

Stefano Gaiarsa

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5194770/stefano-gaiarsa-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36
papers

1,034
citations

18
h-index

32
g-index

40
ext. papers

1,519
ext. citations

7.7
avg, IF

4.24
L-index

#	Paper	IF	Citations
36	Spread of multiple SARS-CoV-2 lineages April-August 2020 anticipated the second pandemic wave in Lombardy (Italy).. <i>Pediatric Allergy and Immunology</i> , 2022 , 33 Suppl 27, 89-92	4.2	0
35	EBV DNA increase in COVID-19 patients with impaired lymphocyte subpopulation count. <i>International Journal of Infectious Diseases</i> , 2021 , 104, 315-319	10.5	22
34	Bispecific IgG neutralizes SARS-CoV-2 variants and prevents escape in mice. <i>Nature</i> , 2021 , 593, 424-428	50.4	36
33	Epidemiological Characterization of Infections in Pavia Province in 2017 Reveals the Presence of Multiple Concurrently Circulating Strains. <i>Foodborne Pathogens and Disease</i> , 2021 , 18, 267-275	3.8	0
32	Bispecific antibody neutralizes circulating SARS-CoV-2 variants, prevents escape and protects mice from disease 2021 ,		2
31	Genomic epidemiology of SARS-CoV-2 reveals multiple lineages and early spread of SARS-CoV-2 infections in Lombardy, Italy. <i>Nature Communications</i> , 2021 , 12, 434	17.4	44
30	Tocilizumab for Treatment of Severe COVID-19 Patients: Preliminary Results from SMAtteo Covid19 Registry (SMACORE). <i>Microorganisms</i> , 2020 , 8,	4.9	157
29	Emergency Department and Out-of-Hospital Emergency System (112-AREU 118) integrated response to Coronavirus Disease 2019 in a Northern Italy centre. <i>Internal and Emergency Medicine</i> , 2020 , 15, 825-833	3.7	31
28	Lack of SARS-CoV-2 RNA environmental contamination in a tertiary referral hospital for infectious diseases in Northern Italy. <i>Journal of Hospital Infection</i> , 2020 ,	6.9	39
27	SARS Cov-2 infection in a renal-transplanted patient: A case report. <i>American Journal of Transplantation</i> , 2020 , 20, 1882-1884	8.7	67
26	Clinical characteristics of coronavirus disease (COVID-19) early findings from a teaching hospital in Pavia, North Italy, 21 to 28 February 2020. <i>Eurosurveillance</i> , 2020 , 25,	19.8	86
25	Severe acute respiratory syndrome coronavirus 2 RNA contamination of inanimate surfaces and virus viability in a health care emergency unit. <i>Clinical Microbiology and Infection</i> , 2020 , 26, 1094.e1-1094.e5	9.5	86
24	Detection of the SARS-CoV-2 in different biologic specimens from positive patients with COVID-19, in Northern Italy. <i>Pediatric Allergy and Immunology</i> , 2020 , 31, 72-74	4.2	3
23	Rickettsia buchneri, symbiont of the deer tick Ixodes scapularis, can colonise the salivary glands of its host. <i>Ticks and Tick-borne Diseases</i> , 2020 , 11, 101299	3.6	10
22	Comparative Analysis of the Two Multilocus Sequence Typing (MLST) Schemes. <i>Frontiers in Microbiology</i> , 2019 , 10, 930	5.7	47
21	Deianiraea, an extracellular bacterium associated with the ciliate Paramecium, suggests an alternative scenario for the evolution of Rickettsiales. <i>ISME Journal</i> , 2019 , 13, 2280-2294	11.9	27
20	Can Insertion Sequences Proliferation Influence Genomic Plasticity? Comparative Analysis of Sequence Type 78, a Persistent Clone in Italian Hospitals. <i>Frontiers in Microbiology</i> , 2019 , 10, 2080	5.7	5

19	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen <i>Klebsiella pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2019 , 11, 3240-3251	3.9	8
18	Multiple KPC Clones Contribute to an Extended Hospital Outbreak. <i>Frontiers in Microbiology</i> , 2019 , 10, 2767	5.7	15
17	Characterization of an Outbreak of Extended-Spectrum β -Lactamase-Producing <i>Klebsiella pneumoniae</i> in a Neonatal Intensive Care Unit in Italy. <i>Microbial Drug Resistance</i> , 2018 , 24, 1128-1136	2.9	8
16	Shifts of Faecal Microbiota During Sporadic Colorectal Carcinogenesis. <i>Scientific Reports</i> , 2018 , 8, 10329	4.9	39
15	ST405 NDM-5 producing <i>Escherichia coli</i> in Northern Italy: the first two clinical cases. <i>Clinical Microbiology and Infection</i> , 2017 , 23, 489-490	9.5	23
14	A Novel IncA/C1 Group Conjugative Plasmid, Encoding VIM-1 Metallo-Beta-Lactamase, Mediates the Acquisition of Carbapenem Resistance in ST104 Isolates from Neonates in the Intensive Care Unit of V. Monaldi Hospital in Naples. <i>Frontiers in Microbiology</i> , 2017 , 8, 2135	5.7	18
13	Genomic Characterization Helps Dissecting an Outbreak of Listeriosis in Northern Italy. <i>PLOS Currents</i> , 2017 , 9,		3
12	Tracking Nosocomial <i>Klebsiella pneumoniae</i> Infections and Outbreaks by Whole-Genome Analysis: Small-Scale Italian Scenario within a Single Hospital. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 2861-8	9.7	37
11	Differential single nucleotide polymorphism-based analysis of an outbreak caused by <i>Salmonella enterica</i> serovar Manhattan reveals epidemiological details missed by standard pulsed-field gel electrophoresis. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 1227-38	9.7	16
10	Genomic epidemiology of <i>Klebsiella pneumoniae</i> in Italy and novel insights into the origin and global evolution of its resistance to carbapenem antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 389-96	5.9	51
9	Draft Genome Sequence of <i>Clostridium tyrobutyricum</i> Strain DIVETGP, Isolated from Cow's Milk for Grana Padano Production. <i>Genome Announcements</i> , 2015 , 3,		3
8	Bacterial genomic epidemiology, from local outbreak characterization to species-history reconstruction. <i>Pathogens and Global Health</i> , 2015 , 109, 319-27	3.1	6
7	Acetic acid bacteria genomes reveal functional traits for adaptation to life in insect guts. <i>Genome Biology and Evolution</i> , 2014 , 6, 912-20	3.9	53
6	Presence of <i>Wolbachia</i> in three hymenopteran species: <i>Diprion pini</i> (Hymenoptera: Diprionidae), <i>Neodiprion sertifer</i> (Hymenoptera: Diprionidae), and <i>Dahlbominus fuscipennis</i> (Hymenoptera: Eulophidae). <i>Journal of Insect Science</i> , 2014 , 14, 147	2	2
5	Effects of global changes on the climatic niche of the tick <i>Ixodes ricinus</i> inferred by species distribution modelling. <i>Parasites and Vectors</i> , 2013 , 6, 271	4	75
4	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain EPM1, Found in Association with a Culture of the Human Parasite <i>Giardia duodenalis</i> . <i>Genome Announcements</i> , 2013 , 1, e0018213		6
3	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Manhattan Strain 111113, from an Outbreak of Human Infections in Northern Italy. <i>Genome Announcements</i> , 2013 , 1,		2
2	Insurgence and worldwide diffusion of genomic variants in SARS-CoV-2 genomes		4

1 Genomic epidemiology of SARS-CoV-2 reveals multiple lineages and early spread of SARS-CoV-2 infections in Lombardy, Italy

2