Maurizio Zazzi

List of Publications by Year
in descending order

264 papers	5,560 citations	101543 36 h-index	138484 58 g-index
273 all docs	273 docs citations	273 times ranked	5906 citing authors

#	Article	IF	Citations
1	Prevalence of Drug-Resistant HIV-1 Variants in Untreated Individuals in Europe: Implications for Clinical Management. Journal of Infectious Diseases, 2005, 192, 958-966.	4.0	385
2	European guidelines on the clinical management of HIV-1 tropism testing. Lancet Infectious Diseases, The, 2011, 11, 394-407.	9.1	218
3	Transmission of HIV Drug Resistance and the Predicted Effect on Current First-line Regimens in Europe. Clinical Infectious Diseases, 2016, 62, 655-663.	5.8	135
4	A novel methodology for large-scale phylogeny partition. Nature Communications, 2011, 2, 321.	12.8	118
5	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. Retrovirology, 2009, 6, 49.	2.0	114
6	Antiretroviral Resistance Mutations in Human Immunodeficiency Virus Type 1 Reverse Transcriptase and Protease from Paired Cerebrospinal Fluid and Plasma Samples. Journal of Infectious Diseases, 2000, 181, 740-745.	4.0	106
7	Human DDX3 protein is a valuable target to develop broad spectrum antiviral agents. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5388-5393.	7.1	100
8	The Calculated Genetic Barrier for Antiretroviral Drug Resistance Substitutions Is Largely Similar for Different HIV-1 Subtypes. Journal of Acquired Immune Deficiency Syndromes (1999), 2006, 41, 352-360.	2.1	90
9	SARS-CoV-2 RNA-dependent RNA polymerase as a therapeutic target for COVID-19. Expert Opinion on Therapeutic Patents, 2021, 31, 325-337.	5.0	84
10	Fatal herpesvirus 6 encephalitis after unrelated bone marrow transplant. Bone Marrow Transplantation, 1998, 22, 285-288.	2.4	66
11	Evaluation of the Abbott Real-Time HIV-1 quantitative assay with dried blood spot specimens. Clinical Microbiology and Infection, 2009, 15, 93-97.	6.0	66
12	Targeting the RdRp of Emerging RNA Viruses: The Structure-Based Drug Design Challenge. Molecules, 2020, 25, 5695.	3.8	64
13	New findings in HCV genotype distribution in selected West European, Russian and Israeli regions. Journal of Clinical Virology, 2016, 81, 82-89.	3.1	60
14	The global spread of HIV-1 subtype B epidemic. Infection, Genetics and Evolution, 2016, 46, 169-179.	2.3	60
15	Clinically Validated Genotype Analysis: Guiding Principles and Statistical Concerns. Antiviral Therapy, 2004, 9, 465-478.	1.0	58
16	Comparison of HIV-1 Genotypic Resistance Test Interpretation Systems in Predicting Virological Outcomes Over Time. PLoS ONE, 2010, 5, e11505.	2.5	56
17	Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study. Journal of Antimicrobial Chemotherapy, 2011, 66, 1886-1896.	3.0	56
18	Impact of the M184V Resistance Mutation on Virological Efficacy and Durability of Lamivudine-Based Dual Antiretroviral Regimens as Maintenance Therapy in Individuals With Suppressed HIV-1 RNA: A Cohort Study. Open Forum Infectious Diseases, 2018, 5, ofy113.	0.9	56

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19	HIV-associated malignant lymphomas in Kenya (Equatorial Africa). Human Pathology, 1998, 29, 1285-1289.	2.0	55
20	A comparison of three computational modelling methods for the prediction of virological response to combination HIV therapy. Artificial Intelligence in Medicine, 2009, 47, 63-74.	6.5	55
21	Changing patterns in HIVâ€1 nonâ€B clade prevalence and diversity in Italy over three decades*. HIV Medicine, 2010, 11, 593-602.	2.2	54
22	Naturally occurring hepatitis C virus (HCV) NS3/4A protease inhibitor resistance-related mutations in HCV genotype 1-infected subjects in Italy. Journal of Antimicrobial Chemotherapy, 2012, 67, 984-987.	3.0	54
23	Declining Prevalence of HIV-1 Drug Resistance in Antiretroviral Treatment-exposed Individuals in Western Europe. Journal of Infectious Diseases, 2013, 207, 1216-1220.	4.0	53
24	Selecting anti-HIV therapies based on a variety of genomic and clinical factors. Bioinformatics, 2008, 24, i399-i406.	4.1	50
25	Comparative determination of HIV-1 co-receptor tropism by Enhanced Sensitivity Trofile, gp120 V3-loop RNA and DNA genotyping. Retrovirology, 2010, 7, 56.	2.0	50
26	Plasma levels of soluble CD27: a simple marker to monitor immune activation during potent antiretroviral therapy in HIV-1-infected subjects. Clinical and Experimental Immunology, 2002, 127, 486-494.	2.6	47
27	Comparative analysis of different cell systems for Zika virus (ZIKV) propagation and evaluation of anti-ZIKV compounds in vitro. Virus Research, 2018, 244, 64-70.	2.2	47
28	Broad Nucleosideâ€Analogue Resistance Implications for Human Immunodeficiency Virus Type 1 Reverseâ€Transcriptase Mutations at Codons 44 and 118. Journal of Infectious Diseases, 2002, 185, 898-904.	4.0	46
29	Immunoglobulin Gene Rearrangement Analysis in Composite Hodgkin Disease and Large B-Cell Lymphoma: Evidence for Receptor Revision of Immunoglobulin Heavy Chain Variable Region Genes in Hodgkin-Reed-Sternberg Cells?. Diagnostic Molecular Pathology, 2002, 11, 2-8.	2.1	46
30	Molecular Tracing of SARS-CoV-2 in Italy in the First Three Months of the Epidemic. Viruses, 2020, 12, 798.	3.3	46
31	Comparison of Classifier Fusion Methods for Predicting Response to Anti HIV-1 Therapy. PLoS ONE, 2008, 3, e3470.	2.5	45
32	Dosage of Tn916 Circular Intermediates in Enterococcus faecalis. Plasmid, 1995, 34, 48-57.	1.4	43
33	Predicting Response to Antiretroviral Treatment by Machine Learning: The EuResist Project. Intervirology, 2012, 55, 123-127.	2.8	43
34	Predicting the Response to Combination Antiretroviral Therapy: Retrospective Validation of geno2phenoâ€THEO on a Large Clinical Database. Journal of Infectious Diseases, 2009, 199, 999-1006.	4.0	40
35	Antigenicity and Immunogenicity of the V3 Domain of HIV Type 1 Glycoprotein 120 Expressed on the Surface of Streptococcus gordonii. AIDS Research and Human Retroviruses, 1999, 15, 451-459.	1.1	39
36	HIV-1 Subtype Is an Independent Predictor of Reverse Transcriptase Mutation K65R in HIV-1 Patients Treated with Combination Antiretroviral Therapy Including Tenofovir. Antimicrobial Agents and Chemotherapy, 2013, 57, 1053-1056.	3.2	39

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37	Comparative evaluation of three computerized algorithms for prediction of antiretroviral susceptibility from HIV type 1 genotype. Journal of Antimicrobial Chemotherapy, 2004, 53, 356-360.	3.0	36
38	Prevalence of Single and Multiple Natural NS3, NS5A and NS5B Resistance-Associated Substitutions in Hepatitis C Virus Genotypes 1â€"4 in Italy. Scientific Reports, 2018, 8, 8988.	3.3	36
39	Circulating SARS-CoV-2 variants in Italy, October 2020â€"March 2021. Virology Journal, 2021, 18, 168.	3.4	36
40	Investigation of expert rule bases, logistic regression, and non-linear machine learning techniques for predicting response to antiretroviral treatment. Antiviral Therapy, 2009, 14, 433-442.	1.0	35
41	Rules-based HIV-1 genotypic resistance interpretation systems predict 8 week and 24 week virological antiretroviral treatment outcome and benefit from drug potency weighting. Journal of Antimicrobial Chemotherapy, 2009, 64, 616-624.	3.0	34
42	Evolution of transmitted HIVâ€1 drug resistance and viral subtypes circulation in Italy from 2006 to 2016. HIV Medicine, 2018, 19, 619-628.	2.2	34
43	Simultaneous Amplification of Multiple HIV-1 DNA Sequences from Clinical Specimens by Using Nested-Primer Polymerase Chain Reaction. AIDS Research and Human Retroviruses, 1993, 9, 315-320.	1.1	33
44	Antiretroviral therapy with protease inhibitors in human immunodeficiency virus type 1- and human herpesvirus 8-coinfected patients. , 1999, 57, 140-144.		33
45	Development and significance of resistance to protease inhibitors in HIV-1-infected adults under triple-drug therapy in clinical practice. Journal of Medical Virology, 2002, 66, 143-150.	5.0	33
46	Both Human Immunodeficiency Virus Cellular DNA Sequencing and Plasma RNA Sequencing Are Useful for Detection of Drug Resistance Mutations in Blood Samples from Antiretroviral-Drug-Naive Patients. Journal of Clinical Microbiology, 2007, 45, 1783-1788.	3.9	33
47	Prevalence of transmitted HIV-1 drug resistance in HIV-1-infected patients in Italy: evolution over 12 years and predictors. Journal of Antimicrobial Chemotherapy, 2009, 64, 607-615.	3.0	33
48	Evaluation of the presence of 2-LTR HIV-1 unintegrated DNA as a simple molecular predictor of disease progression. , 1997, 52, 20-25.		32
49	Emerging mutations at virological failure of HAART combinations containing tenofovir and lamivudine or emtricitabine. Aids, 2010, 24, 1013-1018.	2.2	32
50	Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study). HIV Medicine, 2011, 12, 211-218.	2.2	32
51	Synthesis and Antiviral Activity of Novel 1,3,4-Thiadiazole Inhibitors of DDX3X. Molecules, 2019, 24, 3988.	3.8	31
52	Faster decay of neutralizing antibodies in never infected than previously infected healthcare workers three months after the second BNT162b2 mRNA COVID-19 vaccine dose. International Journal of Infectious Diseases, 2021, 112, 40-44.	3.3	31
53	Two Distinct Hepatitis C Virus Genotype 1a Clades Have Different Geographical Distribution and Association With Natural Resistance to NS3 Protease Inhibitors. Open Forum Infectious Diseases, 2015, 2, ofv043.	0.9	30
54	Evaluation of sofosbuvir activity and resistance profile against West Nile virus in vitro. Antiviral Research, 2020, 175, 104708.	4.1	30

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55	RegaDB: community-driven data management and analysis for infectious diseases. Bioinformatics, 2013, 29, 1477-1480.	4.1	29
56	Computational models can predict response to HIV therapy without a genotype and may reduce treatment failure in different resource-limited settings. Journal of Antimicrobial Chemotherapy, 2013, 68, 1406-1414.	3.0	29
57	Phylogenetic analysis provides evidence of interactions between Italian heterosexual and South American homosexual males as the main source of national HIVâ€1 subtype C epidemics. Journal of Medical Virology, 2014, 86, 729-736.	5.0	29
58	Identification of a new HIV-1 BC circulating recombinant form (CRF60_BC) in Italian young men having sex with men. Infection, Genetics and Evolution, 2014, 23, 176-181.	2.3	29
59	Frequent NS5A and multiclass resistance in almost all HCV genotypes at DAA failures: What are the chances for second-line regimens?. Journal of Hepatology, 2018, 68, 597-600.	3.7	28
60	The global burden of HIV-1 drug resistance in the past 20 years. PeerJ, 2018, 6, e4848.	2.0	28
61	Impact of the M184V/I Mutation on the Efficacy of Abacavir/Lamivudine/Dolutegravir Therapy in HIV Treatment-Experienced Patients. Open Forum Infectious Diseases, 2019, 6, ofz330.	0.9	28
62	Cross-neutralization of SARS-CoV-2 B.1.1.7 and P.1 variants in vaccinated, convalescent and P.1 infected. Journal of Infection, 2021, 83, 467-472.	3.3	28
63	DDX3X inhibitors, an effective way to overcome HIV-1 resistance targeting host proteins. European Journal of Medicinal Chemistry, 2020, 200, 112319.	5.5	27
64	Divergent Distribution of HIV-1 Drug-Resistant Variants on and off Antiretroviral Therapy. Antiviral Therapy, 2002, 7, 245-250.	1.0	27
65	Low frequency of plasma nerve-growth factor detection is associated with death of memory B lymphocytes in HIV-1 infection. Clinical and Experimental Immunology, 2003, 132, 297-303.	2.6	26
66	Frequency and Treatmentâ€Related Predictors of Thymidineâ€Analogue Mutation Patterns in HIVâ€1 Isolates after Unsuccessful Antiretroviral Therapy. Journal of Infectious Diseases, 2006, 193, 1219-1222.	4.0	26
67	Use of Peripheral Blood DNA for Genotype Antiretroviral Resistance Testing in Drug-Naive HIV-Infected Subjects. Clinical Infectious Diseases, 2007, 44, 1657-1661.	5.8	26
68	Prevalence of predicted resistance to doravirine in HIV-1-positive patients after exposure to non-nucleoside reverse transcriptase inhibitors. International Journal of Antimicrobial Agents, 2019, 53, 515-519.	2.5	26
69	Failure on voxilaprevir, velpatasvir, sofosbuvir and efficacy of rescue therapy. Journal of Hepatology, 2021, 74, 801-810.	3.7	26
70	Single-dose BNT162b2 mRNA COVID-19 vaccine significantly boosts neutralizing antibody response in health care workers recovering from asymptomatic or mild natural SARS-CoV-2 infection. International Journal of Infectious Diseases, 2021, 108, 176-178.	3.3	26
71	The development of artificial neural networks to predict virological response to combination HIV therapy. Antiviral Therapy, 2007, 12, 15-24.	1.0	26
72	HIV-1 A1 Subtype Epidemic in Italy Originated from Africa and Eastern Europe and Shows a High Frequency of Transmission Chains Involving Intravenous Drug Users. PLoS ONE, 2016, 11, e0146097.	2.5	25

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73	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. Scientific Reports, 2018, 8, 1702.	3.3	24
74	The development of an expert system to predict virological response to HIV therapy as part of an online treatment support tool. Aids, 2011, 25, 1855-1863.	2.2	23
75	Identification and Structural Characterization of Novel Genetic Elements in the HIV-1 V3 Loop Regulating Coreceptor Usage. Antiviral Therapy, 2011, 16, 1035-1045.	1.0	23
76	Rare occurrence of doravirine resistance-associated mutations in HIV-1-infected treatment-naive patients. Journal of Antimicrobial Chemotherapy, 2019, 74, 614-617.	3.0	23
77	Determinants of HIV-1 Late Presentation in Patients Followed in Europe. Pathogens, 2021, 10, 835.	2.8	23
78	Long-read direct infrared sequencing of crude PCR products for prediction of resistance to HIV-1 reverse transcriptase and protease inhibitors. Molecular Biotechnology, 1998, 10, 1-8.	2.4	22
79	Identification of a Possible Ancestor of the Subtype A1 HIV Type 1 Variant Circulating in the Former Soviet Union. AIDS Research and Human Retroviruses, 2008, 24, 1319-1325.	1.1	22
80	Prevalence of HIV-1 integrase mutations related to resistance to dolutegravir in raltegravir naïve and pretreated patients. Clinical Microbiology and Infection, 2012, 18, E428-E430.	6.0	22
81	HIV-1 Subtype F1 Epidemiological Networks among Italian Heterosexual Males Are Associated with Introduction Events from South America. PLoS ONE, 2012, 7, e42223.	2.5	22
82	Agreement between an in‐house replication competent and a reference replication defective recombinant virus assay for measuring phenotypic resistance to <scp>HIV</scp>‐1 protease, reverse transcriptase, and integrase inhibitors. Journal of Clinical Laboratory Analysis, 2018, 32, .	2.1	22
83	Neuronal intranuclear inclusion disease: Polymerase chain reaction and ultrastructural study of rectal biopsy specimen in a new case. Acta Neuropathologica, 1996, 91, 215-218.	7.7	21
84	Robust Supervised and Unsupervised Statistical Learning for HIV Type 1 Coreceptor Usage Analysis. AIDS Research and Human Retroviruses, 2009, 25, 305-314.	1.1	21
85	Antiretroviral Therapy Optimisation without Genotype Resistance Testing: A Perspective on Treatment History Based Models. PLoS ONE, 2010, 5, e13753.	2.5	21
86	Performance of an in-house genotypic antiretroviral resistance assay in patients pretreated with multiple human immunodeficiency virus type 1 protease and reverse transcriptase inhibitors. Journal of Clinical Virology, 2002, 25, 57-62.	3.1	20
87	Surrogate Markers as a Guide to Evaluate Response to Antiretroviral Therapy. Current Medicinal Chemistry, 2003, 10, 349-365.	2.4	20
88	Gln145Met/Leu Changes in Human Immunodeficiency Virus Type 1 Reverse Transcriptase Confer Resistance to Nucleoside and Nonnucleoside Analogs and Impair Virus Replication. Antimicrobial Agents and Chemotherapy, 2004, 48, 4611-4617.	3.2	20
89	Prevalence of skin allograft discards as a result of serological and molecular microbiological screening in a regional skin bank in Italy. Burns, 2006, 32, 348-351.	1.9	20
90	HIV-1 Sub-Subtype A6: Settings for Normalised Identification and Molecular Epidemiology in the Southern Federal District, Russia. Viruses, 2020, 12, 475.	3.3	20

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91	Low human immunodeficiency virus type 1 (HIV-1) DNA burden as a major cause for failure to detect HIV-1 DNA in clinical specimens by PCR. Journal of Clinical Microbiology, 1995, 33, 205-208.	3.9	20
92	Clinically validated genotype analysis: guiding principles and statistical concerns. Antiviral Therapy, 2004, 9, 465-78.	1.0	20
93	Development and Significance of the HIV-1 Reverse Transcriptase M184V Mutation During Combination Therapy With Lamivudine, Zidovudine, and Protease Inhibitors. Journal of Acquired Immune Deficiency Syndromes (1999), 1999, 21, 203.	2.1	19
94	Genotypic resistance profiles associated with virological failure to darunavir-containing regimens: a cross-sectional analysis. Infection, 2012, 40, 311-318.	4.7	19
95	The role of baseline HIV-1 RNA, drug resistance, and regimen type as determinants of response to first-line antiretroviral therapy. Journal of Medical Virology, 2014, 86, 1648-1655.	5.0	19
96	Exploring the Implication of DDX3X in DENV Infection: Discovery of the First-in-Class DDX3X Fluorescent Inhibitor. ACS Medicinal Chemistry Letters, 2020, 11, 956-962.	2.8	19
97	Investigation of expert rule bases, logistic regression, and non-linear machine learning techniques for predicting response to antiretroviral treatment. Antiviral Therapy, 2009, 14, 433-42.	1.0	19
98	Nested polymerase chain reaction for detection of human immunodeficiency virus type 1 DNA in clinical specimens. Journal of Medical Virology, 1992, 38, 172-174.	5.0	18
99	Focal myositis: A polymerase chain reaction analysis for a viral etiology. Human Pathology, 1997, 28, 111-113.	2.0	18
100	Evaluation of Cell–Free and Cell–Associated Peripheral Blood Human Immunodeficiency Virus Type 1 RNA Response to Antiretroviral Therapy. Journal of Infectious Diseases, 1999, 179, 361-366.	4.0	18
101	High Plasma Levels of Soluble Fas in HIV Type 1-Infected Subjects Are Not Normalized during Highly Active Antiretroviral Therapy. AIDS Research and Human Retroviruses, 2000, 16, 1379-1384.	1.1	18
102	Computer-Aided Optimization of Combined Anti-Retroviral Therapy for HIV: New Drugs, New Drug Targets and Drug Resistance. Current HIV Research, 2016, 14, 101-109.	0.5	18
103	Dysfunctional phenotypes of CD4+ and CD8+ T cells are comparable in patients initiating ART during early or chronic HIV-1 infection. Medicine (United States), 2016, 95, e3738.	1.0	18
104	Detection of genotypically drug-resistant HIV-1 variants and non-B subtypes in recently infected antiretroviral-naive adults in Italy. Aids, 2000, 14, 2204.	2.2	18
105	Clinical Evaluation of Rega 8: An Updated Genotypic Interpretation System That Significantly Predicts HIV-Therapy Response. PLoS ONE, 2013, 8, e61436.	2.5	17
106	Recombination analysis and structure prediction show correlation between breakpoint clusters and RNA hairpins in the pol gene of human immunodeficiency virus type 1 unique recombinant forms. Journal of General Virology, 2008, 89, 3119-3125.	2.9	16
107	Longitudinal analysis of HIV-1 coreceptor tropism by single and triplicate HIV-1 RNA and DNA sequencing in patients undergoing successful first-line antiretroviral therapy. Journal of Antimicrobial Chemotherapy, 2014, 69, 735-741.	3.0	16
108	Burden of Disease in PWH Harboring a Multidrug-Resistant Virus: Data From the PRESTIGIO Registry. Open Forum Infectious Diseases, 2020, 7, ofaa456.	0.9	16

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109	Evidence of Differential Selection of HIV-1 Variants Carrying Drug-Resistant Mutations in Seroconverters. Antiviral Therapy, 2006, 11, 329-334.	1.0	16
110	Zidovudine resistance mutations and human immunodeficiency virus type 1 DNA burden: Longitudinal evaluation of six patients under treatment. Infection, 1996, 24, 419-425.	4.7	15
111	Analysis of the HIV-1nef gene in five intravenous drug users with long-term nonprogressive HIV-1 infection in Italy. , 2000, 60, 294-299.		15
112	Cutaneous leishmaniasis: usefulnes<i>s</i> of PCR on paraffin-embedded skin biopsies as part of routine investigation. Annals of Tropical Medicine and Parasitology, 2007, 101, 745-749.	1.6	15
113	Impact of transmitted HIV-1 drug resistance on the efficacy of first-line antiretroviral therapy with two nucleos(t)ide reverse transcriptase inhibitors plus an integrase inhibitor or a protease inhibitor. Journal of Antimicrobial Chemotherapy, 2018, 73, 2480-2484.	3.0	15
114	Comparable <i>In Vitro</i> Activities of Second-Generation HIV-1 Integrase Strand Transfer Inhibitors (INSTIs) on HIV-1 Clinical Isolates with INSTI Resistance Mutations. Antimicrobial Agents and Chemotherapy, 2019, 64, .	3.2	15
115	Trends of Transmitted and Acquired Drug Resistance in Europe From 1981 to 2019: A Comparison Between the Populations of Late Presenters and Non-late Presenters. Frontiers in Microbiology, 2022, 13, 846943.	3.5	15
116	Efficacy of Licensed Monoclonal Antibodies and Antiviral Agents against the SARS-CoV-2 Omicron Sublineages BA.1 and BA.2. Viruses, 2022, 14, 1374.	3.3	15
117	Optimal conditions for detection of human immunodeficiency virus type 1 DNA by polymerase chain reaction with nested primers. Molecular and Cellular Probes, 1993, 7, 431-437.	2.1	14
118	Duration of first-line antiretroviral therapy with tenofovir and emtricitabine combined with atazanavir/ritonavir, efavirenz or lopinavir/ritonavir in the Italian ARCA cohort. Journal of Antimicrobial Chemotherapy, 2013, 68, 200-205.	3.0	14
119	Development of an internally controlled quantitative PCR to measure total cell-associated HIV-1 DNA in blood. Clinical Chemistry and Laboratory Medicine, 2018, 56, e75-e77.	2.3	14
120	Evolution and predictors of HIV type-1 drug resistance in patients failing combination antiretroviral therapy in Italy. Antiviral Therapy, 2009, 14, 359-369.	1.0	14
121	An update to the HIV-TRePS system: the development of new computational models that do not require a genotype to predict HIV treatment outcomes. Journal of Antimicrobial Chemotherapy, 2014, 69, 1104-1110.	3.0	13
122	Trends and correlates of HIV-1 resistance among subjects failing an antiretroviral treatment over the 2003â€"2012 decade in Italy. BMC Infectious Diseases, 2014, 14, 398.	2.9	13
123	Structure-Based Identification of HIV-1 Nucleocapsid Protein Inhibitors Active against Wild-Type and Drug-Resistant HIV-1 Strains. ACS Chemical Biology, 2018, 13, 253-266.	3.4	13
124	Development of a Cell-Based Immunodetection Assay for Simultaneous Screening of Antiviral Compounds Inhibiting Zika and Dengue Virus Replication. SLAS Discovery, 2020, 25, 506-514.	2.7	13
125	Zika Virus in West Africa: A Seroepidemiological Study between 2007 and 2012. Viruses, 2020, 12, 641.	3.3	13
126	Bithiazole Inhibitors of Phosphatidylinositol 4â€"Kinase (PI4KIIIÎ²) as Broadâ€"Spectrum Antivirals Blocking the Replication of SARSâ€"CoVâ€"2, Zika Virus, and Human Rhinoviruses. ChemMedChem, 2021, 16, 3548-3552.	3.2	13

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127	Identification of Mycobacterium tuberculosis complex, Mycobacterium avium and Mycobacterium intracellulare by selective nested polymerase chain reaction. Molecular and Cellular Probes, 1995, 9, 321-326.	2.1	12
128	A child with vestibular neuritis. Is adenovirus implicated?. Brain and Development, 2006, 28, 410-412.	1.1	12
129	HIV-1 mutational pathways under multidrug therapy. AIDS Research and Therapy, 2011, 8, 26.	1.7	12
130	Future research and collaboration: the "SINERGIE" project on HCV (South Italian Network for) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.9	12
131	Efficacy of tenofovir and efavirenz in combination with lamivudine or emtricitabine in antiretroviral-naive patients in Europe. Journal of Antimicrobial Chemotherapy, 2015, 70, 1850-7.	3.0	12
132	The HIV-1 integrase E157Q polymorphism per se does not alter susceptibility to raltegravir and dolutegravir in vitro. Aids, 2017, 31, 2307-2309.	2.2	12
133	Evaluation of HIV-1 integrase resistance emergence and evolution in patients treated with integrase inhibitors. Journal of Global Antimicrobial Resistance, 2020, 20, 163-169.	2.2	12
134	<i>In vitro</i> cross-resistance to doravirine in a panel of HIV-1 clones harbouring multiple NNRTI resistance mutations. Journal of Antimicrobial Chemotherapy, 2021, 76, 130-134.	3.0	12
135	Serum Neutralizing Activity against B.1.1.7, B.1.351, and P.1 SARS-CoV-2 Variants of Concern in Hospitalized COVID-19 Patients. Viruses, 2021, 13, 1347.	3.3	12
136	Combining Kernel and Model Based Learning for HIV Therapy Selection. AMIA Summits on Translational Science Proceedings, 2017, 2017, 239-248.	0.4	12
137	Ultrasensitive in-house reverse transcription-competitive PCR for quantitation of HIV-1 RNA in plasma. Journal of Virological Methods, 2000, 87, 91-97.	2.1	11
138	Treatment with Lopinavir/Ritonavir in Heavily Pretreated Subjects Failing Multiple Antiretroviral Regimens in Clinical Practice. Journal of Acquired Immune Deficiency Syndromes (1999), 2002, 30, 533-535.	2.1	11
139	Immunological recovery despite virological failure is independent of human immunodeficiency virus-type 1 resistant mutants in children receiving highly active antiretroviral therapy. Journal of Medical Virology, 2003, 70, 506-512.	5.0	11
140	Dolutegravir (DTG)-containing regimens after receiving raltegravir (RAL) or elvitegravir (EVG): Durability and virological response in a large Italian HIV drug resistance network (ARCA). Journal of Clinical Virology, 2018, 105, 112-117.	3.1	11
141	In vitro susceptibility to fostemsavir is not affected by long-term exposure to antiviral therapy in MDR HIV-1-infected patients. Journal of Antimicrobial Chemotherapy, 2020, 75, 2547-2553.	3.0	11
142	Drug resistance testing through remote genotyping and predicted treatment options in human immunodeficiency virus type 1 infected Tanzanian subjects failing first or second line antiretroviral therapy. PLoS ONE, 2017, 12, e0178942.	2.5	11
143	Switch to maraviroc with darunavir/r, both QD, in patients with suppressed HIV-1 was well tolerated but virologically inferior to standard antiretroviral therapy: 48-week results of a randomized trial. PLoS ONE, 2017, 12, e0187393.	2.5	11
144	SARS-CoV-2 Infection of Human Ovarian Cells: A Potential Negative Impact on Female Fertility. Cells, 2022, 11, 1431.	4.1	11

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145	Detection of a Drug-Resistant Human Immunodeficiency Virus Variant in a Newly Infected Heterosexual Couple. Clinical Infectious Diseases, 2002, 34, 116-117.	5.8	10
146	Stochastic modelling of genotypic drug-resistance for human immunodeficiency virus towards long-term combination therapy optimization. Bioinformatics, 2009, 25, 1040-1047.	4.1	10
147	Impact of extensive HIV-1 variability on molecular diagnosis in the Congo basin. Journal of Clinical Virology, 2010, 47, 372-375.	3.1	10
148	Interpretation of Genotypic HIV-1 Resistance to Darunavir and Virological Response: Validation of Available Systems and of a New Score. Antiviral Therapy, 2011, 16, 489-497.	1.0	10
149	Factors associated with virological success with raltegravir-containing regimens and prevalence of raltegravir-resistance-associated mutations at failure in the ARCA database. Clinical Microbiology and Infection, 2013, 19, 936-942.	6.0	10
150	Susceptibility to HIV-1 integrase strand transfer inhibitors (INSTIs) in highly treatment-experienced patients who failed an INSTI-based regimen. International Journal of Antimicrobial Agents, 2020, 56, 106027.	2.5	10
151	The second dose of the BNT162b2 mRNA vaccine does not boost SARS-CoV-2 neutralizing antibody response in previously infected subjects. Infection, 2022, 50, 541-543.	4.7	10
152	Clinical Evaluation of an In-House Reverse Transcription-Competitive PCR for Quantitation of Human Immunodeficiency Virus Type 1 RNA in Plasma. Journal of Clinical Microbiology, 1999, 37, 333-338.	3.9	10
153	Advantages of predicted phenotypes and statistical learning models in inferring virological response to antiretroviral therapy from HIV genotype. Antiviral Therapy, 2009, 14, 273-283.	1.0	10
154	Natural Variability in the HR-1 and HR-2 Domains of HIV Type 1 gp41 from Different Clades Circulating in Italy. AIDS Research and Human Retroviruses, 2007, 23, 558-563.	1.1	9
155	Natural NS5A inhibitor resistance associated substitutions in hepatitis C virus genotype 1 infected patients from Italy. Clinical Microbiology and Infection, 2018, 24, 308.e5-308.e8.	6.0	9
156	Clinical use, efficacy, and durability of maraviroc for antiretroviral therapy in routine care: A European survey. PLoS ONE, 2019, 14, e0225381.	2.5	9
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