

Anne-Mieke Vandamme

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5551359/anne-mieke-vandamme-publications-by-citations.pdf>

Version: 2024-04-24

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.

401
papers

16,422
citations

67
h-index

108
g-index

517
ext. papers

18,470
ext. citations

5.3
avg, IF

6.03
L-index

#	Paper	IF	Citations
401	Drug resistance mutations for surveillance of transmitted HIV-1 drug-resistance: 2009 update. <i>PLoS ONE</i> , 2009 , 4, e4724	3.7	706
400	Global trends in molecular epidemiology of HIV-1 during 2000-2007. <i>Aids</i> , 2011 , 25, 679-89	3.5	535
399	Human T-lymphotropic virus 1: recent knowledge about an ancient infection. <i>Lancet Infectious Diseases, The</i> , 2007 , 7, 266-81	25.5	461
398	An automated genotyping system for analysis of HIV-1 and other microbial sequences. <i>Bioinformatics</i> , 2005 , 21, 3797-800	7.2	416
397	Prevalence of drug-resistant HIV-1 variants in untreated individuals in Europe: implications for clinical management. <i>Journal of Infectious Diseases</i> , 2005 , 192, 958-66	7	356
396	Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event. <i>Journal of Virology</i> , 2005 , 79, 1595-604	6.6	344
395	Tracing the origin and history of the HIV-2 epidemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6588-92	11.5	254
394	Assessing substitution saturation with DAMBE615-630		237
393	Impact of HIV-1 subtype and antiretroviral therapy on protease and reverse transcriptase genotype: results of a global collaboration. <i>PLoS Medicine</i> , 2005 , 2, e112	11.6	234
392	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, 337-48	4.5	229
391	European guidelines on the clinical management of HIV-1 tropism testing. <i>Lancet Infectious Diseases, The</i> , 2011 , 11, 394-407	25.5	194
390	Transmission of drug-resistant HIV-1 is stabilizing in Europe. <i>Journal of Infectious Diseases</i> , 2009 , 200, 1503-8	7	186
389	Potent and highly selective human immunodeficiency virus type 1 (HIV-1) inhibition by a series of alpha-anilinophenylacetamide derivatives targeted at HIV-1 reverse transcriptase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993 , 90, 1711-5	11.5	184
388	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	11.6	163
387	2P5PBis-O-(tert-butyl dimethylsilyl)-3Pspiro-5P(4Pamino-1P2P oxathiole-2P2Pdioxide)pyrimidine (TSAO) nucleoside analogues: highly selective inhibitors of human immunodeficiency virus type 1 that are targeted at the viral reverse transcriptase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993 , 90, 1239-44	11.5	153
386	HIV-1-specific reverse transcriptase inhibitors show differential activity against HIV-1 mutant strains containing different amino acid substitutions in the reverse transcriptase. <i>Virology</i> , 1993 , 192, 246-53	3.6	152
385	Clinical and laboratory guidelines for the use of HIV-1 drug resistance testing as part of treatment management: recommendations for the European setting. The EuroGuidelines Group for HIV resistance. <i>Aids</i> , 2001 , 15, 309-20	3.5	141

384	Global and regional molecular epidemiology of HIV-1, 1990-2015: a systematic review, global survey, and trend analysis. <i>Lancet Infectious Diseases, The</i> , 2019 , 19, 143-155	25.5	135
383	Relating increasing hantavirus incidences to the changing climate: the mast connection. <i>International Journal of Health Geographics</i> , 2009 , 8, 1	3.5	134
382	DEB025 (Alisporivir) inhibits hepatitis C virus replication by preventing a cyclophilin A induced cis-trans isomerisation in domain II of NS5A. <i>PLoS ONE</i> , 2010 , 5, e13687	3.7	133
381	A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , 2009 , 37, W634-42	20.1	128
380	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	11.6	117
379	Characterization of a novel simian immunodeficiency virus with a vpu gene from greater spot-nosed monkeys (<i>Cercopithecus nictitans</i>) provides new insights into simian/human immunodeficiency virus phylogeny. <i>Journal of Virology</i> , 2002 , 76, 8298-309	6.6	112
378	Genetic variability and molecular evolution of the human respiratory syncytial virus subgroup B attachment G protein. <i>Journal of Virology</i> , 2005 , 79, 9157-67	6.6	111
377	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019 , 35, 871-873	7.2	109
376	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalized epidemics. <i>Retrovirology</i> , 2013 , 10, 7	3.6	103
375	A synthetic HIV-1 Rev inhibitor interfering with the CRM1-mediated nuclear export. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 14440-5	11.5	103
374	U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains. <i>Journal of Virology</i> , 2003 , 77, 6359-66	6.6	100
373	Transmission of drug-resistant HIV-1 in Europe remains limited to single classes. <i>Aids</i> , 2008 , 22, 625-35	3.5	97
372	Molecular evolution and circulation patterns of human respiratory syncytial virus subgroup a: positively selected sites in the attachment g glycoprotein. <i>Journal of Virology</i> , 2004 , 78, 4675-83	6.6	95
371	European recommendations for the clinical use of HIV drug resistance testing: 2011 update. <i>AIDS Reviews</i> , 2011 , 13, 77-108	1.5	95
370	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , 2009 , 6, 49	3.6	94
369	Prevalence and characteristics of multinucleoside-resistant human immunodeficiency virus type 1 among European patients receiving combinations of nucleoside analogues. <i>Antimicrobial Agents and Chemotherapy</i> , 2000 , 44, 2109-17	5.9	91
368	A primate T-lymphotropic virus, PTLV-L, different from human T-lymphotropic viruses types I and II, in a wild-caught baboon (<i>Papio hamadryas</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 2848-52	11.5	91
367	Dating the common ancestor of SIVcpz and HIV-1 group M and the origin of HIV-1 subtypes using a new method to uncover clock-like molecular evolution. <i>FASEB Journal</i> , 2001 , 15, 276-8	0.9	90

366	The molecular population genetics of HIV-1 group O. <i>Genetics</i> , 2004 , 167, 1059-68	4	89
365	The simian origins of the pathogenic human T-cell lymphotropic virus type I. <i>Trends in Microbiology</i> , 1998 , 6, 477-83	12.4	88
364	Resistance-related mutations in the HIV-1 protease gene of patients treated for 1 year with the protease inhibitor ritonavir (ABT-538). <i>Aids</i> , 1996 , 10, 995-9	3.5	86
363	Extensive survey on the prevalence and genetic diversity of SIVs in primate bushmeat provides insights into risks for potential new cross-species transmissions. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 386-96	4.5	84
362	The calculated genetic barrier for antiretroviral drug resistance substitutions is largely similar for different HIV-1 subtypes. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2006 , 41, 352-60	3.1	84
361	Primate T-lymphotropic virus type I LTR sequence variation and its phylogenetic analysis: compatibility with an African origin of PTLV-I. <i>Virology</i> , 1994 , 202, 212-23	3.6	83
360	A Genotypic Drug Resistance Interpretation Algorithm that Significantly Predicts Therapy Response in HIV-1-Infected Patients. <i>Antiviral Therapy</i> , 2002 , 7, 123-129	1.6	83
359	Profile of resistance of human immunodeficiency virus to mannose-specific plant lectins. <i>Journal of Virology</i> , 2004 , 78, 10617-27	6.6	82
358	Human immunodeficiency virus type 1 (HIV-1) strains selected for resistance against the HIV-1-specific [2P5Pbis-O-(tert-butyldimethylsilyl)-3Pspiro-5P(4Pamino-1P2Poxathiole-2P2Pdioxide)]-beta-D-pentofurano syl (TSAO) nucleoside analogues retain sensitivity to HIV-1-specific nonnucleoside inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993 , 90, 6952-6	11.5	80
357	The characteristics of the HIV subtype B epidemic in Slovenia. <i>BMC Infectious Diseases</i> , 2014 , 14,	4	78
356	B cell costimulatory molecules as potential biomarkers in HAM/TSP. <i>Retrovirology</i> , 2011 , 8,	3.6	78
355	CD64 as a biomarker and therapeutic target in HAM/TSP and HTLV-1-associated Infective Dermatitis. <i>Retrovirology</i> , 2011 , 8,	3.6	78
354	env Chimeric Virus Technology for Evaluating Human Immunodeficiency Virus Susceptibility to Entry Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2003 , 47, 1177-1177	5.9	78
353	Quantifying differences in the tempo of human immunodeficiency virus type 1 subtype evolution. <i>Journal of Virology</i> , 2009 , 83, 12917-24	6.6	77
352	Rapid, phenotypic HIV-1 drug sensitivity assay for protease and reverse transcriptase inhibitors. <i>Journal of Clinical Virology</i> , 1999 , 13, 71-80	14.5	77
351	Managing resistance to anti-HIV drugs: an important consideration for effective disease management. <i>Drugs</i> , 1999 , 57, 337-61	12.1	77
350	HTLV-II seroprevalence in pygmies across Africa since 1970. <i>AIDS Research and Human Retroviruses</i> , 1993 , 9, 709-13	1.6	77
349	HIV-1 protease and reverse transcriptase mutation patterns responsible for discordances between genotypic drug resistance interpretation algorithms. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2003 , 33, 8-14	3.1	76

348	Recombination confounds the early evolutionary history of human immunodeficiency virus type 1: subtype G is a circulating recombinant form. <i>Journal of Virology</i> , 2007 , 81, 8543-51	6.6	75
347	Clinical characteristics of patients in Peru with human T cell lymphotropic virus type 1-associated tropical spastic paraparesis. <i>Clinical Infectious Diseases</i> , 2004 , 39, 939-44	11.6	75
346	Diagnostic value of different adherence measures using electronic monitoring and virologic failure as reference standards. <i>AIDS Patient Care and STDs</i> , 2008 , 22, 735-43	5.8	73
345	Phylogenetic surveillance of viral genetic diversity and the evolving molecular epidemiology of human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2007 , 81, 13050-6	6.6	72
344	Hepatitis E virus infection in work horses in Egypt. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 368-73	4.5	71
343	Discordances between interpretation algorithms for genotypic resistance to protease and reverse transcriptase inhibitors of human immunodeficiency virus are subtype dependent. <i>Antimicrobial Agents and Chemotherapy</i> , 2006 , 50, 694-701	5.9	71
342	Two new human T-lymphotropic virus type I phylogenetic subtypes in seroindeterminates, a Mbuti pygmy and a Gabonese, have closest relatives among African STLV-I strains. <i>Virology</i> , 1998 , 246, 277-87	3.6	70
341	Activity of non-nucleoside reverse transcriptase inhibitors against HIV-2 and SIV. <i>Aids</i> , 1999 , 13, 1477-83	3.5	70
340	Different population dynamics of human T cell lymphotropic virus type II in intravenous drug users compared with endemically infected tribes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 13253-8	11.5	70
339	Development of resistance of human immunodeficiency virus type 1 to dextran sulfate associated with the emergence of specific mutations in the envelope gp120 glycoprotein. <i>Molecular Pharmacology</i> , 1997 , 52, 98-104	4.3	69
338	Multiple dideoxynucleoside analogue-resistant (MddNR) HIV-1 strains isolated from patients from different European countries. <i>Aids</i> , 1998 , 12, 2007-15	3.5	69
337	Selective regimen shift and demographic growth increase associated with the emergence of high-fitness variants of canine parvovirus. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 399-409	4.5	68
336	The three human T-lymphotropic virus type I subtypes arose from three geographically distinct simian reservoirs. <i>Journal of General Virology</i> , 1996 , 77 (Pt 2), 359-68	4.9	68
335	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015 , 12, 18	3.6	67
334	Standardisation of primers and an algorithm for HIV-1 diagnostic PCR evaluated in patients harbouring strains of diverse geographical origin. The Belgian AIDS Reference Laboratories. <i>Journal of Virological Methods</i> , 1995 , 51, 305-16	2.6	67
333	African origin of human T-lymphotropic virus type 2 (HTLV-2) supported by a potential new HTLV-2d subtype in Congolese Bambutu Efe Pygmies. <i>Journal of Virology</i> , 1998 , 72, 4327-40	6.6	67
332	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	5	66
331	Protease mutation M89I/V is linked to therapy failure in patients infected with the HIV-1 non-B subtypes C, F or G. <i>Aids</i> , 2005 , 19, 1799-806	3.5	66

330	Increasing prevalence of non-clade B HIV-1 strains in heterosexual men and women, as monitored by analysis of reverse transcriptase and protease sequences. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2001 , 27, 499-505	3.1	66
329	Phylogeography and evolutionary history of dengue virus type 3. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 716-25	4.5	63
328	Prevalence and correlates of nonadherence to antiretroviral therapy in a population of HIV patients using Medication Event Monitoring System. <i>AIDS Patient Care and STDs</i> , 2004 , 18, 644-57	5.8	63
327	Tenofovir resistance and resensitization. <i>Antimicrobial Agents and Chemotherapy</i> , 2003 , 47, 3478-84	5.9	63
326	Quantification of HIV-1 RNA in plasma: comparable results with the NASBA HIV-1 RNA QT and the AMPLICOR HIV monitor test. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1996 , 13, 127-39		63
325	Hepatitis C virus evolutionary patterns studied through analysis of full-genome sequences. <i>Journal of Molecular Evolution</i> , 2002 , 54, 62-70	3.1	61
324	Circulation of genetically distinct contemporary human coronavirus OC43 strains. <i>Virology</i> , 2005 , 337, 85-92	3.6	61
323	Molecular footprint of drug-selective pressure in a human immunodeficiency virus transmission chain. <i>Journal of Virology</i> , 2005 , 79, 11981-9	6.6	61
322	Use of a generic polymerase chain reaction assay detecting human T-lymphotropic virus (HTLV) types I, II and divergent simian strains in the evaluation of individuals with indeterminate HTLV serology 1997 , 52, 1-7		59
321	Failure to quantify viral load with two of the three commercial methods in a pregnant woman harboring an HIV type 1 subtype G strain. <i>AIDS Research and Human Retroviruses</i> , 1998 , 14, 453-9	1.6	59
320	Detection of HIV-1 RNA in plasma and serum samples using the NASBA amplification system compared to RNA-PCR. <i>Journal of Virological Methods</i> , 1995 , 52, 121-32	2.6	58
319	HIV forensics: pitfalls and acceptable standards in the use of phylogenetic analysis as evidence in criminal investigations of HIV transmission. <i>HIV Medicine</i> , 2007 , 8, 382-7	2.7	57
318	The presence of a divergent T-lymphotropic virus in a wild-caught pygmy chimpanzee (<i>Pan paniscus</i>) supports an African origin for the human T-lymphotropic/simian T-lymphotropic group of viruses. <i>Journal of General Virology</i> , 1996 , 77 (Pt 5), 1089-99	4.9	57
317	In vivo characteristics of human immunodeficiency virus type 1 intersubtype recombination: determination of hot spots and correlation with sequence similarity. <i>Journal of General Virology</i> , 2003 , 84, 2715-2722	4.9	56
316	Analysis of HIV-1 pol sequences using Bayesian Networks: implications for drug resistance. <i>Bioinformatics</i> , 2006 , 22, 2975-9	7.2	55
315	Pharmacy refill adherence outperforms self-reported methods in predicting HIV therapy outcome in resource-limited settings. <i>BMC Public Health</i> , 2014 , 14, 1035	4.1	54
314	Phylogeography of circulating populations of human echovirus 30 over 50 years: nucleotide polymorphism and signature of purifying selection in the VP1 capsid protein gene. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 699-708	4.5	53
313	Analysis of the serotype and genotype correlation of VP1 and the 5'noncoding region in an epidemiological survey of the human enterovirus B species. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 963-71	9.7	53

312	Simian T-cell leukemia virus (STLV) infection in wild primate populations in Cameroon: evidence for dual STLV type 1 and type 3 infection in agile mangabeys (<i>Cercocebus agilis</i>). <i>Journal of Virology</i> , 2004 , 78, 4700-9	6.6	52
311	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	2.6	52
310	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, 5018-39	6.2	51
309	Resistance of human immunodeficiency virus type 1 reverse transcriptase to TIBO derivatives induced by site-directed mutagenesis. <i>Virology</i> , 1992 , 188, 900-4	3.6	51
308	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, 1735-44	7	50
307	New findings in HCV genotype distribution in selected West European, Russian and Israeli regions. <i>Journal of Clinical Virology</i> , 2016 , 81, 82-9	14.5	50
306	Evolutionary rate and genetic drift of hepatitis C virus are not correlated with the host immune response: studies of infected donor-recipient clusters. <i>Journal of Virology</i> , 2000 , 74, 2541-9	6.6	49
305	Comparison of HIV-1 genotypic resistance test interpretation systems in predicting virological outcomes over time. <i>PLoS ONE</i> , 2010 , 5, e11505	3.7	48
304	Primary resistance to integrase strand-transfer inhibitors in Europe. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 2885-8	5.1	47
303	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	4.1	47
302	Declining prevalence of HIV-1 drug resistance in antiretroviral treatment-exposed individuals in Western Europe. <i>Journal of Infectious Diseases</i> , 2013 , 207, 1216-20	7	47
301	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	11.5	46
300	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	4.9	46
299	Seroprevalence and risk factors for human T-cell lymphotropic virus (HTLV-I) infection among ethnically and geographically diverse Peruvian women. <i>International Journal of Infectious Diseases</i> , 2003 , 7, 132-7	10.5	46
298	The low evolutionary rate of human T-cell lymphotropic virus type-1 confirmed by analysis of vertical transmission chains. <i>Molecular Biology and Evolution</i> , 2004 , 21, 603-11	8.3	46
297	Phylogenetics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 453-60	4.5	45
296	Bayesian phylogenetic analysis using MRBAYES210-266		45
295	Algorithms for the interpretation of HIV-1 genotypic drug resistance information. <i>Antiviral Research</i> , 2006 , 71, 335-42	10.8	45

294	Functional conservation of HIV-1 Gag: implications for rational drug design. <i>Retrovirology</i> , 2013 , 10, 126	3.6	44
293	Cell type-dependent effect of sodium valproate on human immunodeficiency virus type 1 replication in vitro. <i>AIDS Research and Human Retroviruses</i> , 1997 , 13, 187-92	1.6	44
292	Rising prevalence of HIV-1 non-B subtypes in Belgium: 1983-2001. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2004 , 35, 279-85	3.1	44
291	Human retroviruses (HIV and HTLV) in Brazilian Indians: seroepidemiological study and molecular epidemiology of HTLV type 2 isolates. <i>AIDS Research and Human Retroviruses</i> , 2002 , 18, 71-7	1.6	44
290	Characterization of HIV-1 strains isolated from patients treated with TIBO R82913. <i>AIDS Research and Human Retroviruses</i> , 1994 , 10, 39-46	1.6	44
289	Complete genome sequence, taxonomic assignment, and comparative analysis of the untranslated regions of the Modoc virus, a flavivirus with no known vector. <i>Virology</i> , 2002 , 293, 125-40	3.6	43
288	Different epidemic potentials of the HIV-1B and C subtypes. <i>Journal of Molecular Evolution</i> , 2005 , 60, 598-605	3.1	43
287	New retroviruses in human and simian T-lymphotropic viruses. <i>Lancet, The</i> , 1994 , 344, 265-6	4.0	43
286	Familial transmission and minimal sequence variability of human T-lymphotropic virus type I (HTLV-I) in Zaire. <i>AIDS Research and Human Retroviruses</i> , 1994 , 10, 1135-42	1.6	42
285	Mapping sites of positive selection and amino acid diversification in the HIV genome: an alternative approach to vaccine design?. <i>Genetics</i> , 2004 , 167, 1047-58	4	41
284	Increasing Prevalence of Non-1ade B HIV-1 Strains in Heterosexual Men and Women, as Monitored by Analysis of Reverse Transcriptase and Protease Sequences. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2001 , 27, 499-505	3.1	41
283	Investigation of Baseline Susceptibility to Protease Inhibitors in HIV-1 Subtypes C, F, G and Crf02_Ag. <i>Antiviral Therapy</i> , 2006 , 11, 581-589	1.6	41
282	Evolutionary rate and genetic heterogeneity of human T-cell lymphotropic virus type II (HTLV-II) using isolates from European injecting drug users. <i>Journal of Molecular Evolution</i> , 1998 , 46, 602-11	3.1	40
281	Fas 670 promoter polymorphism is associated to susceptibility, clinical presentation, and survival in adult T cell leukemia. <i>Journal of Leukocyte Biology</i> , 2008 , 83, 220-2	6.5	40
280	Simple algorithm derived from a geno-/phenotypic database to predict HIV-1 protease inhibitor resistance. <i>Aids</i> , 2000 , 14, 1731-8	3.5	40
279	Limited cross-border infections in patients newly diagnosed with HIV in Europe. <i>Retrovirology</i> , 2013 , 10, 36	3.6	39
278	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, 1886-96	5.1	39
277	Use of electronic monitoring induces a 40-day intervention effect in HIV patients. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2006 , 43, 247-8	3.1	39

276	Molecular testing of multiple HIV-1 transmissions in a criminal case. <i>Aids</i> , 2005 , 19, 1649-58	3.5	39
275	High GUD incidence in the early 20 century created a particularly permissive time window for the origin and initial spread of epidemic HIV strains. <i>PLoS ONE</i> , 2010 , 5, e9936	3.7	39
274	CRF19_cpx is an Evolutionary fit HIV-1 Variant Strongly Associated With Rapid Progression to AIDS in Cuba. <i>EBioMedicine</i> , 2015 , 2, 244-54	8.8	38
273	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	5.4	38
272	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	4	38
271	Highly divergent subtypes and new recombinant forms prevail in the HIV/AIDS epidemic in Angola: new insights into the origins of the AIDS pandemic. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 672-82	4.5	38
270	Early sequential development of infective dermatitis, human T cell lymphotropic virus type 1-associated myelopathy, and adult T cell leukemia/lymphoma. <i>Clinical Infectious Diseases</i> , 2008 , 46, 440-2 ^{11.6}		38
269	Isolation, cloning, and complete nucleotide sequence of a phenotypically distinct Brazilian isolate of human T-lymphotropic virus type II (HTLV-II). <i>Virology</i> , 2000 , 271, 142-54	3.6	38
268	A genotypic drug resistance interpretation algorithm that significantly predicts therapy response in HIV-1-infected patients. <i>Antiviral Therapy</i> , 2002 , 7, 123-9	1.6	38
267	The incidence of multidrug and full class resistance in HIV-1 infected patients is decreasing over time (2001-2006) in Portugal. <i>Retrovirology</i> , 2008 , 5, 12	3.6	37
266	Genotypic drug resistance interpretation algorithms display high levels of discordance when applied to non-B strains from HIV-1 naive and treated patients. <i>FEMS Immunology and Medical Microbiology</i> , 2006 , 46, 53-62		37
265	A genotypic resistance assay for the detection of drug resistance in the human immunodeficiency virus type 1 envelope gene. <i>Journal of Virological Methods</i> , 2005 , 123, 25-34	2.6	37
264	Antiviral activity of the bicyclam derivative JM3100 against drug-resistant strains of human immunodeficiency virus type 1. <i>Antiviral Research</i> , 1996 , 29, 297-307	10.8	37
263	Evaluation of two commercial kits for the detection of genotypic drug resistance on a panel of HIV type 1 subtypes A through J. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2001 , 28, 254-8	3.1	36
262	env chimeric virus technology for evaluating human immunodeficiency virus susceptibility to entry inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2002 , 46, 3954-62	5.9	36
261	The origin and evolution of human T-cell lymphotropic virus type II (HTLV-II) and the relationship with its replication strategy. <i>Gene</i> , 1999 , 234, 11-21	3.8	36
260	Detection and molecular characterisation of noroviruses and sapoviruses in asymptomatic swine and cattle in Slovenian farms. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 413-20	4.5	35
259	No response to first-line tenofovir+lamivudine+efavirenz despite optimization according to baseline resistance testing: impact of resistant minority variants on efficacy of low genetic barrier drugs. <i>Journal of Clinical Virology</i> , 2007 , 39, 43-7	14.5	35

258	The genomic structure of a new simian T-lymphotropic virus, STLV-PH969, differs from that of human T-lymphotropic virus types I and II. <i>Journal of General Virology</i> , 1996 , 77 (Pt 2), 347-58	4.9	35
257	A genotypic assay for the amplification and sequencing of integrase from diverse HIV-1 group M subtypes. <i>Journal of Virological Methods</i> , 2008 , 153, 176-81	2.6	34
256	Mosaic genomes of the six major primate lentivirus lineages revealed by phylogenetic analyses. <i>Journal of Virology</i> , 2003 , 77, 7202-13	6.6	34
255	The simian T-lymphotropic virus STLV-PP1664 from Pan paniscus is distinctly related to HTLV-2 but differs in genomic organization. <i>Virology</i> , 1998 , 243, 366-79	3.6	33
254	Prevalence and origin of HIV-1 group M subtypes among patients attending a Belgian hospital in 1999. <i>Virus Research</i> , 2002 , 85, 95-107	6.4	33
253	Complete genome sequence of Montana Myotis leukoencephalitis virus, phylogenetic analysis and comparative study of the 3Puntranslated region of flaviviruses with no known vector. <i>Journal of General Virology</i> , 2002 , 83, 1875-1885	4.9	33
252	Impact of HCV genotype on treatment regimens and drug resistance: a snapshot in time. <i>Reviews in Medical Virology</i> , 2016 , 26, 408-434	11.7	32
251	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016 , 46, 169-179	4.5	32
250	Evolution and dispersal of St. Louis encephalitis virus in the Americas. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 709-15	4.5	32
249	Limitations to contact tracing and phylogenetic analysis in establishing HIV type 1 transmission networks in Cuba. <i>AIDS Research and Human Retroviruses</i> , 2007 , 23, 347-56	1.6	32
248	HIV-1 compartmentalization in diverse leukocyte populations during antiretroviral therapy. <i>Journal of Leukocyte Biology</i> , 2004 , 76, 562-70	6.5	32
247	Detection of shrew-borne hantavirus in Eurasian pygmy shrew (<i>Sorex minutus</i>) in Central Europe. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 403-10	4.5	31
246	Hepatitis C virus infections in the Democratic Republic of Congo exhibit a cohort effect. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 386-94	4.5	31
245	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, 1053-6	5.9	31
244	Stabilisation of emulsions using hydrophobically modified inulin (polyfructose). <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2004 , 250, 133-140	5.1	31
243	A new ensemble coevolution system for detecting HIV-1 protein coevolution. <i>Biology Direct</i> , 2015 , 10, 1	7.2	30
242	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	3.7	30
241	Predictive value of HIV-1 genotypic resistance test interpretation algorithms. <i>Journal of Infectious Diseases</i> , 2009 , 200, 453-63	7	30

240	Comparison of the LiPA HIV-1 RT test, selective PCR and direct solid phase sequencing for the detection of HIV-1 drug resistance mutations. <i>Journal of Virological Methods</i> , 1998 , 73, 77-82	2.6	30
239	Prevalence and epidemiology of HIV type 1 drug resistance among newly diagnosed therapy-naive patients in Belgium from 2003 to 2006. <i>AIDS Research and Human Retroviruses</i> , 2008 , 24, 355-62	1.6	30
238	Identification in gelada baboons (<i>Theropithecus gelada</i>) of a distinct simian T-cell lymphotropic virus type 3 with a broad range of Western blot reactivity. <i>Journal of General Virology</i> , 2004 , 85, 507-519	4.9	30
237	A Bayesian statistical analysis of human T-cell lymphotropic virus evolutionary rates. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 291-8	4.5	30
236	Evolutionary strategies of human T-cell lymphotropic virus type II. <i>Gene</i> , 2000 , 261, 171-80	3.8	30
235	Investigation of expert rule bases, logistic regression, and non-linear machine learning techniques for predicting response to antiretroviral treatment. <i>Antiviral Therapy</i> , 2009 , 14, 433-442	1.6	30
234	Phylogeny of primate T lymphotropic virus type 1 (PTLV-1) including various new Asian and African non-human primate strains. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 374-81	4.5	29
233	Complete nucleotide sequence of the Italian human T-cell lymphotropic virus type II isolate Gu and phylogenetic identification of a possible origin of South European epidemics. <i>Journal of General Virology</i> , 1996 , 77 (Pt 6), 1193-201	4.9	29
232	Patterns of transmitted HIV drug resistance in Europe vary by risk group. <i>PLoS ONE</i> , 2014 , 9, e94495	3.7	28
231	Development and validation of a multiplex real-time PCR assay for simultaneous genotyping and human T-lymphotropic virus type 1, 2, and 3 proviral load determination. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 3682-91	9.7	27
230	Differences in molecular evolution between switch (R5 to R5X4/X4-tropic) and non-switch (R5-tropic only) HIV-1 populations during infection. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 356-64	4.5	27
229	Assessment of automated genotyping protocols as tools for surveillance of HIV-1 genetic diversity. <i>Aids</i> , 2006 , 20, 1521-9	3.5	27
228	Brazilian HTLV type 2a strains from intravenous drug users (IDUs) appear to have originated from two sources: Brazilian Amerindians and European/North American IDUs. <i>AIDS Research and Human Retroviruses</i> , 2003 , 19, 519-23	1.6	27
227	The discovery of two new divergent STLVs has implications for the evolution and epidemiology of HTLVs. <i>Reviews in Medical Virology</i> , 1999 , 9, 155-70	11.7	27
226	Genetic analyses reveal structured HIV-1 populations in serially sampled T lymphocytes of patients receiving HAART. <i>Virology</i> , 2006 , 348, 35-46	3.6	26
225	Estimating the relative contribution of dNTP pool imbalance and APOBEC3G/3F editing to HIV evolution in vivo. <i>Journal of Computational Biology</i> , 2007 , 14, 1105-14	1.7	26
224	A quantitative GFP-based bioassay for the detection of HIV-1 Tat transactivation inhibitors. <i>Journal of Virological Methods</i> , 2001 , 96, 183-8	2.6	26
223	Evidence for a second simian T-cell lymphotropic virus type 3 in <i>Cercopithecus nictitans</i> from Cameroon. <i>Journal of Virology</i> , 2001 , 75, 11939-41	6.6	26

222	Human immunodeficiency virus gene regulation as a target for antiviral chemotherapy. <i>Antiviral Chemistry and Chemotherapy</i> , 1999 , 10, 1-14	3.5	26
221	A prospect on the use of antiviral drugs to control local outbreaks of COVID-19. <i>BMC Medicine</i> , 2020 , 18, 191	11.4	25
220	The impact of HIV-1 within-host evolution on transmission dynamics. <i>Current Opinion in Virology</i> , 2018 , 28, 92-101	7.5	25
219	Intra-host evolutionary rates in HIV-1C env and gag during primary infection. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 361-8	4.5	25
218	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013 , 29, 1477-80	7.2	25
217	Science in court: the myth of HIV fingerprinting. <i>Lancet Infectious Diseases</i> , 2011 , 11, 78-9	25.5	25
216	Bayesian network analysis of resistance pathways against HIV-1 protease inhibitors. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 382-90	4.5	25
215	Full-genome analysis of a highly divergent simian T-cell lymphotropic virus type 1 strain in <i>Macaca arctoides</i> . <i>Journal of General Virology</i> , 2005 , 86, 1953-1959	4.9	25
214	HIV-1 genotypic drug resistance testing: digging deep, reaching wide?. <i>Current Opinion in Virology</i> , 2015 , 14, 16-23	7.5	24
213	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, 211-8	2.7	24
212	S-adenosylhomocysteine hydrolase inhibitors interfere with the replication of human immunodeficiency virus type 1 through inhibition of the LTR transactivation. <i>Molecular Pharmacology</i> , 1997 , 52, 1157-63	4.3	24
211	Performance of ViroSeq HIV-1 Genotyping System in routine practice at a Belgian clinical laboratory. <i>Journal of Virological Methods</i> , 2004 , 119, 45-9	2.6	24
210	Phylogenetic reconstruction of a known HIV-1 CRF04_cpx transmission network using maximum likelihood and Bayesian methods. <i>Journal of Molecular Evolution</i> , 2004 , 59, 709-17	3.1	24
209	Current levels of drug resistance among therapy-naïve HIV-infected patients have significant impact on treatment response. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2004 , 37, 1664-6 ¹	2.1	24
208	Evolutionary dynamics of human retroviruses investigated through full-genome scanning. <i>Molecular Biology and Evolution</i> , 2005 , 22, 942-51	8.3	24
207	A stably expressed llama single-domain intrabody targeting Rev displays broad-spectrum anti-HIV activity. <i>Antiviral Research</i> , 2014 , 112, 91-102	10.8	23
206	Estimation of an in vivo fitness landscape experienced by HIV-1 under drug selective pressure useful for prediction of drug resistance evolution during treatment. <i>Bioinformatics</i> , 2008 , 24, 34-41	7.2	23
205	Analysis of the evolutionary relationships of HIV-1 and SIVcpz sequences using bayesian inference: implications for the origin of HIV-1. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1986-96	8.3	23

204	Patient HIV-1 strains carrying the multiple nucleoside resistance mutations are cross-resistant to abacavir. <i>Aids</i> , 2000 , 14, 469-71	3.5	23
203	Prevalence of antiretroviral drug resistance mutations and HIV-1 non-B subtypes in newly diagnosed drug-naïve patients in Slovenia, 2000-2004. <i>Virus Research</i> , 2006 , 118, 156-63	6.4	22
202	Nonadherence to highly active antiretroviral therapy: clinically relevant patient categorization based on electronic event monitoring. <i>AIDS Research and Human Retroviruses</i> , 2002 , 18, 327-30	1.6	22
201	Evaluating Clinical Isolates for Their Phenotypic and Genotypic Resistance Against Anti-HIV Drugs. <i>Methods in Molecular Medicine</i> , 2000 , 24, 223-58		22
200	Frequent HTLV-1 infection in the offspring of Peruvian women with HTLV-1-associated myelopathy/tropical spastic paraparesis or strongyloidiasis. <i>Revista Panamericana De Salud Publica/Pan American Journal of Public Health</i> , 2007 , 22, 223-30	4.1	22
199	Ethical considerations in global HIV phylogenetic research. <i>Lancet HIV,the</i> , 2018 , 5, e656-e666	7.8	22
198	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	3.6	21
197	Comparison of CREB- and NF-kappaB-mediated transactivation by human T lymphotropic virus type II (HTLV-II) and type I (HTLV-I) tax proteins. <i>Virology</i> , 2002 , 295, 182-9	3.6	21
196	Site-directed mutagenesis of human immunodeficiency virus type 1 reverse transcriptase at amino acid position 138. <i>Virology</i> , 2001 , 280, 97-106	3.6	21
195	Investigation of baseline susceptibility to protease inhibitors in HIV-1 subtypes C, F, G and CRF02_AG. <i>Antiviral Therapy</i> , 2006 , 11, 581-9	1.6	21
194	Large cluster outbreaks sustain the HIV epidemic among MSM in Quebec. <i>Aids</i> , 2017 , 31, 707-717	3.5	20
193	Phylogenetic analysis as a forensic tool in HIV transmission investigations. <i>Aids</i> , 2018 , 32, 543-554	3.5	20
192	Antiretroviral drug resistance in HIV-1 therapy-naive patients in Cuba. <i>Infection, Genetics and Evolution</i> , 2013 , 16, 144-50	4.5	20
191	Phylogenetic analysis of the full-length SARS-CoV sequences: evidence for phylogenetic discordance in three genomic regions. <i>Journal of Medical Virology</i> , 2004 , 74, 369-72	19.7	20
190	Optimization of a genotypic assay applicable to all human immunodeficiency virus type 1 protease and reverse transcriptase subtypes. <i>Journal of Virological Methods</i> , 2005 , 128, 47-53	2.6	20
189	SlidingBayes: exploring recombination using a sliding window approach based on Bayesian phylogenetic inference. <i>Bioinformatics</i> , 2005 , 21, 1274-5	7.2	20
188	Initiation of HAART in drug-naive HIV type 1 patients prevents viral breakthrough for a median period of 35.5 months in 60% of the patients. <i>AIDS Research and Human Retroviruses</i> , 2002 , 18, 419-26	1.6	20
187	Quasispecies of hepatitis C virus genotype 1 and treatment outcome with peginterferon and ribavirin. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 689-98	4.5	19

186	Globin haplotypes of human T-cell lymphotropic virus type I-infected individuals in Salvador, Bahia, Brazil, suggest a post-Columbian African origin of this virus. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2003 , 33, 536-42	3.1	19
185	Comparative rates of nucleotide sequence variation in the hypervariable region of E1/E2 and the NS5b region of hepatitis C virus in patients with a spectrum of liver disease resulting from a common source of infection. <i>Virology</i> , 2002 , 301, 354-64	3.6	19
184	Investigation of expert rule bases, logistic regression, and non-linear machine learning techniques for predicting response to antiretroviral treatment. <i>Antiviral Therapy</i> , 2009 , 14, 433-42	1.6	19
183	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	10.1	18
182	Antiretroviral therapy optimisation without genotype resistance testing: a perspective on treatment history based models. <i>PLoS ONE</i> , 2010 , 5, e13753	3.7	18
181	Discordant genotypic interpretation and phenotypic role of protease mutations in HIV-1 subtypes B and G. <i>Journal of Antimicrobial Chemotherapy</i> , 2009 , 63, 593-9	5.1	18
180	Bayesian network analyses of resistance pathways against efavirenz and nevirapine. <i>Aids</i> , 2008 , 22, 2107-15	3.15	18
179	Antiretroviral resistance in different HIV-1 subtypes: impact on therapy outcomes and resistance testing interpretation. <i>Current Opinion in HIV and AIDS</i> , 2007 , 2, 123-9	4.2	18
178	Role of viral evolutionary rate in HIV-1 disease progression in a linked cohort. <i>Retrovirology</i> , 2005 , 2, 41	3.6	18
177	Blinded, multicenter quality control study for the quantification of human immunodeficiency virus type 1 RNA in plasma by the Belgian AIDS reference laboratories. <i>Clinical Microbiology and Infection</i> , 2000 , 6, 213-7	9.5	18
176	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007231	4.8	17
175	Assessing transmissibility of HIV-1 drug resistance mutations from treated and from drug-naive individuals. <i>Aids</i> , 2015 , 29, 2045-52	3.5	17
174	Phylogenetic inference using maximum likelihood methods181-209		17
173	Impact of HIV-1 protease mutations A71V/T and T74S on M89I/V-mediated protease inhibitor resistance in subtype G isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2008 , 61, 1201-4	5.1	17
172	Testing tree topologies381-404		17
171	Efficacy of triple combination therapy with zidovudine (ZDV) plus zalcitabine (ddC) plus lamivudine (3TC) versus double (ZDV+3TC) combination therapy in patients previously treated with ZDV+ddC. <i>Aids</i> , 1996 , 10, F61-6	3.5	17
170	Interpreting resistance data for HIV-1 therapy management--know the limitations. <i>AIDS Reviews</i> , 2006 , 8, 37-43	1.5	17
169	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	3.7	16

168	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	16
167	Clinical evaluation of Rega 8: an updated genotypic interpretation system that significantly predicts HIV-therapy response. <i>PLoS ONE</i> , 2013 , 8, e61436	3.7	16
166	A genotypic assay for the amplification and sequencing of gag and protease from diverse human immunodeficiency virus type 1 group M subtypes. <i>Journal of Virological Methods</i> , 2006 , 132, 181-6	2.6	16
165	A combination of poor adherence and a low baseline susceptibility score is highly predictive for HAART failure. <i>Antiviral Chemistry and Chemotherapy</i> , 2002 , 13, 231-40	3.5	16
164	Mutations selected in HIV-2-infected patients failing a regimen including atazanavir. <i>Journal of Antimicrobial Chemotherapy</i> , 2013 , 68, 190-2	5.1	15
163	Resistance pathways of human immunodeficiency virus type 1 against the combination of zidovudine and lamivudine. <i>Journal of General Virology</i> , 2010 , 91, 1898-1908	4.9	15
162	Ascorbic acid has superior ex vivo antiproliferative, cell death-inducing and immunomodulatory effects over IFN- β in HTLV-1-associated myelopathy. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1729	4.8	15
161	Adult T-cell leukemia/lymphoma with a mixed CD4+ and CD8+ phenotype and indolent course. <i>Journal of Clinical Oncology</i> , 2007 , 25, 2480-2	2.2	15
160	A rapid and convenient variant of fusion-PCR to construct chimeric flaviviruses. <i>Journal of Virological Methods</i> , 2003 , 108, 67-74	2.6	15
159	HIV-1 genetic variants circulation in the North of Angola. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 231-74.5		15
158	Mutations in the non-nucleoside binding-pocket interfere with the multi-nucleoside resistance phenotype. <i>Aids</i> , 2001 , 15, 553-61	3.5	15
157	Sequence analysis of the first HTLV-I infection in Germany without relations to endemic areas. <i>AIDS Research and Human Retroviruses</i> , 1998 , 14, 1199-203	1.6	15
156	IFN- β induces greater antiproliferative and proapoptotic effects and increased p53 signaling compared with IFN- β in PBMCs of Adult T-cell Leukemia/Lymphoma patients. <i>Blood Cancer Journal</i> , 2017 , 7, e519	7	14
155	Sub-Epidemics Explain Localized High Prevalence of Reduced Susceptibility to Rilpivirine in Treatment-Naive HIV-1-Infected Patients: Subtype and Geographic Compartmentalization of Baseline Resistance Mutations. <i>AIDS Research and Human Retroviruses</i> , 2016 , 32, 427-33	1.6	14
154	High inpatient HIV-1 evolutionary rate is associated with CCR5-to-CXCR4 coreceptor switch. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 369-77	4.5	14
153	The epidemic history of hepatitis C among injecting drug users in Flanders, Belgium. <i>Journal of Viral Hepatitis</i> , 2008 , 15, 399-408	3.4	14
152	Full-length HIV type 1 genome analysis showing evidence for HIV type 1 transmission from a nonprogressor to two recipients who progressed to AIDS. <i>AIDS Research and Human Retroviruses</i> , 2005 , 21, 575-9	1.6	14
151	Phylogenetic classification of TT virus groups based on the N22 region is unreliable. <i>Virus Research</i> , 2002 , 85, 47-59	6.4	14

150	Baseline HIV type 1 genotypic resistance to a newly added nucleoside analog is predictive of virologic failure of the new therapy. <i>AIDS Research and Human Retroviruses</i> , 2000 , 16, 529-37	1.6	14
149	HTLV-negative and HTLV type I-positive tropical spastic paraparesis in northeastern Brazil. <i>AIDS Research and Human Retroviruses</i> , 1995 , 11, 315-8	1.6	14
148	Global and regional epidemiology of HIV-1 recombinants in 1990-2015: a systematic review and global survey. <i>Lancet HIV</i> , 2020 , 7, e772-e781	7.8	14
147	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.e1-8	9.5	13
146	Phylogenetic analysis of G1P[6] group A rotavirus strains detected in Northeast Brazilian children fully vaccinated with Rotarix. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 395-402	4.5	13
145	PhyloGeoTool: interactively exploring large phylogenies in an epidemiological context. <i>Bioinformatics</i> , 2017 , 33, 3993-3995	7.2	13
144	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015 , 29, 1549-56	3.5	13
143	Selecting models of evolution	345-361	13
142	Novel recombinant virus assay for measuring susceptibility of human immunodeficiency virus type 1 group M subtypes to clinically approved drugs. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 2232-42	9.7	13
141	HIV-1 gp120 N-linked glycosylation differs between plasma and leukocyte compartments. <i>Virology Journal</i> , 2008 , 5, 14	6.1	13
140	The close relationship between South African and Latin American HTLV type 1 strains corroborated in a molecular epidemiological study of the HTLV type 1 isolates from a blood donor cohort. <i>AIDS Research and Human Retroviruses</i> , 2007 , 23, 503-7	1.6	13
139	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,	6.3	13
138	Viral phylogeny in court: the unusual case of the Valencian anesthetist. <i>BMC Biology</i> , 2013 , 11, 83	7.3	12
137	Asparagine 42 of the conserved endo-inulinase INU2 motif WMNDPN from <i>Aspergillus ficuum</i> plays a role in activity specificity. <i>FEBS Open Bio</i> , 2013 , 3, 467-72	2.7	12
136	Origins of HTLV-1 in South America. <i>Nature Medicine</i> , 2000 , 6, 232-3	50.5	12
135	Long-term stability of human immunodeficiency virus viral load and infectivity in whole blood. <i>European Journal of Clinical Investigation</i> , 1999 , 29, 445-52	4.6	12
134	Family Aggregation of Human T-Lymphotropic Virus 1-Associated Diseases: A Systematic Review. <i>Frontiers in Microbiology</i> , 2016 , 7, 1674	5.7	12
133	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	7	11

132	Relapse or reinfection after failing hepatitis C direct acting antiviral treatment: Unravalled by phylogenetic analysis. <i>PLoS ONE</i> , 2018 , 13, e0201268	3.7	11
131	A near-full length genotypic assay for HCV1b. <i>Journal of Virological Methods</i> , 2014 , 209, 126-35	2.6	11
130	Molecular typing of the local HIV-1 epidemic in Serbia. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 378-85	4.5	11
129	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	3.6	11
128	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	6.1	11
127	Basic concepts of molecular evolution	3-30	11
126	Comparative performance of the REGA subtyping tool version 2 versus version 1. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 380-5	4.5	11
125	Exploring full-genome sequences for phylogenetic support of HIV-1 transmission events. <i>Aids</i> , 2005 , 19, 1551-2	3.5	11
124	Construction and characterization of a functional chimeric murine-human antibody directed against human fibrin fragment-D dimer. <i>FEBS Journal</i> , 1991 , 195, 235-42		11
123	A public HTLV-1 molecular epidemiology database for sequence management and data mining. <i>PLoS ONE</i> , 2012 , 7, e42123	3.7	11
122	Questions on the evolution of primate T-lymphotropic viruses raised by molecular and epidemiological studies of divergent strains. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1996 , 13 Suppl 1, S242-7		11
121	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016 , 8,	6.2	11
120	Modelled in vivo HIV Fitness under drug Selective Pressure and Estimated Genetic Barrier Towards Resistance are Predictive for Virological Response. <i>Antiviral Therapy</i> , 2008 , 13, 399-408	1.6	11
119	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	2.9	10
118	Genetic distances and nucleotide substitution models	111-141	10
117	Bayesian evolutionary analysis by sampling trees	564-591	10
116	Enhanced heterosexual transmission hypothesis for the origin of pandemic HIV-1. <i>Viruses</i> , 2012 , 4, 1950-83		10
115	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. <i>BMC Bioinformatics</i> , 2010 , 11, 409	3.6	10

114	Phylogenetic analysis of a simian T lymphotropic virus type I from a hamadryas baboon. <i>AIDS Research and Human Retroviruses</i> , 1997 , 13, 1545-8	1.6	10
113	Sequence analysis of two HTLV type I infections imported to Germany. <i>AIDS Research and Human Retroviruses</i> , 1997 , 13, 1255-8	1.6	10
112	Western blot seroindeterminate individuals for human T-lymphotropic virus I/II (HTLV-I/II) in Fortaleza (Brazil): a serological and molecular diagnostic and epidemiological approach. <i>Brazilian Journal of Infectious Diseases</i> , 2003 , 7, 202-9	2.8	10
111	Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer. <i>FEBS Journal</i> , 1990 , 192, 767-75		10
110	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	4	9
109	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>Oncotmmunology</i> , 2018 , 7, e1426423	7.2	9
108	A Fas Lymphoproliferative Phenotype Reveals Non-Apoptotic Fas Signaling in HTLV-1-Associated Neuroinflammation. <i>Frontiers in Immunology</i> , 2017 , 8, 97	8.4	9
107	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, 348-55	14.5	9
106	Comparison of three ELISAs for the routine diagnosis of human T-lymphotropic virus infection in a high-prevalence setting in Peru. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2009 , 103, 420-2	2	9
105	Evolution of genotypic resistance to enfuvirtide in HIV-1 isolates from different group M subtypes. <i>Journal of Clinical Virology</i> , 2009 , 44, 325-8	14.5	9
104	Effect of human immunodeficiency virus type 1 protease inhibitor therapy and subtype on development of resistance in subtypes B and G. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 373-9	4.5	9
103	Simian T cell leukemia virus type I from naturally infected feral monkeys from central and west Africa encodes a 91-amino acid p12 (ORF-I) protein as opposed to a 99-amino acid protein encoded by HTLV type I from humans. <i>AIDS Research and Human Retroviruses</i> , 1997 , 13, 425-32	1.6	9
102	Introduction to recombination detection493-518		9
101	Change in hepatitis C virus genotype in hemodialysis patients after end-of-treatment response to interferon monotherapy--relapse or re-infection?. <i>Journal of Medical Virology</i> , 2008 , 80, 80-6	19.7	9
100	Proviral HTLV-I and HTLV-II in the Efe pygmies of northeastern Zaire. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1996 , 12, 208-9		9
99	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	5.7	8
98	Zika genomics urgently need standardized and curated reference sequences. <i>PLoS Pathogens</i> , 2017 , 13, e1006528	7.6	8
97	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	4.9	8

96	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, 2205-9	5.1	8
95	Phylogenetic inference based on distance methods	142-180	8
94	The rise and fall of K65R in a Portuguese HIV-1 Drug Resistance database, despite continuously increasing use of tenofovir. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 683-8	4.5	8
93	The rare HIV-1 gp41 mutations 43T and 50V elevate enfuvirtide resistance levels of common enfuvirtide resistance mutations that did not impact susceptibility to sifuvirtide. <i>Antiviral Research</i> , 2010 , 86, 253-60	10.8	8
92	Fatal brain necrosis in primary HIV infection. <i>Lancet, The</i> , 2005 , 366, 866	40	8
91	Site stripping based on likelihood ratio reduction is a useful tool to evaluate the impact of non-clock-like behavior on viral phylogenetic reconstructions. <i>FEMS Immunology and Medical Microbiology</i> , 2003 , 39, 125-32		8
90	Performance of the VERSANT HIV-1 resistance assays (LiPA) for detecting drug resistance in therapy-naive patients infected with different HIV-1 subtypes. <i>FEMS Immunology and Medical Microbiology</i> , 2003 , 39, 119-24		8
89	Lack of evidence for infection with simian immunodeficiency virus in bonobos. <i>AIDS Research and Human Retroviruses</i> , 2002 , 18, 213-6	1.6	8
88	Inhibition of HIV type 1 Tat-mediated trans-activation by oncostatin M in HLtat cells. <i>AIDS Research and Human Retroviruses</i> , 1995 , 11, 1355-8	1.6	8
87	Characterization of a recombinant chimeric plasminogen activator composed of a fibrin fragment-D-dimer-specific humanized monoclonal antibody and a truncated single-chain urokinase. <i>FEBS Journal</i> , 1992 , 205, 139-46		8
86	Cellular HIV-1 DNA levels in drug sensitive strains are equivalent to those in drug resistant strains in newly-diagnosed patients in Europe. <i>PLoS ONE</i> , 2010 , 5, e10976	3.7	8
85	Evolution of HIV drug Resistance in Zidovudine/Zalcitabine- and Zidovudine/Didanosine-Experienced Patients Receiving Lamivudine-Containing Combination Therapy. <i>Antiviral Therapy</i> , 1998 , 3, 81-88	1.6	8
84	Male Circumcision and the Epidemic Emergence of HIV-2 in West Africa. <i>PLoS ONE</i> , 2016 , 11, e0166805	3.7	8
83	Time to Harmonize Dengue Nomenclature and Classification. <i>Viruses</i> , 2018 , 10,	6.2	8
82	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	4.5	7
81	Molecular Epidemiology of HIV-1 Infected Migrants Followed up in Portugal: Trends between 2001-2017. <i>Viruses</i> , 2020 , 12,	6.2	7
80	On the contribution of Angola to the initial spread of HIV-1. <i>Infection, Genetics and Evolution</i> , 2016 , 46, 219-222	4.5	7
79	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019 , 7, 208	6	7

78	HIV-1 protease mutation 82M contributes to phenotypic resistance to protease inhibitors in subtype G. <i>Journal of Antimicrobial Chemotherapy</i> , 2012 , 67, 1075-9	5.1	7
77	Diagnosis of human immunodeficiency virus infection by a polymerase chain reaction assay evaluated in patients harbouring strains of diverse geographical origin. <i>Journal of Virological Methods</i> , 1998 , 70, 153-66	2.6	7
76	Split networks. A tool for exploring complex evolutionary relationships in molecular data	631-653	7
75	Mutations at 65 and 70 within the context of a Q151M cluster in human immunodeficiency virus type 1 reverse transcriptase impact the susceptibility to the different nucleoside reverse transcriptase inhibitors in distinct ways. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 600-3	4.5	7
74	Presence of 2P5PBis-O-(tert-butyldimethylsilyl)-3Pspiro-5''-(4''-amino-1'',2''-oxathiole-2'',2''-dioxide) (TSAO)-resistant virus strains in TSAO-inexperienced HIV patients. <i>AIDS Research and Human Retroviruses</i> , 2000 , 16, 825-33	1.6	7
73	High prevalence of CRF02_AG and many minor resistance-related mutations at the protease gene among HIV-infected treatment-naive immigrants in Madrid. <i>Aids</i> , 2003 , 17, 1105-7	3.5	7
72	Modelled in vivo HIV fitness under drug selective pressure and estimated genetic barrier towards resistance are predictive for virological response. <i>Antiviral Therapy</i> , 2008 , 13, 399-407	1.6	7
71	State of the Art in HIV Drug Resistance: Science and Technology Knowledge Gap. <i>AIDS Reviews</i> , 2018 , 20, 27-42	1.5	7
70	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 (1999)</i> , 2018 , 77, 514-522	3.1	6
69	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	13.4	6
68	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, 845-52	2.3	6
67	The demise of multidrug-resistant HIV-1: the national time trend in Portugal. <i>Journal of Antimicrobial Chemotherapy</i> , 2013 , 68, 911-4	5.1	6
66	Impact on replicative fitness of the G48E substitution in the protease of HIV-1: an in vitro and in silico evaluation. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008 , 48, 255-62	3.1	6
65	Mutations in both env and gag genes are required for HIV-1 resistance to the polysulfonic dendrimer SPL2923, as corroborated by chimeric virus technology. <i>Antiviral Chemistry and Chemotherapy</i> , 2005 , 16, 253-66	3.5	6
64	Full-length genomic sequence of an HIV type 1 subtype G from Kinshasa. <i>AIDS Research and Human Retroviruses</i> , 1999 , 15, 585-9	1.6	6
63	Doubt at the core: Unspoken vaccine hesitancy among healthcare workers.. <i>Lancet Regional Health - Europe, The</i> , 2022 , 12, 100289		6
62	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	4.1	6
61	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 , 10, 79-88	1.6	6

60	Natural selection and adaptation of molecular sequences407-418		5
59	Population genetic tests suggest that the epidemiologies of JCV and BKV are strikingly different. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 397-403	4.5	5
58	Phylogenetic analysis using protein sequences313-342		5
57	Molecular clock analysis362-380		5
56	Differentiating between viruses and virus species by writing their names correctly.. <i>Archives of Virology</i> , 2022 , 167, 1231	2.6	5
55	Scenario-driven forecasting: modeling peaks and paths. Insights from the COVID-19 pandemic in Belgium. <i>Scientometrics</i> , 2020 , 124, 1-13	3	5
54	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,	6.2	5
53	Determinants of HIV-1 Late Presentation in Patients Followed in Europe. <i>Pathogens</i> , 2021 , 10,	4.5	5
52	The epidemic emergence of HIV: what novel enabling factors were involved?. <i>Future Virology</i> , 2017 , 12, 685-707	2.4	4
51	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	5.4	4
50	Re-analysis of 34 full-length HIV-1 intersubtype recombinant sequences. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 225-9	4.5	4
49	Increasing Prevalence of HIV-1 Transmitted Drug Resistance in Portugal: Implications for First Line Treatment Recommendations. <i>Viruses</i> , 2020 , 12,	6.2	4
48	A21 HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017 , 3,	3.7	3
47	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, 310-8	3.6	3
46	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, 349-60	4.5	3
45	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	3.7	3
44	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, 419-23	5.1	3
43	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	4	3

42	LAMARC: Estimating population genetic parameters from molecular data	592-612		3
41	Detecting and characterizing individual recombination events	519-548		3
40	Analysis of complex HIV-1 intersubtype recombinants using a Bayesian scanning method. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 219-24		4.5	3
39	Factors Associated with HIV Drug Resistance in Dar es Salaam, Tanzania: Analysis of a Complex Adaptive System.. <i>Pathogens</i> , 2021 , 10,		4.5	3
38	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		4.5	3
37	A Rapid Phenotypic Assay for Detecting Multiple Nucleoside Analogue Reverse Transcriptase Inhibitor-Resistant HIV-1 in Plasma. <i>Antiviral Therapy</i> , 2002 , 7, 131-139		1.6	3
36	Discovery and characterization of auxiliary proteins encoded by type 3 simian T-cell lymphotropic viruses. <i>Journal of Virology</i> , 2015 , 89, 931-51		6.6	2
35	Quality Control of Next-Generation Sequencing-Based HIV-1 Drug Resistance Data in Clinical Laboratory Information Systems Framework. <i>Viruses</i> , 2020 , 12,		6.2	2
34	Characterization of amino acids Arg, Ser and Thr at position 70 within HIV-1 reverse transcriptase. <i>Acta Clinica Belgica</i> , 2014 , 69, 348-57		1.8	2
33	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, O22		3.6	2
32	Ascorbic acid has superior antiviral and antiproliferative effects over IFN-alpha in HAM/TSP PBMC ex vivo. <i>Retrovirology</i> , 2011 , 8,		3.6	2
31	Association between specific HIV-1 Env traits and virologic control in vivo. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 365-72		4.5	2
30	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		1	2
29	HIV-related Peer Support in Dar es Salaam: A Pilot Questionnaire Inquiry. <i>Transdisciplinary Insights</i> , 2019 , 3, 1-18		0.7	2
28	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020 , 143, 110164		3.8	2
27	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		3.5	2
26	Clinical use, efficacy, and durability of maraviroc for antiretroviral therapy in routine care: A European survey. <i>PLoS ONE</i> , 2019 , 14, e0225381		3.7	2
25	A collaborative environment allowing clinical investigations on integrated biomedical databases. <i>Studies in Health Technology and Informatics</i> , 2009 , 147, 51-61		0.5	2

24	State of the Art in HIV Drug Resistance: Surveillance and Regional Gaps. <i>AIDS Reviews</i> , 2018 , 20, 43-57	1.5	2
23	A18 Random amplification with next-generation sequencing to cover HIV and HCV full-length genomes. <i>Virus Evolution</i> , 2017 , 3,	3.7	1
22	Evaluation of the automatic editing tool RECall for HIV-1 pol and V3 loop sequences. <i>Journal of Virological Methods</i> , 2013 , 193, 135-9	2.6	1
21	A Bayesian network approach to study host and viral genetic correlates of HIV-1 disease progression. <i>Retrovirology</i> , 2011 , 8, P70	3.6	1
20	Sequence databases and database searching33-67		1
19	The coalescent: population genetic inference using genealogies551-563		1
18	Profile of Resistance of Human Immunodeficiency Virus to Mannose-Specific Plant Lectins. <i>Journal of Virology</i> , 2004 , 78, 12724-12724	6.6	1
17	Virologic therapy response significantly correlates with the number of active drugs as evaluated using a LiPA HIV-1 resistance scoring system. <i>Journal of Clinical Virology</i> , 2004 , 31 Suppl 1, S7-15	14.5	1
16	Stereospecificity of 6PC-neplanocin A analogues as inhibitors of S-adenosylhomocysteine hydrolase activity and human immunodeficiency virus replication. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 1998 , 17, 479-86	1.4	1
15	BaEV is a relic from an ancient retrovirus that crossed species barriers. <i>Trends in Microbiology</i> , 1996 , 4, 478	12.4	1
14	Evaluation of Two Commercial Kits for the Detection of Genotypic Drug Resistance on a Panel of HIV Type 1 Subtypes A Through J. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2001 , 28, 254-258	3.1	1
13	Comparison of two individual-based model simulators for HIV epidemiology in a population with HSV-2 using as case study YaoundeCameroon, 1980-2005		1
12	Comparison of two simulators for individual based models in HIV epidemiology in a population with HSV 2 in Yaounde(Cameroon). <i>Scientific Reports</i> , 2021 , 11, 14696	4.9	1
11	Multi-science decision support for HIV drug resistance treatment. <i>Studies in Health Technology and Informatics</i> , 2008 , 138, 188-98	0.5	1
10	Qualitative systems mapping for complex public health problems: A practical guide.. <i>PLoS ONE</i> , 2022 , 17, e0264463	3.7	1
9	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	4.1	1
8	Virus genetic variability involvement in transmissibility of HIV-1 immune activation and disease progression. <i>Future Virology</i> , 2015 , 10, 1259-1262	2.4	0
7	Sexually transmitted infections, their treatment and urban change in colonial Leopoldville, 1910-1960. <i>Medical History</i> , 2021 , 65, 178-196	0.2	0

- 6 Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal.. *Virus Evolution*, **2022**, 8, veac029 3.7 0
- 5 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. *AIDS Research and Human Retroviruses*, **2011**, 27, 1223-9 1.6
- 4 Bioinformatics tools for the investigation of emerging and re-emerging infectious diseases. Introduction. *Infection, Genetics and Evolution*, **2009**, 9, 671 4.5
- 3 Impact of genetic variation of HIV-1 on drug resistance development. *Future Virology*, **2007**, 2, 303-310 2.4
- 2 Reanalysis of the HIV-1 Circulating Recombinant Form A/E (CRF01_AE): Evidence of A/E/G Recombination. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2002**, 30, 124-129 3.1
- 1 Clinical Implications of Reverse Transcriptase Inhibitor Resistance **2009**, 589-619