

# Anne-Mieke Vandamme

## List of Publications by Year in descending order

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Version: 2024-02-01

419  
papers

19,970  
citations

11639

70  
h-index

20943

115  
g-index

517  
all docs

517  
docs citations

517  
times ranked

14750  
citing authors

#	ARTICLE	IF	CITATIONS
1	Doubt at the core: Unspoken vaccine hesitancy among healthcare workers. <i>Lancet Regional Health - Europe</i> , 2022, 12, 100289.	3.0	45
2	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	0.9	33
3	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. <i>Virus Evolution</i> , 2022, 8, veac029.	2.2	5
4	Qualitative systems mapping for complex public health problems: A practical guide. <i>PLoS ONE</i> , 2022, 17, e0264463.	1.1	14
5	The Impact of Genital Ulcers on HIV Transmission Has Been Underestimated – A Critical Review. <i>Viruses</i> , 2022, 14, 538.	1.5	2
6	Exploring the mechanisms behind HIV drug resistance in sub-Saharan Africa: conceptual mapping of a complex adaptive system based on multi-disciplinary expert insights. <i>BMC Public Health</i> , 2022, 22, 455.	1.2	10
7	Women in the European Virus Bioinformatics Center. <i>Viruses</i> , 2022, 14, 1522.	1.5	1
8	Sexually transmitted infections, their treatment and urban change in colonial Leopoldville, 1910–1960. <i>Medical History</i> , 2021, 65, 178-196.	0.1	2
9	Behavioral changes before lockdown and decreased retail and recreation mobility during lockdown contributed most to controlling COVID-19 in Western countries. <i>BMC Public Health</i> , 2021, 21, 654.	1.2	18
10	A Comprehensive Molecular Epidemiological Analysis of SARS-CoV-2 Infection in Cyprus from April 2020 to January 2021: Evidence of a Highly Polyphyletic and Evolving Epidemic. <i>Viruses</i> , 2021, 13, 1098.	1.5	11
11	Comparison of two simulators for individual based models in HIV epidemiology in a population with HSV 2 in Yaoundé (Cameroon). <i>Scientific Reports</i> , 2021, 11, 14696.	1.6	3
12	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021, 166, 2633-2648.	0.9	219
13	Determinants of HIV-1 Late Presentation in Patients Followed in Europe. <i>Pathogens</i> , 2021, 10, 835.	1.2	23
14	Newly Discovered Archival Data Show Coincidence of a Peak of Sexually Transmitted Diseases with the Early Epicenter of Pandemic HIV-1. <i>Viruses</i> , 2021, 13, 1701.	1.5	0
15	Factors Associated with HIV Drug Resistance in Dar es Salaam, Tanzania: Analysis of a Complex Adaptive System. <i>Pathogens</i> , 2021, 10, 1535.	1.2	9
16	Development of HIV Drug Resistance in a Cohort of Adults on First-Line Antiretroviral Therapy in Tanzania during the Stavudine Era. <i>Microbiology Research</i> , 2021, 12, 847-861.	0.8	5
17	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020, 143, 110164.	0.8	3
18	Increasing Prevalence of HIV-1 Transmitted Drug Resistance in Portugal: Implications for First Line Treatment Recommendations. <i>Viruses</i> , 2020, 12, 1238.	1.5	7

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19	Scenario-driven forecasting: modeling peaks and paths. Insights from the COVID-19 pandemic in Belgium. <i>Scientometrics</i> , 2020, 124, 2703-2715.	1.6	5
20	Global and regional epidemiology of HIV-1 recombinants in 1990â€“2015: a systematic review and global survey. <i>Lancet HIV</i> , 2020, 7, e772-e781.	2.1	51
21	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
22	Quality Control of Next-Generation Sequencing-Based HIV-1 Drug Resistance Data in Clinical Laboratory Information Systems Framework. <i>Viruses</i> , 2020, 12, 645.	1.5	7
23	Molecular Epidemiology of HIV-1 Infected Migrants Followed Up in Portugal: Trends between 2001â€“2017. <i>Viruses</i> , 2020, 12, 268.	1.5	12
24	A prospect on the use of antiviral drugs to control local outbreaks of COVID-19. <i>BMC Medicine</i> , 2020, 18, 191.	2.3	47
25	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019, 35, 871-873.	1.8	254
26	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208.	1.3	15
27	Cross-country migration linked to people who inject drugs challenges the long-term impact of national HCV elimination programmes. <i>Journal of Hepatology</i> , 2019, 71, 1270-1272.	1.8	7
28	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
29	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. <i>Frontiers in Microbiology</i> , 2019, 10, 613.	1.5	21
30	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019, 220, 233-243.	1.9	23
31	The effect of primary drug resistance on CD4+ cell decline and the viral load set-point in HIV-positive individuals before the start of antiretroviral therapy. <i>Aids</i> , 2019, 33, 315-326.	1.0	4
32	Clinical use, efficacy, and durability of maraviroc for antiretroviral therapy in routine care: A European survey. <i>PLoS ONE</i> , 2019, 14, e0225381.	1.1	9
33	Global and regional molecular epidemiology of HIV-1, 1990â€“2015: a systematic review, global survey, and trend analysis. <i>Lancet Infectious Diseases</i> , 2019, 19, 143-155.	4.6	255
34	HIV-related Peer Support in Dar es Salaam: A Pilot Questionnaire Inquiry. <i>Transdisciplinary Insights</i> , 2019, 3, 1-18.	0.1	4
35	A genetic IFN/STAT1/FAS axis determines CD4 T stem cell memory levels and apoptosis in healthy controls and Adult T-cell Leukemia patients. <i>Oncimmunology</i> , 2018, 7, e1426423.	2.1	17
36	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. <i>Scientific Reports</i> , 2018, 8, 1702.	1.6	24

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37	Transmission Networks of HCV Genotype 1a Enriched With Pre-existing Polymorphism Q80K Among HIV-Infected Patients With Acute Hepatitis C in Poland. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2018, 77, 514-522.	0.9	8
38	The impact of HIV-1 within-host evolution on transmission dynamics. <i>Current Opinion in Virology</i> , 2018, 28, 92-101.	2.6	47
39	Phylogenetic analysis as a forensic tool in HIV transmission investigations. <i>Aids</i> , 2018, 32, 543-554.	1.0	28
40	Predictors of non adherence to antiretroviral therapy at an urban HIV care and treatment center in Tanzania. <i>Drug, Healthcare and Patient Safety</i> , 2018, Volume 10, 79-88.	1.0	18
41	Time to Harmonize Dengue Nomenclature and Classification. <i>Viruses</i> , 2018, 10, 569.	1.5	14
42	Ethical considerations in global HIV phylogenetic research. <i>Lancet HIV</i> , 2018, 5, e656-e666.	2.1	39
43	Relapse or reinfection after failing hepatitis C direct acting antiviral treatment: Unravelling by phylogenetic analysis. <i>PLoS ONE</i> , 2018, 13, e0201268.	1.1	14
44	Expert consensus statement on the science of HIV in the context of criminal law. <i>Journal of the International AIDS Society</i> , 2018, 21, e25161.	1.2	59
45	Origin and Distribution of HIV-1 Subtypes. , 2018, , 1589-1603.		0
46	State of the Art in HIV Drug Resistance: Surveillance and Regional Gaps. <i>AIDS Reviews</i> , 2018, 20, 43-57.	0.5	2
47	State of the Art in HIV Drug Resistance: Science and Technology Knowledge Gap. <i>AIDS Reviews</i> , 2018, 20, 27-42.	0.5	11
48	IFN- $\gamma$ induces greater antiproliferative and proapoptotic effects and increased p53 signaling compared with IFN- $\alpha$ in PBMCs of Adult T-cell Leukemia/Lymphoma patients. <i>Blood Cancer Journal</i> , 2017, 7, e519-e519.	2.8	17
49	Exploring resistance pathways for first-generation NS3/4A protease inhibitors boceprevir and telaprevir using Bayesian network learning. <i>Infection, Genetics and Evolution</i> , 2017, 53, 15-23.	1.0	14
50	Large cluster outbreaks sustain the HIV epidemic among MSM in Quebec. <i>Aids</i> , 2017, 31, 707-717.	1.0	31
51	Phylogenetic evidence for underreporting of male-to-male sex among human immunodeficiency virus-infected donors in the Netherlands and Flanders. <i>Transfusion</i> , 2017, 57, 1235-1247.	0.8	11
52	The epidemic emergence of HIV: what novel enabling factors were involved?. <i>Future Virology</i> , 2017, 12, 685-707.	0.9	7
53	Implications of hepatitis C virus subtype 1a migration patterns for virus genetic sequencing policies in Italy. <i>BMC Evolutionary Biology</i> , 2017, 17, 70.	3.2	21
54	PhyloGeoTool: interactively exploring large phylogenies in an epidemiological context. <i>Bioinformatics</i> , 2017, 33, 3993-3995.	1.8	16

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55	A Fashi Lymphoproliferative Phenotype Reveals Non-Apoptotic Fas Signaling in HTLV-1-Associated Neuroinflammation. <i>Frontiers in Immunology</i> , 2017, 8, 97.	2.2	14
56	A36â€fPrevalence of HIV-1 subtypes in Slovenia with an emphasis on molecular and phylogenetic investigation of subtype A. <i>Virus Evolution</i> , 2017, 3, .	2.2	0
57	A21â€fHIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017, 3, .	2.2	6
58	Zika genomics urgently need standardized and curated reference sequences. <i>PLoS Pathogens</i> , 2017, 13, e1006528.	2.1	10
59	A18â€fRandom amplification with next-generation sequencing to cover HIV and HCV full-length genomes. <i>Virus Evolution</i> , 2017, 3, .	2.2	1
60	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	1.5	13
61	Family Aggregation of Human T-Lymphotropic Virus 1-Associated Diseases: A Systematic Review. <i>Frontiers in Microbiology</i> , 2016, 7, 1674.	1.5	20
62	Detection of Natural Resistance-Associated Substitutions by Ion Semiconductor Technology in HCV1b Positive, Direct-Acting Antiviral Agents-Naïve Patients. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1416.	1.8	14
63	Male Circumcision and the Epidemic Emergence of HIV-2 in West Africa. <i>PLoS ONE</i> , 2016, 11, e0166805.	1.1	10
64	New findings in HCV genotype distribution in selected West European, Russian and Israeli regions. <i>Journal of Clinical Virology</i> , 2016, 81, 82-89.	1.6	60
65	HCV1b genome evolution under selective pressure of the cyclophilin inhibitor alisporivir during the DEB-025-HCV-203 phase II clinical trial. <i>Infection, Genetics and Evolution</i> , 2016, 44, 169-181.	1.0	3
66	On the contribution of Angola to the initial spread of HIV-1. <i>Infection, Genetics and Evolution</i> , 2016, 46, 219-222.	1.0	11
67	Impact of HCV genotype on treatment regimens and drug resistance: a snapshot in time. <i>Reviews in Medical Virology</i> , 2016, 26, 408-434.	3.9	34
68	Mapping the genomic diversity of HCV subtypes 1a and 1b: Implications of structural and immunological constraints for vaccine and drug development. <i>Virus Evolution</i> , 2016, 2, vew024.	2.2	17
69	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 46, 169-179.	1.0	60
70	Transmission of HIV Drug Resistance and the Predicted Effect on Current First-line Regimens in Europe. <i>Clinical Infectious Diseases</i> , 2016, 62, 655-663.	2.9	135
71	Sub-Epidemics Explain Localized High Prevalence of Reduced Susceptibility to Rilpivirine in Treatment-Naïve HIV-1-Infected Patients: Subtype and Geographic Compartmentalization of Baseline Resistance Mutations. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 427-433.	0.5	19
72	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015, 29, 1549-1556.	1.0	16

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73	Virus genetic variability involvement in transmissibility of HIV-1 immune activation and disease progression. <i>Future Virology</i> , 2015, 10, 1259-1262.	0.9	2
74	Assessing transmissibility of HIV-1 drug resistance mutations from treated and from drug-naive individuals. <i>Aids</i> , 2015, 29, 2045-2052.	1.0	21
75	Genetic Diversity and Selective Pressure in Hepatitis C Virus Genotypes 1-6: Significance for Direct-Acting Antiviral Treatment and Drug Resistance. <i>Viruses</i> , 2015, 7, 5018-5039.	1.5	59
76	Performance of an In-House Human Immunodeficiency Virus Type 1 Genotyping System for Assessment of Drug Resistance in Cuba. <i>PLoS ONE</i> , 2015, 10, e0117176.	1.1	4
77	Geographic and Temporal Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted HIV-1 Drug Resistance: An Individual-Patient- and Sequence-Level Meta-Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001810.	3.9	188
78	HIV-1 genotypic drug resistance testing: digging deep, reaching wide?. <i>Current Opinion in Virology</i> , 2015, 14, 16-23.	2.6	36
79	Bridging epidemiology with population genetics in a low incidence MSM-driven HIV-1 subtype B epidemic in Central Europe. <i>BMC Infectious Diseases</i> , 2015, 15, 65.	1.3	11
80	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	0.9	90
81	A new ensemble coevolution system for detecting HIV-1 protein coevolution. <i>Biology Direct</i> , 2015, 10, 1.	1.9	78
82	CRF19_cpx is an Evolutionary fit HIV-1 Variant Strongly Associated With Rapid Progression to AIDS in Cuba. <i>EBioMedicine</i> , 2015, 2, 244-254.	2.7	56
83	Primary resistance to integrase strand-transfer inhibitors in Europe: Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2885-2888.	1.3	61
84	Predicted residual activity of rilpivirine in HIV-1 infected patients failing therapy including NNRTIs efavirenz or nevirapine. <i>Clinical Microbiology and Infection</i> , 2015, 21, 607.e1-607.e8.	2.8	13
85	Global Dispersal Pattern of HIV Type 1 Subtype CRF01_AE: A Genetic Trace of Human Mobility Related to Heterosexual Sexual Activities Centralized in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 1735-1744.	1.9	62
86	Discovery and Characterization of Auxiliary Proteins Encoded by Type 3 Simian T-Cell Lymphotropic Viruses. <i>Journal of Virology</i> , 2015, 89, 931-951.	1.5	2
87	Origin and Distribution of HIV-1 Subtypes. , 2015, , 1-16.		0
88	Trends and Predictors of Transmitted Drug Resistance (TDR) and Clusters with TDR in a Local Belgian HIV-1 Epidemic. <i>PLoS ONE</i> , 2014, 9, e101738.	1.1	36
89	High frequency of antiviral drug resistance and non-b subtypes in HIV-1 patients failing antiviral therapy in Cuba. <i>Journal of the International AIDS Society</i> , 2014, 17, 19754.	1.2	6
90	Pharmacy refill adherence outperforms self-reported methods in predicting HIV therapy outcome in resource-limited settings. <i>BMC Public Health</i> , 2014, 14, 1035.	1.2	82

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91	HIV-1 Gag C-terminal amino acid substitutions emerging under selective pressure of protease inhibitors in patient populations infected with different HIV-1 subtypes. <i>Retrovirology</i> , 2014, 11, 79.	0.9	11
92	The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. <i>PLoS Computational Biology</i> , 2014, 10, e1003505.	1.5	79
93	Clinical and virological response to antiretroviral drugs among HIV patients on first-line treatment in Dar-es-Salaam, Tanzania. <i>Journal of Infection in Developing Countries</i> , 2014, 8, 845-852.	0.5	8
94	Bioinformatics tools for the investigation of viral evolution and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2014, 28, 349-350.	1.0	0
95	HAM/TSP in relatives of HAM/TSP cases and in relatives of asymptomatic HTLV-1 carriers. <i>Retrovirology</i> , 2014, 11, .	0.9	2
96	Superior antiviral and antiproliferative activity of IFN-beta vs. IFN-alpha in primary ATL cells occurs downstream of STAT1 signaling. <i>Retrovirology</i> , 2014, 11, .	0.9	4
97	A selective defect in Fas-mediated apoptosis in HAM/TSP: An ex vivo, in vitro and in silico study. <i>Retrovirology</i> , 2014, 11, P78.	0.9	1
98	CD80+ and CD86+B cells as biomarkers and possible therapeutic targets in HTLV-1 associated myelopathy/tropical spastic paraparesis and multiple sclerosis. <i>Journal of Neuroinflammation</i> , 2014, 11, 18.	3.1	25
99	A stably expressed llama single-domain intrabody targeting Rev displays broad-spectrum anti-HIV activity. <i>Antiviral Research</i> , 2014, 112, 91-102.	1.9	24
100	Increase in transmitted resistance to non-nucleoside reverse transcriptase inhibitors among newly diagnosed HIV-1 infections in Europe. <i>BMC Infectious Diseases</i> , 2014, 14, 407.	1.3	43
101	The characteristics of the HIV subtype B epidemic in Slovenia. <i>BMC Infectious Diseases</i> , 2014, 14, .	1.3	0
102	A near-full length genotypic assay for HCV1b. <i>Journal of Virological Methods</i> , 2014, 209, 126-135.	1.0	11
103	Horizontal gene transfer from human host to HIV-1 reverse transcriptase confers drug resistance and partly compensates for replication deficits. <i>Virology</i> , 2014, 456-457, 310-318.	1.1	5
104	Characterization of amino acids Arg, Ser and Thr at position 70 within HIV-1 reverse transcriptase. <i>Acta Clinica Belgica</i> , 2014, 69, 348-357.	0.5	3
105	Patterns of Transmitted HIV Drug Resistance in Europe Vary by Risk Group. <i>PLoS ONE</i> , 2014, 9, e94495.	1.1	32
106	Limited cross-border infections in patients newly diagnosed with HIV in Europe. <i>Retrovirology</i> , 2013, 10, 36.	0.9	52
107	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalized epidemics. <i>Retrovirology</i> , 2013, 10, 7.	0.9	129
108	Gender differences in HIV disease progression and treatment outcomes among HIV patients one year after starting antiretroviral treatment (ART) in Dar es Salaam, Tanzania. <i>BMC Public Health</i> , 2013, 13, 38.	1.2	58

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109	HIV-1 fitness landscape models for indinavir treatment pressure using observed evolution in longitudinal sequence data are predictive for treatment failure. <i>Infection, Genetics and Evolution</i> , 2013, 19, 349-360.	1.0	4
110	Detection of shrew-borne hantavirus in Eurasian pygmy shrew ( <i>Sorex minutus</i> ) in Central Europe. <i>Infection, Genetics and Evolution</i> , 2013, 19, 403-410.	1.0	43
111	Phylogenetic analysis of G1P[6] group A rotavirus strains detected in Northeast Brazilian children fully vaccinated with Rotarix <sup>®</sup> . <i>Infection, Genetics and Evolution</i> , 2013, 19, 395-402.	1.0	13
112	Viral phylogeny in court: the unusual case of the Valencian anesthetist. <i>BMC Biology</i> , 2013, 11, 83.	1.7	14
113	Antiretroviral drug resistance in HIV-1 therapy-naïve patients in Cuba. <i>Infection, Genetics and Evolution</i> , 2013, 16, 144-150.	1.0	23
114	Mutations selected in HIV-2-infected patients failing a regimen including atazanavir. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 190-192.	1.3	17
115	International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 19, 335-336.	1.0	1
116	Automated subtyping of HIV-1 genetic sequences for clinical and surveillance purposes: Performance evaluation of the new REGA version 3 and seven other tools. <i>Infection, Genetics and Evolution</i> , 2013, 19, 337-348.	1.0	313
117	High inpatient HIV-1 evolutionary rate is associated with CCR5-to-CXCR4 coreceptor switch. <i>Infection, Genetics and Evolution</i> , 2013, 19, 369-377.	1.0	18
118	Asparagine 42 of the conserved endo- $\alpha$ -manninase INU2 motif WMNDPN from <i>Aspergillus ficuum</i> plays a role in activity specificity. <i>FEBS Open Bio</i> , 2013, 3, 467-472.	1.0	14
119	Molecular typing of the local HIV-1 epidemic in Serbia. <i>Infection, Genetics and Evolution</i> , 2013, 19, 378-385.	1.0	15
120	Evaluation of the automatic editing tool RECall for HIV-1 pol and V3 loop sequences. <i>Journal of Virological Methods</i> , 2013, 193, 135-139.	1.0	1
121	Hepatitis C virus infections in the Democratic Republic of Congo exhibit a cohort effect. <i>Infection, Genetics and Evolution</i> , 2013, 19, 386-394.	1.0	32
122	Intra-host evolutionary rates in HIV-1C env and gag during primary infection. <i>Infection, Genetics and Evolution</i> , 2013, 19, 361-368.	1.0	31
123	HIV-1 drug resistance: where do polymorphisms fit in?. <i>Future Microbiology</i> , 2013, 8, 303-306.	1.0	11
124	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013, 29, 1477-1480.	1.8	29
125	Decreasing population selection rates of resistance mutation K65R over time in HIV-1 patients receiving combination therapy including tenofovir. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 419-423.	1.3	4
126	The demise of multidrug-resistant HIV-1: the national time trend in Portugal. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 911-914.	1.3	6



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127	Declining Prevalence of HIV-1 Drug Resistance in Antiretroviral Treatment-exposed Individuals in Western Europe. <i>Journal of Infectious Diseases</i> , 2013, 207, 1216-1220.	1.9	53
128	Structural modifications induced by specific HIV-1 protease-compensatory mutations have an impact on the virological response to a first-line lopinavir/ritonavir-containing regimen. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2205-2209.	1.3	8
129	HIV-1 Subtype Is an Independent Predictor of Reverse Transcriptase Mutation K65R in HIV-1 Patients Treated with Combination Antiretroviral Therapy Including Tenofovir. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1053-1056.	1.4	39
130	Superinfection with drug-resistant HIV is rare and does not contribute substantially to therapy failure in a large European cohort. <i>BMC Infectious Diseases</i> , 2013, 13, 537.	1.3	8
131	Functional conservation of HIV-1 Gag: implications for rational drug design. <i>Retrovirology</i> , 2013, 10, 126.	0.9	56
132	Clinical Evaluation of Rega 8: An Updated Genotypic Interpretation System That Significantly Predicts HIV-Therapy Response. <i>PLoS ONE</i> , 2013, 8, e61436.	1.1	17
133	Ascorbic Acid Has Superior Ex Vivo Antiproliferative, Cell Death-Inducing and Immunomodulatory Effects over IFN- $\gamma$ in HTLV-1-Associated Myelopathy. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1729.	1.3	18
134	Enhanced Heterosexual Transmission Hypothesis for the Origin of Pandemic HIV-1. <i>Viruses</i> , 2012, 4, 1950-1983.	1.5	11
135	HIV-1 protease mutation 82M contributes to phenotypic resistance to protease inhibitors in subtype G. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1075-1079.	1.3	8
136	Treatment-associated polymorphisms in protease are significantly associated with higher viral load and lower CD4 count in newly diagnosed drug-naive HIV-1 infected patients. <i>Retrovirology</i> , 2012, 9, 81.	0.9	23
137	Simultaneous RNA quantification of human and retroviral genomes reveals intact interferon signaling in HTLV-1-infected CD4+ T cell lines. <i>Virology Journal</i> , 2012, 9, 171.	1.4	21
138	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. <i>Journal of General Virology</i> , 2012, 93, 889-899.	1.3	56
139	High frequency of antiviral drug resistance and non-B subtypes in HIV-1 patients failing antiviral therapy in Cuba. <i>Journal of Clinical Virology</i> , 2012, 55, 348-355.	1.6	10
140	Phylodynamics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012, 12, 453-460.	1.0	52
141	A Public HTLV-1 Molecular Epidemiology Database for Sequence Management and Data Mining. <i>PLoS ONE</i> , 2012, 7, e42123.	1.1	16
142	Science in court: the myth of HIV fingerprinting. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 78-79.	4.6	26
143	European guidelines on the clinical management of HIV-1 tropism testing. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 394-407.	4.6	218
144	Appearance of a Single Amino Acid Insertion at Position 33 in HIV Type 1 Protease Under a Lopinavir-Containing Regimen, Associated with Reduced Protease Inhibitor Susceptibility. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 1223-1229.	0.5	0

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145	Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study). <i>HIV Medicine</i> , 2011, 12, 211-218.	1.0	32
146	B cell costimulatory molecules as potential biomarkers in HAM/TSP. <i>Retrovirology</i> , 2011, 8, .	0.9	0
147	Ascorbic acid has superior antiviral and antiproliferative effects over IFN-alpha in HAM/TSP PBMC ex vivo. <i>Retrovirology</i> , 2011, 8, .	0.9	3
148	CD64 as a biomarker and therapeutic target in HAM/TSP and HTLV-1-associated Infective Dermatitis. <i>Retrovirology</i> , 2011, 8, .	0.9	0
149	A Bayesian network approach to study host and viral genetic correlates of HIV-1 disease progression. <i>Retrovirology</i> , 2011, 8, .	0.9	1
150	Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1886-1896.	1.3	56
151	Global trends in molecular epidemiology of HIV-1 during 2000-2007. <i>Aids</i> , 2011, 25, 679-689.	1.0	602
152	European recommendations for the clinical use of HIV drug resistance testing: 2011 update. <i>AIDS Reviews</i> , 2011, 13, 77-108.	0.5	106
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