discovery in Respiratory Clinical Samples. PLoS ONE, 2011, 6, e16118.	1.1	80
52	Rapid molecular evolution of human bocavirus revealed by Bayesian coalescent inference. Infection, Genetics and Evolution, 2010, 10, 215-220.	1.0	20
53	Viable Newcastle Disease Vaccine Strains in a Pharmaceutical Dump. Emerging Infectious Diseases, 2007, 13, 1901-1903.	2.0	0
54	Molecular Evidence for SARS-CoV-2 in Samples Collected From Patients With Morbilliform Eruptions Since Late Summer 2019 in Lombardy, Northern Italy. SSRN Electronic Journal, 0, , .	0.4	8