Ivano de Filippis

List of Publications by Year
in descending order

45 papers	1,559 citations	567281 15 h-index	302126 39 g-index
45 all docs	45 docs citations	45 times ranked	3126 citing authors

#	Article	IF	Citations
1	Detection and sequencing of Zika virus from amniotic fluid of fetuses with microcephaly in Brazil: a case study. Lancet Infectious Diseases, The, 2016, 16, 653-660.	9.1	981
2	Isolation, molecular and phenotypic characterization, and antibiotic susceptibility of Cronobacter spp. from Brazilian retail foods. Food Microbiology, 2017, 63, 129-138.	4.2	70
3	Evaluation of the potential for use in biocatalysis of a lipase from a wild strain of Bacillus megaterium. Journal of Molecular Catalysis B: Enzymatic, 2004, 31, 53-61.	1.8	45
4	Presence of qacEÎ”1 Gene and Susceptibility to a Hospital Biocide in Clinical Isolates of Pseudomonas aeruginosa Resistant to Antibiotics. Current Microbiology, 2011, 63, 16-21.	2.2	43
5	Molecular Epidemiology of Neisseria meningitidis Serogroup B in Brazil. PLoS ONE, 2012, 7, e33016.	2.5	37
6	PCR Analyses of tRNA Intergenic Spacer, 16S-23S Internal Transcribed Spacer, and Randomly Amplified Polymorphic DNA Reveal Inter- and Intraspecific Relationships of Enterobacter cloacae Strains. Journal of Clinical Microbiology, 2001, 39, 3865-3870.	3.9	34
7	Genotypic characteristics of multidrug-resistantPseudomonas aeruginosafrom hospital wastewater treatment plant in Rio de Janeiro, Brazil. Journal of Applied Microbiology, 2015, 118, 1276-1286.	3.1	34
8	Rapid detection of Neisseria meningitidis in cerebrospinal fluid by one-step polymerase chain reaction of the nspA gene. Diagnostic Microbiology and Infectious Disease, 2005, 51, 85-90.	1.8	29
9	Phenotypic characterization of Cronobacter spp. strains isolated from foods and clinical specimens in Brazil. Food Research International, 2017, 102, 61-67.	6.2	28
10	Molecular and phenotypical characterization ofCronobacterspecies isolated with high occurrence from oats and linseeds. FEMS Microbiology Letters, 2019, 366, .	1.8	26
11	Molecular Characterization of Quinolone-Resistant Neisseria gonorrhoeae Isolates from Brazil. Journal of Clinical Microbiology, 2011, 49, 4208-4212.	3.9	25
12	Occurrence of Haemophilus influenzae strains in three Brazilian states since the introduction of a conjugate Haemophilus influenzae type b vaccine. Brazilian Journal of Medical and Biological Research, 2005, 38, 777-781.	1.5	20
13	HIV-1 Genetic Diversity and Transmitted Drug Resistance in Antiretroviral Treatment-Naive Individuals from AmapÃ¡ State, Northern Brazil. AIDS Research and Human Retroviruses, 2016, 32, 373-376.	1.1	18
14	Multilocus sequence typing and repetitive element-based polymerase chain reaction analysis of Neisseria meningitidis isolates in Brazil reveal the emergence of 11 new sequence types genetically related to the ST-32 and ST-41/44 complexes and high prevalence of strains related to hypervirulent lineages. Diagnostic Microbiology and Infectious Disease, 2005, 53, 161-167.	1.8	17
15	Comparison of PCR-based methods for the simultaneous detection of Neisseria meningitidis, Haemophilus influenzae, and Streptococcus pneumoniae in clinical samples. Brazilian Journal of Infectious Diseases, 2016, 20, 335-341.	0.6	17
16	Methicillin- and vancomycin-resistantStaphylococcus aureusin health care workers and medical devices. Jornal Brasileiro De Patologia E Medicina Laboratorial, 2015, 51, 143-152.	0.3	16
17	Extended genetic analysis of Brazilian isolates of Bacillus cereus and Bacillus thuringiensis. Memorias Do Instituto Oswaldo Cruz, 2013, 108, 65-72.	1.6	13
18	Genetic Relatedness of NDM-Producing Klebsiella pneumoniae Co-Occurring VIM, KPC, and OXA-48 Enzymes from Surveillance Cultures from an Intensive Care Unit. Microbial Drug Resistance, 2020, 26, 1219-1226.	2.0	11

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19	PorA Variable Antigenic Regions VR1, VR2, and VR3 of Neisseria meningitidis Serogroups B and C Isolated in Brazil from 1999 to 2004. Infection and Immunity, 2007, 75, 3683-3685.	2.2	10
20	Septic arthritis due to Haemophilus influenzae serotype a in the post-vaccination era in Brazil. Journal of Medical Microbiology, 2008, 57, 1311-1312.	1.8	10
21	Characterization of strains of Neisseria meningitidis causing meningococcal meningitis in Mozambique, 2014: Implications for vaccination against meningococcal meningitis. PLoS ONE, 2018, 13, e0197390.	2.5	10
22	PorA VR3 Typing Database: A web-based resource for the determination of PorA VR3 alleles of Neisseria meningitidis. Infection, Genetics and Evolution, 2011, 11, 248-249.	2.3	9
23	Detection of antimicrobial resistance genes in betalactamase- and carbapenemase-producing Klebsiella pneumoniae by patient surveillance cultures at an intensive care unit in Rio de Janeiro, Brazil. Jornal Brasileiro De Patologia E Medicina Laboratorial, 2016, 52, 284-292.	0.3	9
24	The invasive Neisseria meningitidis MenC CC103 from Brazil is characterized by an accessory gene repertoire. Scientific Reports, 2017, 7, 1617.	3.3	5
25	Quest for a broad-range vaccine against Neisseria meningitidis serogroup B: implications of genetic variations of the surface-exposed proteins. Journal of Medical Microbiology, 2009, 58, 1127-1132.	1.8	5
26	Urinary tract infection caused by nontypable Haemophilus influenzae in the elderly. Journal of Medical Microbiology, 2010, 59, 1132-1133.	1.8	4
27	Replacement of Neisseria meningitidis C cc11/ET-15 variant by a cc103 hypervirulent clone, Brazil 2005â€“2011. Diagnostic Microbiology and Infectious Disease, 2013, 76, 524-525.	1.8	4
28	Development of a collection of bacteria causing meningitis in Rio de Janeiro from 1990 to 1991. Memorias Do Instituto Oswaldo Cruz, 1995, 90, 21-24.	1.6	3
29	Antimicrobial susceptibility of Haemophilus influenzae isolates collected from 4 centers in Brazil (1990â€“2003). Diagnostic Microbiology and Infectious Disease, 2006, 54, 57-62.	1.8	3
30	Isolation of Brevibacillus brevis from tracheal aspirates of a hospitalized patient. Apmis, 2011, 119, 901-902.	2.0	3
31	InvestigaÃ§Ã£o de um surto causado por Cronobacter malonaticus em um hospital maternidade em Teresina, PiauÃ: caracterizaÃ§Ã£o e tipificaÃ§Ã£o por eletroforese em gel de campo pulsado. VigilÃ¢ncia SanitÃ¡ria Em Debate: Sociedade, CiÃªncia & Tecnologia, 2015, .	0.1	3
32	Haemophilus influenzae serotype b and a capsule-deficient type mutant (bâ¯) invasive disease in a partially vaccinated child in Brazil. Journal of Medical Microbiology, 2013, 62, 655-657.	1.8	2
33	Cronobacter spp.: infecÃ§Ãµes, ocorrÃªncia e regulaÃ§Ã£o em alimentos â€' uma revisÃ£o no Brasil. Brazilian Journal of Food Technology, 2017, 21, .	0.8	2
34	Epidemiology and molecular characterization of Neisseria lactamica carried in 11â€“19 years old students in Salvador, Brazil. International Journal of Medical Microbiology, 2018, 308, 454-458.	3.6	2
35	Molecular surveillance of brazilian meningococcal isolates serogroup c in the pre and post-men-c-vaccination period: Emergence of ST-3780. Infection, Genetics and Evolution, 2020, 78, 104079.	2.3	2
36	Flow-Cytometric Method for Viability Analysis of Mycoplasma gallisepticum and Other Cell-Culture-Contaminant Mollicutes. Current Microbiology, 2021, 78, 67-77.	2.2	2

#	Article	IF	Citations
37	Genetic diversity of Listeria monocytogenes serotype 1/2a strains collected in Brazil by Multiâ€Virulenceâ€Locus Sequence Typing. Letters in Applied Microbiology, 2021, 72, 316-324.	2.2	2
38	Genetic diversity of Neisseria meningitidis strains isolated in Rio de Janeiro, Brazil, evaluated by multilocus enzyme electrophoresis. Letters in Applied Microbiology, 2004, 39, 232-239.	2.2	1
39	NeisseriameningitidisporA variable regions: rapid detection of P1Â·7 and P1Â·19 variants by PCR. Letters in Applied Microbiology, 2007, 45, 426-431.	2.2	1
40	Changes in Haemophilus influenzae capsule locus: possible emergence of novel variants in Brazil. Diagnostic Microbiology and Infectious Disease, 2010, 68, 97-102.	1.8	1
41	Molecular characterization and evaluation of antimicrobial susceptibility of enteropathogenic E. coli (EPEC) isolated from minas soft cheese. Food Science and Technology, 2012, 32, 747-753.	1.7	1
42	The 2010 Meningococcal outbreak in Bahia, Brazil, was caused by 2 different STs belonging to Clonal Complex ST-103. VigilÃ¢ncia SanitÃ¡ria Em Debate: Sociedade, CiÃªncia & Tecnologia, 2013, 1, .	0.1	1
43	Fatal meningococcal meningitis in a HIV-infected patient caused by serogroup C Neisseria meningitidis belonging to the non-hypervirulent clonal complex ST-60 (cc60). Brazilian Journal of Infectious Diseases, 2011, 15, 178-180.	0.6	0
44	Fatal meningococcal meningitis in a HIV-infected patient caused by serogroup C Neisseria meningitidis belonging to the non-hypervirulent clonal complex ST-60 (cc60). Brazilian Journal of Infectious Diseases, 2011, 15, 178-180.	0.6	0
45	The invasive MenC cc103 lineage with penicillin reduced susceptibility persisting in Brazil. International Journal of Medical Microbiology, 2017, 307, 287-290.	3.6	0