

Marta Giovanetti

List of Publications by Year in descending order

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Version: 2024-02-01

112
papers

10,853
citations

136950

32
h-index

46799

89
g-index

139
all docs

139
docs citations

139
times ranked

18097
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessment of core and support functions of the communicable disease surveillance system in the Kurdistan Region of Iraq. <i>Journal of Medical Virology</i> , 2022, 94, 469-479.	5.0	4
2	The first Italian outbreak of SARS-CoV-2 B.1.1.7 lineage in Corzano, Lombardy. <i>Journal of Medical Virology</i> , 2022, 94, 413-416.	5.0	6
3	SARS-CoV-2 AY.4.2 variant circulating in Italy: Genomic preliminary insight. <i>Journal of Medical Virology</i> , 2022, 94, 1689-1692.	5.0	15
4	West Nile virus transmission potential in Portugal. <i>Communications Biology</i> , 2022, 5, 6.	4.4	18
5	Prisoners of variants, or free to act as prisoners of swabs? The case of Italy. <i>Journal of Medical Virology</i> , 2022, 94, 2334-2335.	5.0	1
6	SARS-CoV-2 serological cross-reactivity testing in Brazilian blood donors, October-December, 2019. <i>Journal of Infection</i> , 2022, , .	3.3	0
7	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
8	Metavirome composition of Brazilian blood donors positive for the routinely tested blood-borne infections. <i>Virus Research</i> , 2022, 311, 198689.	2.2	3
9	Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic. <i>Virus Evolution</i> , 2022, 8, veac024.	4.9	37
10	The SARS-CoV-2 Mu variant should not be left aside: It warrants attention for its immuno-escaping ability. <i>Journal of Medical Virology</i> , 2022, 94, 2479-2486.	5.0	6
11	Molecular Identification and Ecology of Portuguese Wild-Caught Phlebotomine Sandfly Specimens. , 2022, 2, 19-31.		4
12	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0015522.	3.0	4
13	Analysis of HIV-1 integrase genotypes and polymorphisms among integrase inhibitors-based antiretroviral treatment naïve patients in South Sudan. <i>Journal of Medical Virology</i> , 2022, 94, 3320-3327.	5.0	2
14	Molecular detection of SARS-CoV-2 eta VOI in Northern Italy: a case report. <i>Clinical Chemistry and Laboratory Medicine</i> , 2022, 60, 61-63.	2.3	0
15	The unresolved question on COVID-19 virus origin: The three cards game?. <i>Journal of Medical Virology</i> , 2022, 94, 1257-1260.	5.0	19
16	SARS-CoV-2 epidemic in Brazil: how the displacement of variants has driven distinct epidemic waves. <i>Virus Research</i> , 2022, 315, 198785.	2.2	26
17	Competition for dominance within replicating quasispecies during prolonged SARS-CoV-2 infection in an immunocompromised host. <i>Virus Evolution</i> , 2022, 8, .	4.9	21
18	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. <i>Nature Medicine</i> , 2022, 28, 1785-1790.	30.7	456

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19	Retrospective Investigation in Horses with Encephalitis Reveals Unnoticed Circulation of West Nile Virus in Brazil. <i>Viruses</i> , 2022, 14, 1540.	3.3	1
20	The Divergent Pattern of SARS-CoV-2 Variant Predominance and Transmission Dynamics in the Brazilian Island of Ilhabela. <i>Viruses</i> , 2022, 14, 1481.	3.3	1
21	Dynamics and Determinants of SARS-CoV-2 RT-PCR Testing on Symptomatic Individuals Attending Healthcare Centers during 2020 in Bahia, Brazil. <i>Viruses</i> , 2022, 14, 1549.	3.3	2
22	Evolution patterns of SARS-CoV-2: Snapshot on its genome variants. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 88-91.	2.1	121
23	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. <i>International Journal of Infectious Diseases</i> , 2021, 103, 234-241.	3.3	63
24	Multi-epitope based vaccine against yellow fever virus applying immunoinformatics approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 219-235.	3.5	34
25	SARS-CoV-2 Lineages and Sub-Lineages Circulating Worldwide: A Dynamic Overview. <i>Chemotherapy</i> , 2021, 66, 3-7.	1.6	39
26	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	30.7	326
27	Animal Hosts and Experimental Models of SARS-CoV-2 Infection. <i>Chemotherapy</i> , 2021, 66, 1-9.	1.6	13
28	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	27.8	1,381
29	Untargeted Metabolomics Insights into Newborns with Congenital Zika Infection. <i>Pathogens</i> , 2021, 10, 468.	2.8	7
30	Short report: Introduction of chikungunya virus ECSA genotype into the Brazilian Midwest and its dispersion through the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009290.	3.0	17
31	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021, 12, 2296.	12.8	29
32	The importance of genomic analysis in cracking the coronavirus pandemic. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 547-562.	3.1	14
33	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489.	4.4	23
34	Genomic surveillance activities unveil the introduction of the SARS-CoV-2 B.1.525 variant of interest in Brazil: Case report. <i>Journal of Medical Virology</i> , 2021, 93, 5523-5526.	5.0	27
35	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021, 27, 1393-1404.	4.3	13
36	Genomic Evidence of SARS-CoV-2 Reinfection Involving E484K Spike Mutation, Brazil. <i>Emerging Infectious Diseases</i> , 2021, 27, 1522-1524.	4.3	181

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37	Betacoronaviruses genome analysis reveals evolution toward specific codons usage: Implications for SARS-CoV-2 mitigation strategies. <i>Journal of Medical Virology</i> , 2021, 93, 5630-5634.	5.0	2
38	COVID-19 sniffer dog experimental training: Which protocol and which implications for reliable identification?. <i>Journal of Medical Virology</i> , 2021, 93, 5924-5930.	5.0	16
39	First detection of SARS-CoV-2 spike protein N501 mutation in Italy in August, 2020. <i>Lancet Infectious Diseases</i> , 2021, 21, e147.	9.1	84
40	The variants question: What is the problem?. <i>Journal of Medical Virology</i> , 2021, 93, 6479-6485.	5.0	26
41	SARS-CoV-2 B.1.617 Indian variants: Are electrostatic potential changes responsible for a higher transmission rate?. <i>Journal of Medical Virology</i> , 2021, 93, 6551-6556.	5.0	79
42	Genomic monitoring unveil the early detection of the SARS-CoV-2 B.1.351 (beta) variant (20H/501Y.V2) in Brazil. <i>Journal of Medical Virology</i> , 2021, 93, 6782-6787.	5.0	24
43	West Nile Virus in Brazil. <i>Pathogens</i> , 2021, 10, 896.	2.8	14
44	Phylogenetic Analysis of Massilia phlebovirus in Portugal. <i>Viruses</i> , 2021, 13, 1412.	3.3	9
45	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	11.0	73
46	Promoting Responsible Research and Innovation (RRI) During Brazilian Activities of Genomic and Epidemiological Surveillance of Arboviruses. <i>Frontiers in Public Health</i> , 2021, 9, 693743.	2.7	4
47	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009591.	3.0	13
48	Detection of a SARS-CoV-2 P.1.1 variant lacking N501Y in a vaccinated health care worker in Italy. <i>Journal of Infection</i> , 2021, , .	3.3	1
49	Molecular surveillance of the on-going SARS-COV-2 epidemic in Ribeirao Preto City, Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104976.	2.3	7
50	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
51	Shortening Epitopes to Survive: The Case of SARS-CoV-2 Lambda Variant. <i>Biomolecules</i> , 2021, 11, 1494.	4.0	5
52	Role of Q675H Mutation in Improving SARS-CoV-2 Spike Interaction with the Furin Binding Pocket. <i>Viruses</i> , 2021, 13, 2511.	3.3	12
53	Return of the founder Chikungunya virus to its place of introduction into Brazil is revealed by genomic characterization of exanthematic disease cases. <i>Emerging Microbes and Infections</i> , 2020, 9, 53-57.	6.5	11
54	The first two cases of 2019-nCoV in Italy: Where they come from?. <i>Journal of Medical Virology</i> , 2020, 92, 518-521.	5.0	263

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55	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016–2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	4.7	39
56	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1824-1834.	6.5	42
57	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	3.0	17
58	Emerging of a SARS-CoV-2 viral strain with a deletion in nsp1. <i>Journal of Translational Medicine</i> , 2020, 18, 329.	4.4	71
59	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020, 11, 949.	2.4	65
60	Co-Circulation of Two Independent Clades and Persistence of CHIKV-ECSA Genotype during Epidemic Waves in Rio de Janeiro, Southeast Brazil. <i>Pathogens</i> , 2020, 9, 984.	2.8	13
61	Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission. <i>Journal of Medical Virology</i> , 2020, 92, 2232-2237.	5.0	28
62	Sars-CoV-2 Envelope and Membrane Proteins: Structural Differences Linked to Virus Characteristics?. <i>BioMed Research International</i> , 2020, 2020, 1-6.	1.9	150
63	A doubt of multiple introduction of SARS-CoV-2 in Italy: A preliminary overview. <i>Journal of Medical Virology</i> , 2020, 92, 1634-1636.	5.0	48
64	Application of the ARIMA model on the COVID-2019 epidemic dataset. <i>Data in Brief</i> , 2020, 29, 105340.	1.0	455
65	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020, 36, 3552-3555.	4.1	129
66	COVID-2019: The role of the nsp2 and nsp3 in its pathogenesis. <i>Journal of Medical Virology</i> , 2020, 92, 584-588.	5.0	308
67	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
68	The global spread of 2019-nCoV: a molecular evolutionary analysis. <i>Pathogens and Global Health</i> , 2020, 114, 64-67.	2.3	161
69	Neonatal surveillance for congenital Zika infection during the 2016 microcephaly outbreak in Salvador, Brazil: Zika virus detection in asymptomatic newborns. <i>International Journal of Gynecology and Obstetrics</i> , 2020, 148, 9-14.	2.3	12
70	The 2019–2020 new coronavirus epidemic: Evidence for virus evolution. <i>Journal of Medical Virology</i> , 2020, 92, 455-459.	5.0	508
71	Evolutionary analysis of SARS-CoV-2: how mutation of Non-Structural Protein 6 (NSP6) could affect viral autophagy. <i>Journal of Infection</i> , 2020, 81, e24-e27.	3.3	211
72	Molecular Epidemiology of HIV-1 in African Countries: A Comprehensive Overview. <i>Pathogens</i> , 2020, 9, 1072.	2.8	28

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73	Severe airport sanitarian control could slow down the spreading of COVID-19 pandemics in Brazil. PeerJ, 2020, 8, e9446.	2.0	28
74	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. Microbiology Spectrum, 2019, 7, .	3.0	14
75	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016â€“2019. Journal of Virology, 2019, 94, .	3.4	62
76	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. PLoS ONE, 2019, 14, e0217871.	2.5	31
77	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. PLoS Neglected Tropical Diseases, 2019, 13, e0007231.	3.0	44
78	Lipidomic Analysis Reveals Serum Alteration of Plasmalogens in Patients Infected With ZIKA Virus. Frontiers in Microbiology, 2019, 10, 753.	3.5	39
79	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. PLoS Neglected Tropical Diseases, 2019, 13, e0007065.	3.0	75
80	Opsoclonus-myoclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. International Journal of Infectious Diseases, 2018, 75, 11-14.	3.3	13
81	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. Infection, Genetics and Evolution, 2017, 48, 95-101.	2.3	9
82	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols, 2017, 12, 1261-1276.	12.0	898
83	Origin and evolution of Nipah virus. Journal of Medical Virology, 2016, 88, 380-388.	5.0	41
84	Genetic diversity of the haemagglutinin (HA) of human influenza a (H1N1) virus in montenegro: Focus on its origin and evolution. Journal of Medical Virology, 2016, 88, 1905-1913.	5.0	20
85	Zika virus complete genome from Salvador, Bahia, Brazil. Infection, Genetics and Evolution, 2016, 41, 142-145.	2.3	24
86	Phylogenesis and homology modeling in Zika virus epidemic: food for thought. Pathogens and Global Health, 2016, 110, 269-274.	2.3	5
87	MISSEL: a method to identify a large number of small species-specific genomic subsequences and its application to viruses classification. BioData Mining, 2016, 9, 38.	4.0	15
88	Zika virus in the Americas: Early epidemiological and genetic findings. Science, 2016, 352, 345-349.	12.6	877
89	Genetic diversity in Ebola virus: Phylogenetic and in silico structural studies of Ebola viral proteins. Asian Pacific Journal of Tropical Medicine, 2016, 9, 337-343.	0.8	11
90	Zika Virus spreading in South America: Evolutionary analysis of emerging neutralizing resistant Phe279Ser strains. Asian Pacific Journal of Tropical Medicine, 2016, 9, 445-452.	0.8	14

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91	Deep Sequencing Analysis of Human T Cell Lymphotropic Virus Type 1 Long Terminal Repeat 5' Region from Patients with Tropical Spastic Paraparesis/Human T Cell Lymphotropic Virus Type 1-Associated Myelopathy and Asymptomatic Carriers. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 279-283.	1.1	4
92	Phylogenetic analysis of human immunodeficiency virus type 2 group B. <i>Journal of Global Infectious Diseases</i> , 2016, 8, 108.	0.5	5
93	Hepatitis E Virus Circulation in Italy: Phylogenetic and Evolutionary Analysis. <i>Hepatitis Monthly</i> , 2016, 16, e31951.	0.2	18
94	An epidemiological investigation to reconstruct a probable human immunodeficiency virus -1 transmission network: a case report. <i>Journal of Medical Case Reports</i> , 2015, 9, 253.	0.8	0
95	Impact of spatial dispersion, evolution and selection on Ebola Zaire Virus epidemic waves. <i>Scientific Reports</i> , 2015, 5, 10170.	3.3	27
96	Reliable timescale inference of HBV genotype A origin and phylodynamics. <i>Infection, Genetics and Evolution</i> , 2015, 32, 361-369.	2.3	24
97	Hepatitis B virus genotype and subgenotype prevalence and distribution in Montenegro. <i>Journal of Medical Virology</i> , 2015, 87, 807-813.	5.0	5
98	Analysis of the ORFK1 hypervariable regions reveal distinct HHV-8 clustering in Kaposi's sarcoma and non-Kaposi's cases. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 1.	8.6	62
99	Amino acid mutations in Ebola virus glycoprotein of the 2014 epidemic. <i>Journal of Medical Virology</i> , 2015, 87, 893-898.	5.0	7
100	Molecular Characterization of the Human Immunodeficiency Virus Type 1 in Women and Their Vertically Infected Children. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 1046-1051.	1.1	5
101	Two Distinct Hepatitis C Virus Genotype 1a Clades Have Different Geographical Distribution and Association With Natural Resistance to NS3 Protease Inhibitors. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv043.	0.9	30
102	Molecular epidemiology and phylogenetic analysis of Hepatitis B virus in a group of migrants in Italy. <i>BMC Infectious Diseases</i> , 2015, 15, 287.	2.9	12
103	Characterization of spotted fever group Rickettsiae in ticks from a city park of Rome, Italy. <i>Annali Dell'Istituto Superiore Di Sanita</i> , 2015, 51, 284-90.	0.4	15
104	Phylogeny of Dengue and Chikungunya viruses in Al Hudayda governorate, Yemen. <i>Infection, Genetics and Evolution</i> , 2014, 27, 395-401.	2.3	19
105	Molecular epidemiology and genetic diversity of human rhinovirus affecting hospitalized children in Rome. <i>Medical Microbiology and Immunology</i> , 2013, 202, 303-311.	4.8	20
106	HIV Type 1 Origin and Transmission Dynamics Among Different Risk Groups in Sardinia: Molecular Epidemiology Within the Close Boundaries of an Italian Island. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 404-410.	1.1	11
107	Epidemiological history and phylogeography of West Nile virus lineage 2. <i>Infection, Genetics and Evolution</i> , 2013, 17, 46-50.	2.3	58
108	Full-Genome Characterization of a G8P[8] Rotavirus That Emerged among Children with Diarrhea in Croatia in 2006. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1583-1588.	3.9	17

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109	Migration patterns of HIV-1 subtype B virus in Northern Italy. <i>New Microbiologica</i> , 2013, 36, 75-9.	0.1	6
110	When phylogenetic analysis complements the epidemiological investigation: a case of HIV-2 infection, Italy. <i>New Microbiologica</i> , 2013, 36, 93-6.	0.1	4
111	HIV-1 non-B subtypes in Italy: a growing trend. <i>New Microbiologica</i> , 2012, 35, 377-86.	0.1	18
112	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 0, , .	27.8	61