

Anne-Mieke Vandamme

List of Publications by Year in descending order

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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	Drug Resistance Mutations for Surveillance of Transmitted HIV-1 Drug-Resistance: 2009 Update. PLoS ONE, 2009, 4, e4724.	1.1	823
2	Human T-lymphotropic virus 1: recent knowledge about an ancient infection. Lancet Infectious Diseases, The, 2007, 7, 266-281.	4.6	622
3	Global trends in molecular epidemiology of HIV-1 during 2000â€“2007. Aids, 2011, 25, 679-689.	1.0	602
4	Complete Genomic Sequence of Human Coronavirus OC43: Molecular Clock Analysis Suggests a Relatively Recent Zoonotic Coronavirus Transmission Event. Journal of Virology, 2005, 79, 1595-1604.	1.5	477
5	An automated genotyping system for analysis of HIV-1 and other microbial sequences. Bioinformatics, 2005, 21, 3797-3800.	1.8	468
6	Prevalence of Drugâ€“Resistant HIVâ€“1 Variants in Untreated Individuals in Europe: Implications for Clinical Management. Journal of Infectious Diseases, 2005, 192, 958-966.	1.9	385
7	Assessing substitution saturation with DAMBE. , 2009, , 615-630.		340
8	Tracing the origin and history of the HIV-2 epidemic. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6588-6592.	3.3	315
9	Automated subtyping of HIV-1 genetic sequences for clinical and surveillance purposes: Performance evaluation of the new REGA version 3 and seven other tools. Infection, Genetics and Evolution, 2013, 19, 337-348.	1.0	313
10	Impact of HIV-1 Subtype and Antiretroviral Therapy on Protease and Reverse Transcriptase Genotype: Results of a Global Collaboration. PLoS Medicine, 2005, 2, e112.	3.9	262
11	Global and regional molecular epidemiology of HIV-1, 1990â€“2015: a systematic review, global survey, and trend analysis. Lancet Infectious Diseases, The, 2019, 19, 143-155.	4.6	255
12	Genome Detective: an automated system for virus identification from high-throughput sequencing data. Bioinformatics, 2019, 35, 871-873.	1.8	254
13	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	0.9	219
14	European guidelines on the clinical management of HIV-1 tropism testing. Lancet Infectious Diseases, The, 2011, 11, 394-407.	4.6	218
15	Transmission of Drugâ€“Resistant HIVâ€“1 Is Stabilizing in Europe. Journal of Infectious Diseases, 2009, 200, 1503-1508.	1.9	213
16	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.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 1711-1715.	3.3	203
17	Relating increasing hantavirus incidences to the changing climate: the mast connection. International Journal of Health Geographics, 2009, 8, 1.	1.2	198
18	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. PLoS Medicine, 2015, 12, e1001810.	3.9	188

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19	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, 246-253.	1.1	169
20	Clinical and laboratory guidelines for the use of HIV-1 drug resistance testing as part of treatment management: recommendations for the European setting. <i>Aids</i> , 2001, 15, 309-320.	1.0	169
21	2',5'-Bis-O-(tert-butyldimethylsilyl)-3'-spiro-5''-(4''-amino-1'',2''-oxathiole-2'',2'-dioxide)pyrimidine (TSAO) nucleoside analogues: highlyselective 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> , 1992, 89, 4392-4396.	3.3	164
22	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.	1.1	151
23	A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , 2009, 37, W634-W642.	6.5	142
24	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
25	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
26	Genetic Variability and Molecular Evolution of the Human Respiratory Syncytial Virus Subgroup B Attachment G Protein. <i>Journal of Virology</i> , 2005, 79, 9157-9167.	1.5	127
27	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, 8298-8309.	1.5	124
28	A Genotypic Drug Resistance Interpretation Algorithm that Significantly Predicts Therapy Response in HIV-1-Infected Patients. <i>Antiviral Therapy</i> , 2002, 7, 123-129.	0.6	122
29	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, 14440-14445.	3.3	120
30	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , 2009, 6, 49.	0.9	114
31	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, 6359-6366.	1.5	112
32	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, 995-999.	1.0	111
33	Dating the common ancestor of SIVcpz and HIVâ€1 group M and the origin of HIVâ€1 subtypes by using a new method to uncover clockâ€like molecular evolution. <i>FASEB Journal</i> , 2001, 15, 276-278.	0.2	111
34	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, 2848-2852.	3.3	110
35	Transmission of drug-resistant HIV-1 in Europe remains limited to single classes. <i>Aids</i> , 2008, 22, 625-635.	1.0	109
36	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, 4675-4683.	1.5	106

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37	European recommendations for the clinical use of HIV drug resistance testing: 2011 update. <i>AIDS Reviews</i> , 2011, 13, 77-108.	0.5	106
38	The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068.	1.2	105
39	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, 212-223.	1.1	102
40	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, 2109-2117.	1.4	101
41	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, 386-396.	1.0	100
42	Managing Resistance to Anti-HIV Drugs. <i>Drugs</i> , 1999, 57, 337-361.	4.9	95
43	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, 127-139.	0.3	95
44	HTLV-II Seroprevalence in Pygmies Across Africa Since 1970. <i>AIDS Research and Human Retroviruses</i> , 1993, 9, 709-713.	0.5	94
45	The simian origins of the pathogenic human T-cell lymphotropic virus type I. <i>Trends in Microbiology</i> , 1998, 6, 477-483.	3.5	94
46	Profile of Resistance of Human Immunodeficiency Virus to Mannose-Specific Plant Lectins. <i>Journal of Virology</i> , 2004, 78, 10617-10627.	1.5	94
47	Rapid, phenotypic HIV-1 drug sensitivity assay for protease and reverse transcriptase inhibitors. <i>Journal of Clinical Virology</i> , 1999, 13, 71-80.	1.6	93
48	Human immunodeficiency virus type 1 (HIV-1) strains selected for resistance against the HIV-1-specific [2',5'-bis-O-(tert-butyldimethylsilyl)-3'-spiro-5''-(4''-amino-1'',2''-oxathiole-2'',2''-dioxide)]-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, 6952-6956.	3.3	91
49	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, 352-360.	0.9	90
50	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	0.9	90
51	Hepatitis E virus Infection in Work Horses in Egypt†. <i>Infection, Genetics and Evolution</i> , 2007, 7, 368-373.	1.0	87
52	Quantifying Differences in the Tempo of Human Immunodeficiency Virus Type 1 Subtype Evolution. <i>Journal of Virology</i> , 2009, 83, 12917-12924.	1.5	87
53	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.	0.9	86
54	Clinical Characteristics of Patients in Peru with Human T Cell Lymphotropic Virus Type 1â€“Associated Tropical Spastic Paraparesis. <i>Clinical Infectious Diseases</i> , 2004, 39, 939-944.	2.9	86

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55	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, 8543-8551.	1.5	84
56	Diagnostic Value of Different Adherence Measures Using Electronic Monitoring and Virologic Failure as Reference Standards. <i>AIDS Patient Care and STDs</i> , 2008, 22, 735-743.	1.1	82
57	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
58	The three human T-lymphotropic virus type I subtypes arose from three geographically distinct simian reservoirs. <i>Journal of General Virology</i> , 1996, 77, 359-368.	1.3	81
59	Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 13050-13056.	1.5	81
60	Standardisation of primers and an algorithm for HIV-1 diagnostic PCR evaluated in patients harbouring strains of diverse geographical origin. <i>Journal of Virological Methods</i> , 1995, 51, 305-316.	1.0	80
61	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, 277-287.	1.1	80
62	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.	1.0	79
63	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
64	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, 13253-13258.	3.3	78
65	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.	1.4	78
66	A new ensemble coevolution system for detecting HIV-1 protein coevolution. <i>Biology Direct</i> , 2015, 10, 1.	1.9	78
67	African Origin of Human T-Lymphotropic Virus Type 2 (HTLV-2) Supported by a Potential New HTLV-2d Subtype in Congolese Mbuti Pygmies. <i>Journal of Virology</i> , 1998, 72, 4327-4340.	1.5	78
68	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. <i>Journal of Medical Virology</i> , 1997, 52, 1-7.	2.5	77
69	Multiple dideoxynucleoside analogue-resistant (MddNR) HIV-1 strains isolated from patients from different European countries. <i>Aids</i> , 1998, 12, 2007-2015.	1.0	77
70	Activity of non-nucleoside reverse transcriptase inhibitors against HIV-2 and SIV. <i>Aids</i> , 1999, 13, 1477-1483.	1.0	77
71	Tenofovir Resistance and Resensitization. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3478-3484.	1.4	77
72	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, 644-657.	1.1	76

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73	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, 1799-1806.	1.0	76
74	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.	1.0	73
75	Hepatitis C Virus Evolutionary Patterns Studied Through Analysis of Full-Genome Sequences. <i>Journal of Molecular Evolution</i> , 2002, 54, 62-70.	0.8	72
76	Circulation of genetically distinct contemporary human coronavirus OC43 strains. <i>Virology</i> , 2005, 337, 85-92.	1.1	71
77	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, 1089-1099.	1.3	70
78	Phylogeography and evolutionary history of dengue virus type 3. <i>Infection, Genetics and Evolution</i> , 2009, 9, 716-725.	1.0	70
79	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</i> (1999), 2001, 27, 499-505.	0.9	69
80	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, 382-387.	1.0	68
81	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
82	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, 453-459.	0.5	67
83	Molecular Footprint of Drug-Selective Pressure in a Human Immunodeficiency Virus Transmission Chain. <i>Journal of Virology</i> , 2005, 79, 11981-11989.	1.5	67
84	Bayesian phylogenetic analysis using MRBAYES. , 2009, , 210-266.		66
85	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, 121-132.	1.0	63
86	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.	1.3	63
87	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, 4700-4709.	1.5	62
88	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
89	Primary resistance to integrase strand-transfer inhibitors in Europe: Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2885-2888.	1.3	61
90	Analysis of HIV-1 pol sequences using Bayesian Networks: implications for drug resistance. <i>Bioinformatics</i> , 2006, 22, 2975-2979.	1.8	60

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91	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.	1.0	60
92	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
93	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 46, 169-179.	1.0	60
94	Genetic Diversity and Selective Pressure in Hepatitis C Virus Genotypes 1â€“6: Significance for Direct-Acting Antiviral Treatment and Drug Resistance. <i>Viruses</i> , 2015, 7, 5018-5039.	1.5	59
95	Expert consensus statement on the science of <scp>HIV</scp> in the context of criminal law. <i>Journal of the International AIDS Society</i> , 2018, 21, e25161.	1.2	59
96	Seroprevalence and risk factors for human T-cell lymphotropic virus (HTLV 1) infection among ethnically and geographically diverse Peruvian women. <i>International Journal of Infectious Diseases</i> , 2003, 7, 132-137.	1.5	58
97	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
98	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.	0.6	58
99	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, 71-77.	0.5	57
100	Analysis of the Serotype and Genotype Correlation of VP1 and the 5â€² Noncoding Region in an Epidemiological Survey of the Human Enterovirus B Species. <i>Journal of Clinical Microbiology</i> , 2004, 42, 963-971.	1.8	57
101	New retroviruses in human and simian T-lymphotropic viruses. <i>Lancet, The</i> , 1994, 344, 265-266.	6.3	56
102	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> , 2003, 21, 603-611.	3.5	56
103	Comparison of HIV-1 Genotypic Resistance Test Interpretation Systems in Predicting Virological Outcomes Over Time. <i>PLoS ONE</i> , 2010, 5, e11505.	1.1	56
104	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
105	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
106	Functional conservation of HIV-1 Gag: implications for rational drug design. <i>Retrovirology</i> , 2013, 10, 126.	0.9	56
107	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
108	Resistance of human immunodeficiency virus type 1 reverse transcriptase to TIBO derivatives induced by site-directed mutagenesis. <i>Virology</i> , 1992, 188, 900-904.	1.1	55

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109	Algorithms for the interpretation of HIV-1 genotypic drug resistance information. <i>Antiviral Research</i> , 2006, 71, 335-342.	1.9	54
110	High GUD Incidence in the Early 20th Century Created a Particularly Permissive Time Window for the Origin and Initial Spread of Epidemic HIV Strains. <i>PLoS ONE</i> , 2010, 5, e9936.	1.1	54
111	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
112	Phylodynamics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012, 12, 453-460.	1.0	52
113	Limited cross-border infections in patients newly diagnosed with HIV in Europe. <i>Retrovirology</i> , 2013, 10, 36.	0.9	52
114	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, 2541-2549.	1.5	51
115	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.	2.1	51
116	Simple algorithm derived from a geno-/phenotypic database to predict HIV-1 protease inhibitor resistance. <i>Aids</i> , 2000, 14, 1731-1738.	1.0	50
117	Characterization of HIV-1 Strains Isolated from Patients Treated with TIBO R82913. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 39-46.	0.5	49
118	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, 1135-1142.	0.5	49
119	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, 602-611.	0.8	49
120	Mapping Sites of Positive Selection and Amino Acid Diversification in the HIV Genome. <i>Genetics</i> , 2004, 167, 1047-1058.	1.2	49
121	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, 176-181.	1.0	49
122	Rising Prevalence of HIV-1 Non-B Subtypes in Belgium: 1983–2001. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2004, 35, 279-285.	0.9	48
123	Cell Type-Dependent Effect of Sodium Valproate on Human Immunodeficiency Virus Type 1 Replication <i>in Vitro</i> . <i>AIDS Research and Human Retroviruses</i> , 1997, 13, 187-192.	0.5	47
124	Different Epidemic Potentials of the HIV-1B and C Subtypes. <i>Journal of Molecular Evolution</i> , 2005, 60, 598-605.	0.8	47
125	The impact of HIV-1 within-host evolution on transmission dynamics. <i>Current Opinion in Virology</i> , 2018, 28, 92-101.	2.6	47
126	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

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127	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, 125-140.	1.1	46
128	Use of Electronic Monitoring Induces a 40-Day Intervention Effect in HIV Patients. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2006, 43, 247-248.	0.9	45
129	Fasâ€“670 promoter polymorphism is associated to susceptibility, clinical presentation, and survival in adult T cell leukemia. <i>Journal of Leukocyte Biology</i> , 2008, 83, 220-222.	1.5	45
130	Doubt at the core: Unspoken vaccine hesitancy among healthcare workers. <i>Lancet Regional Health - Europe, The</i> , 2022, 12, 100289.	3.0	45
131	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, 440-442.	2.9	44
132	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, 672-682.	1.0	44
133	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
134	Molecular testing of multiple HIV-1 transmissions in a criminal case. <i>Aids</i> , 2005, 19, 1649-1658.	1.0	43
135	The incidence of multidrug and full class resistance in HIV-1 infected patients is decreasing over time (2001â€“2006) in Portugal. <i>Retrovirology</i> , 2008, 5, 12.	0.9	43
136	Detection and molecular characterisation of noroviruses and sapoviruses in asymptomatic swine and cattle in Slovenian farms. <i>Infection, Genetics and Evolution</i> , 2010, 10, 413-420.	1.0	43
137	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
138	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
139	A genotypic drug resistance interpretation algorithm that significantly predicts therapy response in HIV-1-infected patients. <i>Antiviral Therapy</i> , 2002, 7, 123-9.	0.6	43
140	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, 347-358.	1.3	42
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