

Marta Giovanetti

List of Publications by Year in descending order

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Version: 2024-02-01

112
papers

10,853
citations

156536

32
h-index

53065

89
g-index

139
all docs

139
docs citations

139
times ranked

19328
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	1,210
3	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276.	5.5	898
4	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	6.0	877
5	The 2019â€œnew coronavirus epidemic: Evidence for virus evolution. <i>Journal of Medical Virology</i> , 2020, 92, 455-459.	2.5	508
6	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. <i>Nature Medicine</i> , 2022, 28, 1785-1790.	15.2	456
7	Application of the ARIMA model on the COVID-2019 epidemic dataset. <i>Data in Brief</i> , 2020, 29, 105340.	0.5	455
8	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	15.2	326
9	COVIDâ€œ2019: The role of the nsp2 and nsp3 in its pathogenesis. <i>Journal of Medical Virology</i> , 2020, 92, 584-588.	2.5	308
10	The first two cases of 2019â€œnCoV in Italy: Where they come from?. <i>Journal of Medical Virology</i> , 2020, 92, 518-521.	2.5	263
11	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.	1.7	211
12	Genomic Evidence of SARS-CoV-2 Reinfection Involving E484K Spike Mutation, Brazil. <i>Emerging Infectious Diseases</i> , 2021, 27, 1522-1524.	2.0	181
13	The global spread of 2019-nCoV: a molecular evolutionary analysis. <i>Pathogens and Global Health</i> , 2020, 114, 64-67.	1.0	161
14	Sars-CoV-2 Envelope and Membrane Proteins: Structural Differences Linked to Virus Characteristics?. <i>BioMed Research International</i> , 2020, 2020, 1-6.	0.9	150
15	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
16	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020, 36, 3552-3555.	1.8	129
17	Evolution patterns of SARS-CoV-2: Snapshot on its genome variants. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 88-91.	1.0	121
18	First detection of SARS-CoV-2 spike protein N501 mutation in Italy in August, 2020. <i>Lancet Infectious Diseases</i> , The, 2021, 21, e147.	4.6	84

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19	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.	2.5	79
20	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	1.3	75
21	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	5.1	73
22	Emerging of a SARS-CoV-2 viral strain with a deletion in nsp1. <i>Journal of Translational Medicine</i> , 2020, 18, 329.	1.8	71
23	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.	1.0	65
24	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.	1.5	63
25	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.	3.5	62
26	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016–2019. <i>Journal of Virology</i> , 2019, 94, .	1.5	62
27	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 0, , .	13.7	61
28	Epidemiological history and phylogeography of West Nile virus lineage 2. <i>Infection, Genetics and Evolution</i> , 2013, 17, 46-50.	1.0	58
29	A doubt of multiple introduction of SARS-CoV-2 in Italy: A preliminary overview. <i>Journal of Medical Virology</i> , 2020, 92, 1634-1636.	2.5	48
30	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007231.	1.3	44
31	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.	3.0	42
32	Origin and evolution of Nipah virus. <i>Journal of Medical Virology</i> , 2016, 88, 380-388.	2.5	41
33	Lipidomic Analysis Reveals Serum Alteration of Plasmalogens in Patients Infected With ZIKA Virus. <i>Frontiers in Microbiology</i> , 2019, 10, 753.	1.5	39
34	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	2.1	39
35	SARS-CoV-2 Lineages and Sub-Lineages Circulating Worldwide: A Dynamic Overview. <i>Chemotherapy</i> , 2021, 66, 3-7.	0.8	39
36	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	2.9	37

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37	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.	2.2	37
38	Multi-epitope based vaccine against yellow fever virus applying immunoinformatics approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 219-235.	2.0	34
39	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019, 14, e0217871.	1.1	31
40	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.	0.4	30
41	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021, 12, 2296.	5.8	29
42	Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission. <i>Journal of Medical Virology</i> , 2020, 92, 2232-2237.	2.5	28
43	Molecular Epidemiology of HIV-1 in African Countries: A Comprehensive Overview. <i>Pathogens</i> , 2020, 9, 1072.	1.2	28
44	Severe airport sanitarian control could slow down the spreading of COVID-19 pandemics in Brazil. <i>PeerJ</i> , 2020, 8, e9446.	0.9	28
45	Impact of spatial dispersion, evolution and selection on Ebola Zaire Virus epidemic waves. <i>Scientific Reports</i> , 2015, 5, 10170.	1.6	27
46	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.	2.5	27
47	The variants question: What is the problem?. <i>Journal of Medical Virology</i> , 2021, 93, 6479-6485.	2.5	26
48	SARS-CoV-2 epidemic in Brazil: how the displacement of variants has driven distinct epidemic waves. <i>Virus Research</i> , 2022, 315, 198785.	1.1	26
49	Reliable timescale inference of HBV genotype A origin and phylodynamics. <i>Infection, Genetics and Evolution</i> , 2015, 32, 361-369.	1.0	24
50	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016, 41, 142-145.	1.0	24
51	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.	2.5	24
52	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.	2.0	23
53	Competition for dominance within replicating quasispecies during prolonged SARS-CoV-2 infection in an immunocompromised host. <i>Virus Evolution</i> , 2022, 8, .	2.2	21
54	Molecular epidemiology and genetic diversity of human rhinovirus affecting hospitalized children in Rome. <i>Medical Microbiology and Immunology</i> , 2013, 202, 303-311.	2.6	20

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55	Genetic diversity of the haemagglutinin (HA) of human influenza A (H1N1) virus in Montenegro: Focus on its origin and evolution. <i>Journal of Medical Virology</i> , 2016, 88, 1905-1913.	2.5	20
56	Phylogeny of Dengue and Chikungunya viruses in Al Hudayda governorate, Yemen. <i>Infection, Genetics and Evolution</i> , 2014, 27, 395-401.	1.0	19
57	The unresolved question on COVID-19 virus origin: The three cards game?. <i>Journal of Medical Virology</i> , 2022, 94, 1257-1260.	2.5	19
58	Hepatitis E Virus Circulation in Italy: Phylogenetic and Evolutionary Analysis. <i>Hepatitis Monthly</i> , 2016, 16, e31951.	0.1	18
59	West Nile virus transmission potential in Portugal. <i>Communications Biology</i> , 2022, 5, 6.	2.0	18
60	HIV-1 non-B subtypes in Italy: a growing trend. <i>New Microbiologica</i> , 2012, 35, 377-86.	0.1	18
61	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.	1.8	17
62	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	1.3	17
63	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.	1.3	17
64	COVID-19 sniffer dog experimental training: Which protocol and which implications for reliable identification?. <i>Journal of Medical Virology</i> , 2021, 93, 5924-5930.	2.5	16
65	MISSEL: a method to identify a large number of small species-specific genomic subsequences and its application to viruses classification. <i>BioData Mining</i> , 2016, 9, 38.	2.2	15
66	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.	0.2	15
67	SARS-CoV-2 AY.4.2 variant circulating in Italy: Genomic preliminary insight. <i>Journal of Medical Virology</i> , 2022, 94, 1689-1692.	2.5	15
68	Zika Virus spreading in South America: Evolutionary analysis of emerging neutralizing resistant Phe279Ser strains. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 445-452.	0.4	14
69	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	14
70	The importance of genomic analysis in cracking the coronavirus pandemic. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 547-562.	1.5	14
71	West Nile Virus in Brazil. <i>Pathogens</i> , 2021, 10, 896.	1.2	14
72	Opsoclonus-myoclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , 2018, 75, 11-14.	1.5	13

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73	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.	1.2	13
74	Animal Hosts and Experimental Models of SARS-CoV-2 Infection. <i>Chemotherapy</i> , 2021, 66, 1-9.	0.8	13
75	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021, 27, 1393-1404.	2.0	13
76	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009591.	1.3	13
77	Molecular epidemiology and phylogenetic analysis of Hepatitis B virus in a group of migrants in Italy. <i>BMC Infectious Diseases</i> , 2015, 15, 287.	1.3	12
78	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.	1.0	12
79	Role of Q675H Mutation in Improving SARS-CoV-2 Spike Interaction with the Furin Binding Pocket. <i>Viruses</i> , 2021, 13, 2511.	1.5	12
80	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.	0.5	11
81	Genetic diversity in Ebola virus: Phylogenetic and in silico structural studies of Ebola viral proteins. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 337-343.	0.4	11
82	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.	3.0	11
83	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. <i>Infection, Genetics and Evolution</i> , 2017, 48, 95-101.	1.0	9
84	Phylogenetic Analysis of Massilia phlebovirus in Portugal. <i>Viruses</i> , 2021, 13, 1412.	1.5	9
85	Amino acid mutations in Ebola virus glycoprotein of the 2014 epidemic. <i>Journal of Medical Virology</i> , 2015, 87, 893-898.	2.5	7
86	Untargeted Metabolomics Insights into Newborns with Congenital Zika Infection. <i>Pathogens</i> , 2021, 10, 468.	1.2	7
87	Molecular surveillance of the on-going SARS-COV-2 epidemic in Ribeirao Preto City, Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104976.	1.0	7
88	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.	2.5	6
89	Migration patterns of HIV-1 subtype B virus in Northern Italy. <i>New Microbiologica</i> , 2013, 36, 75-9.	0.1	6
90	The SARS-CoV-2 Mu variant should not be left aside: It warrants attention for its immunoevading ability. <i>Journal of Medical Virology</i> , 2022, 94, 2479-2486.	2.5	6

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91	Hepatitis B virus genotype and subgenotype prevalence and distribution in Montenegro. <i>Journal of Medical Virology</i> , 2015, 87, 807-813.	2.5	5
92	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.	0.5	5
93	Phylogenesis and homology modeling in Zika virus epidemic: food for thought. <i>Pathogens and Global Health</i> , 2016, 110, 269-274.	1.0	5
94	Phylogenetic analysis of human immunodeficiency virus type 2 group B. <i>Journal of Global Infectious Diseases</i> , 2016, 8, 108.	0.2	5
95	Shortening Epitopes to Survive: The Case of SARS-CoV-2 Lambda Variant. <i>Biomolecules</i> , 2021, 11, 1494.	1.8	5
96	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.	0.5	4
97	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.	1.3	4
98	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.	2.5	4
99	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
100	Molecular Identification and Ecology of Portuguese Wild-Caught Phlebotomine Sandfly Specimens. , 2022, 2, 19-31.		4
101	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0015522.	1.2	4
102	Metavirome composition of Brazilian blood donors positive for the routinely tested blood-borne infections. <i>Virus Research</i> , 2022, 311, 198689.	1.1	3
103	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.	2.5	2
104	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.	2.5	2
105	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.	1.5	2
106	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, , .	1.7	1
107	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.	2.5	1
108	Retrospective Investigation in Horses with Encephalitis Reveals Unnoticed Circulation of West Nile Virus in Brazil. <i>Viruses</i> , 2022, 14, 1540.	1.5	1

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109	The Divergent Pattern of SARS-CoV-2 Variant Predominance and Transmission Dynamics in the Brazilian Island of Ilhabela. <i>Viruses</i> , 2022, 14, 1481.	1.5	1
110	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.	0.4	0
111	SARS-CoV-2 serological cross-reactivity testing in Brazilian blood donors, October-December, 2019. <i>Journal of Infection</i> , 2022, , .	1.7	0
112	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.	1.4	0