## Stefano Gaiarsa

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5194770/publications.pdf

Version: 2024-02-01

34 papers 1,746

<sup>393982</sup>
19
h-index

34 g-index

40 all docs

40 docs citations

40 times ranked

4144 citing authors

#	Article	IF	CITATIONS
1	Tocilizumab for Treatment of Severe COVID-19 Patients: Preliminary Results from SMAtteo COvid19 REgistry (SMACORE). Microorganisms, 2020, 8, 695.	1.6	186
2	Comparative Analysis of the Two Acinetobacter baumannii Multilocus Sequence Typing (MLST) Schemes. Frontiers in Microbiology, 2019, 10, 930.	1.5	133
3	Severe acute respiratory syndrome coronavirus 2 RNA contamination of inanimate surfaces and virus viability in a health care emergency unit. Clinical Microbiology and Infection, 2020, 26, 1094.e1-1094.e5.	2.8	121
4	Clinical characteristics of coronavirus disease (COVID-19) early findings from a teaching hospital in Pavia, North Italy, 21 to 28 February 2020. Eurosurveillance, 2020, 25, .	3.9	119
5	Bispecific IgG neutralizes SARS-CoV-2 variants and prevents escape in mice. Nature, 2021, 593, 424-428.	13.7	108
6	Effects of global changes on the climatic niche of the tick Ixodes ricinus inferred by species distribution modelling. Parasites and Vectors, 2013, 6, 271.	1.0	106
7	Genomic epidemiology of SARS-CoV-2 reveals multiple lineages and early spread of SARS-CoV-2 infections in Lombardy, Italy. Nature Communications, 2021, 12, 434.	5.8	102
8	Shifts of Faecal Microbiota During Sporadic Colorectal Carcinogenesis. Scientific Reports, 2018, 8, 10329.	1.6	99
9	Genomic Epidemiology of Klebsiella pneumoniae in Italy and Novel Insights into the Origin and Global Evolution of Its Resistance to Carbapenem Antibiotics. Antimicrobial Agents and Chemotherapy, 2015, 59, 389-396.	1.4	97
10	SARS Cov-2 infection in a renal-transplanted patient: A case report. American Journal of Transplantation, 2020, 20, 1882-1884.	2.6	76
11	Tracking Nosocomial Klebsiella pneumoniae Infections and Outbreaks by Whole-Genome Analysis: Small-Scale Italian Scenario within a Single Hospital. Journal of Clinical Microbiology, 2015, 53, 2861-2868.	1.8	71
12	<i>Deianiraea</i> , an extracellular bacterium associated with the ciliate <i>Paramecium</i> , suggests an alternative scenario for the evolution of <i>Rickettsiales</i> . ISME Journal, 2019, 13, 2280-2294.	4.4	67
13	Acetic Acid Bacteria Genomes Reveal Functional Traits for Adaptation to Life in Insect Guts. Genome Biology and Evolution, 2014, 6, 912-920.	1.1	66
14	EBV DNA increase in COVID-19 patients with impaired lymphocyte subpopulation count. International Journal of Infectious Diseases, 2021, 104, 315-319.	1.5	66
15	Lack of SARS-CoV-2 RNA environmental contamination in a tertiary referral hospital for infectious diseases in Northern Italy. Journal of Hospital Infection, 2020, 105, 474-476.	1.4	51
16	Emergency Department and Out-of-Hospital Emergency System (112—AREU 118) integrated response to Coronavirus Disease 2019 in a Northern Italy centre. Internal and Emergency Medicine, 2020, 15, 825-833.	1.0	50
17	ST405 NDM-5 producing Escherichia coli in Northern Italy: the first two clinical cases. Clinical Microbiology and Infection, 2017, 23, 489-490.	2.8	28
18	Multiple Klebsiella pneumoniae KPC Clones Contribute to an Extended Hospital Outbreak. Frontiers in Microbiology, 2019, 10, 2767.	1.5	27

#	Article	IF	CITATIONS
19	A Novel IncA/C1 Group Conjugative Plasmid, Encoding VIM-1 Metallo-Beta-Lactamase, Mediates the Acquisition of Carbapenem Resistance in ST104 Klebsiella pneumoniae Isolates from Neonates in the Intensive Care Unit of V. Monaldi Hospital in Naples. Frontiers in Microbiology, 2017, 8, 2135.	1.5	25
20	Can Insertion Sequences Proliferation Influence Genomic Plasticity? Comparative Analysis of Acinetobacter baumannii Sequence Type 78, a Persistent Clone in Italian Hospitals. Frontiers in Microbiology, 2019, 10, 2080.	1.5	23
21	Rickettsia buchneri, symbiont of the deer tick Ixodes scapularis, can colonise the salivary glands of its host. Ticks and Tick-borne Diseases, 2020, 11, 101299.	1.1	21
22	Differential Single Nucleotide Polymorphism-Based Analysis of an Outbreak Caused by Salmonella enterica Serovar Manhattan Reveals Epidemiological Details Missed by Standard Pulsed-Field Gel Electrophoresis. Journal of Clinical Microbiology, 2015, 53, 1227-1238.	1.8	19
23	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen Klebsiella pneumoniae. Genome Biology and Evolution, 2019, 11, 3240-3251.	1.1	18
24	Characterization of an Outbreak of Extended-Spectrum $\hat{l}^2$ -Lactamase-ProducingKlebsiella pneumoniaein a Neonatal Intensive Care Unit in Italy. Microbial Drug Resistance, 2018, 24, 1128-1136.	0.9	13
25	Draft Genome Sequence of Stenotrophomonas maltophilia Strain EPM1, Found in Association with a Culture of the Human Parasite Giardia duodenalis. Genome Announcements, 2013, 1, e0018213.	0.8	8
26	Bacterial genomic epidemiology, from local outbreak characterization to species-history reconstruction. Pathogens and Global Health, 2015, 109, 319-327.	1.0	8
27	Genomic Characterization Helps Dissecting an Outbreak of Listeriosis in Northern Italy. PLOS Currents, 2017, 9, .	1.4	7
28	Draft Genome Sequence of Clostridium tyrobutyricum Strain DIVETGP, Isolated from Cow's Milk for Grana Padano Production. Genome Announcements, 2015, 3, .	0.8	5
29	Detection of the SARSâ€CoVâ€2 in different biologic specimens from positive patients with COVIDâ€19, in Northern Italy. Pediatric Allergy and Immunology, 2020, 31, 72-74.	1.1	4
30	Presence of Wolbachia in Three Hymenopteran Species: Diprion pini (Hymenoptera: Diprionidae), Neodiprion sertifer (Hymenoptera: Diprionidae), and Dahlbominus fuscipennis (Hymenoptera:) Tj ETQq0 0 0 rgB	T / <b>@ve</b> rloc	k 1 <b>9</b> Tf 50 29
31	Spread of multiple SARSâ€CoVâ€2 lineages Aprilâ€August 2020 anticipated the second pandemic wave in Lombardy (Italy). Pediatric Allergy and Immunology, 2022, 33, 89-92.	1.1	3
32	Draft Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Manhattan Strain 111113, from an Outbreak of Human Infections in Northern Italy. Genome Announcements, 2013, 1, .	0.8	2
33	Isolation of a Colistin-Susceptible MDR <i>Pantoea calida</i> Harboring the <i>mcr-9</i> Gene Suggests the Silent Spread of the Resistance Factor. Microbial Drug Resistance, 2022, 28, 408-412.	0.9	2
34	Epidemiological Characterization of Listeria monocytogenes Infections in Pavia Province in 2017 Reveals the Presence of Multiple Concurrently Circulating Strains. Foodborne Pathogens and Disease, 2021, 18, 267-275.	0.8	1