Anne-Mieke Vandamme

List of Publications by Year
in descending order

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419 papers	19,970 citations	11608 70 h-index	20900 115 g-index
517 all docs	517 docs citations	517 times ranked	14750 citing authors

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

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19	Scenario-driven forecasting: modeling peaks and paths. Insights from the COVID-19 pandemic in Belgium. Scientometrics, 2020, 124, 2703-2715.	1.6	5
20	Global and regional epidemiology of HIV-1 recombinants in 1990â€“2015: a systematic review and global survey. Lancet HIV,the, 2020, 7, e772-e781.	2.1	51
21	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	3.3	68
22	Quality Control of Next-Generation Sequencing-Based HIV-1 Drug Resistance Data in Clinical Laboratory Information Systems Framework. Viruses, 2020, 12, 645.	1.5	7
23	Molecular Epidemiology of HIV-1 Infected Migrants Followed Up in Portugal: Trends between 2001â€“2017. Viruses, 2020, 12, 268.	1.5	12
24	A prospect on the use of antiviral drugs to control local outbreaks of COVID-19. BMC Medicine, 2020, 18, 191.	2.3	47
25	Genome Detective: an automated system for virus identification from high-throughput sequencing data. Bioinformatics, 2019, 35, 871-873.	1.8	254
26	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. Frontiers in Public Health, 2019, 7, 208.	1.3	15
27	Cross-country migration linked to people who inject drugs challenges the long-term impact of national HCV elimination programmes. Journal of Hepatology, 2019, 71, 1270-1272.	1.8	7
28	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. PLoS Neglected Tropical Diseases, 2019, 13, e0007231.	1.3	44
29	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. Frontiers in Microbiology, 2019, 10, 613.	1.5	21
30	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. Journal of Infectious Diseases, 2019, 220, 233-243.	1.9	23
31	The effect of primary drug resistance on CD4+ cell decline and the viral load set-point in HIV-positive individuals before the start of antiretroviral therapy. Aids, 2019, 33, 315-326.	1.0	4
32	Clinical use, efficacy, and durability of maraviroc for antiretroviral therapy in routine care: A European survey. PLoS ONE, 2019, 14, e0225381.	1.1	9
33	Global and regional molecular epidemiology of HIV-1, 1990â€“2015: a systematic review, global survey, and trend analysis. Lancet Infectious Diseases, The, 2019, 19, 143-155.	4.6	255
34	HIV-related Peer Support in Dar es Salaam: A Pilot Questionnaire Inquiry. Transdisciplinary Insights, 2019, 3, 1-18.	0.1	4
35	A genetic IFN/STAT1/FAS axis determines CD4 T stem cell memory levels and apoptosis in healthy controls and Adult T-cell Leukemia patients. OncoImmunology, 2018, 7, e1426423.	2.1	17
36	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. Scientific Reports, 2018, 8, 1702.	1.6	24

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37	Transmission Networks of HCV Genotype 1a Enriched With Pre-existing Polymorphism Q80K Among HIV-Infected Patients With Acute Hepatitis C in Poland. Journal of Acquired Immune Deficiency Syndromes (1999), 2018, 77, 514-522.	0.9	8
38	The impact of HIV-1 within-host evolution on transmission dynamics. Current Opinion in Virology, 2018, 28, 92-101.	2.6	47
39	Phylogenetic analysis as a forensic tool in HIV transmission investigations. Aids, 2018, 32, 543-554.	1.0	28
40	Predictors of non adherence to antiretroviral therapy at an urban HIV care and treatment center in Tanzania. Drug, Healthcare and Patient Safety, 2018, Volume 10, 79-88.	1.0	18
41	Time to Harmonize Dengue Nomenclature and Classification. Viruses, 2018, 10, 569.	1.5	14
42	Ethical considerations in global HIV phylogenetic research. Lancet HIV,the, 2018, 5, e656-e666.	2.1	39
43	Relapse or reinfection after failing hepatitis C direct acting antiviral treatment: Unravelled by phylogenetic analysis. PLoS ONE, 2018, 13, e0201268.	1.1	14
44	Expert consensus statement on the science of <scp>HIV</scp> in the context of criminal law. Journal of the International AIDS Society, 2018, 21, e25161.	1.2	59
45	Origin and Distribution of HIV-1 Subtypes. , 2018, , 1589-1603.		0
46	State of the Art in HIV Drug Resistance: Surveillance and Regional Gaps. AIDS Reviews, 2018, 20, 43-57.	0.5	2
47	State of the Art in HIV Drug Resistance: Science and Technology Knowledge Gap. AIDS Reviews, 2018, 20, 27-42.	0.5	11
48	IFN-Î² induces greater antiproliferative and proapoptotic effects and increased p53 signaling compared with IFN-Î± in PBMCs of Adult T-cell Leukemia/Lymphoma patients. Blood Cancer Journal, 2017, 7, e519-e519.	2.8	17
49	Exploring resistance pathways for first-generation NS3/4A protease inhibitors boceprevir and telaprevir using Bayesian network learning. Infection, Genetics and Evolution, 2017, 53, 15-23.	1.0	14
50	Large cluster outbreaks sustain the HIV epidemic among MSM in Quebec. Aids, 2017, 31, 707-717.	1.0	31
51	Phylogenetic evidence for underreporting of maleâ€toâ€male sex among human immunodeficiency virusâ€"infected donors in the Netherlands and Flanders. Transfusion, 2017, 57, 1235-1247.	0.8	11
52	The epidemic emergence of HIV: what novel enabling factors were involved?. Future Virology, 2017, 12, 685-707.	0.9	7
53	Implications of hepatitis C virus subtype 1a migration patterns for virus genetic sequencing policies in Italy. BMC Evolutionary Biology, 2017, 17, 70.	3.2	21
54	PhyloGeoTool: interactively exploring large phylogenies in an epidemiological context. Bioinformatics, 2017, 33, 3993-3995.	1.8	16

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

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

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

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

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

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145	Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study). HIV Medicine, 2011, 12, 211-218.	1.0	32
146	B cell costimulatory molecules as potential biomarkers in HAM/TSP. Retrovirology, 2011, 8, .	0.9	0
147	Ascorbic acid has superior antiviral and antiproliferative effects over IFN-alpha in HAM/TSP PBMC ex vivo. Retrovirology, 2011, 8, .	0.9	3
148	CD64 as a biomarker and therapeutic target in HAM/TSP and HTLV-1-associated Infective Dermatitis. Retrovirology, 2011, 8, .	0.9	0
149	A Bayesian network approach to study host and viral genetic correlates of HIV-1 disease progression. Retrovirology, 2011, 8, .	0.9	1
150	Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study. Journal of Antimicrobial Chemotherapy, 2011, 66, 1886-1896.	1.3	56
151	Global trends in molecular epidemiology of HIV-1 during 2000â€“2007. Aids, 2011, 25, 679-689.	1.0	602
152	European recommendations for the clinical use of HIV drug resistance testing: 2011 update. AIDS Reviews, 2011, 13, 77-108.	0.5	106
153	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. BMC Bioinformatics, 2010, 11, 409.	1.2	12
154	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. Antiviral Research, 2010, 86, 253-260.	1.9	9
155	Extensive survey on the prevalence and genetic diversity of SIVs in primate bushmeat provides insights into risks for potential new cross-species transmissions. Infection, Genetics and Evolution, 2010, 10, 386-396.	1.0	100
156	Effect of human immunodeficiency virus type 1 protease inhibitor therapy and subtype on development of resistance in subtypes B and G. Infection, Genetics and Evolution, 2010, 10, 373-379.	1.0	9
157	Bioinformatics tools for the investigation of viral evolution and molecular epidemiology. Infection, Genetics and Evolution, 2010, 10, 355.	1.0	0
158	Population genetic tests suggest that the epidemiologies of JCV and BKV are strikingly different. Infection, Genetics and Evolution, 2010, 10, 397-403.	1.0	6
159	Differences in molecular evolution between switch (R5 to R5X4/X4-tropic) and non-switch (R5-tropic) Tj ETQq1 1 0.784314 rgBT /Ove	1.0	39
160	Association between specific HIV-1 Env traits and virologic control in vivo. Infection, Genetics and Evolution, 2010, 10, 365-372.	1.0	2
161	Comparative performance of the REGA subtyping tool version 2 versus version 1. Infection, Genetics and Evolution, 2010, 10, 380-385.	1.0	13
162	Detection and molecular characterisation of noroviruses and sapoviruses in asymptomatic swine and cattle in Slovenian farms. Infection, Genetics and Evolution, 2010, 10, 413-420.	1.0	43

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163	Comparison of HIV-1 Genotypic Resistance Test Interpretation Systems in Predicting Virological Outcomes Over Time. PLoS ONE, 2010, 5, e11505.	1.1	56
164	DEB025 (Alisporivir) Inhibits Hepatitis C Virus Replication by Preventing a Cyclophilin A Induced Cis-Trans Isomerisation in Domain II of NS5A. PLoS ONE, 2010, 5, e13687.	1.1	151
165	Antiretroviral Therapy Optimisation without Genotype Resistance Testing: A Perspective on Treatment History Based Models. PLoS ONE, 2010, 5, e13753.	1.1	21
166	Resistance pathways of human immunodeficiency virus type 1 against the combination of zidovudine and lamivudine. Journal of General Virology, 2010, 91, 1898-1908.	1.3	16
167	High GUD Incidence in the Early 20th Century Created a Particularly Permissive Time Window for the Origin and Initial Spread of Epidemic HIV Strains. PLoS ONE, 2010, 5, e9936.	1.1	54
168	Cellular HIV-1 DNA Levels in Drug Sensitive Strains Are Equivalent to Those in Drug Resistant Strains in Newly-Diagnosed Patients in Europe. PLoS ONE, 2010, 5, e10976.	1.1	10
169	Testing tree topologies. , 2009, , 381-404.		18
170	LAMARC: Estimating population genetic parameters from molecular data. , 2009, , 592-612.		3
171	Phylogenetic analysis using protein sequences. , 2009, , 313-342.		10
172	Introduction to recombination detection. , 2009, , 493-518.		9
173	Detecting and characterizing individual recombination events. , 2009, , 519-548.		4
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