

Kristel Van Laethem

List of Publications by Year in descending order

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134
papers

5,130
citations

81743

39
h-index

106150

65
g-index

141
all docs

141
docs citations

141
times ranked

4518
citing authors

#	ARTICLE	IF	CITATIONS
1	Prevalence and Evolution of Transmitted Human Immunodeficiency Virus Drug Resistance in Belgium Between 2013 and 2019. <i>Open Forum Infectious Diseases</i> , 2022, 9, .	0.4	2
2	Nationwide Harmonization Effort for Semi-Quantitative Reporting of SARS-CoV-2 PCR Test Results in Belgium. <i>Viruses</i> , 2022, 14, 1294.	1.5	13
3	The hepatitis C cascade of care in the Belgian HIV population: One step closer to elimination. <i>International Journal of Infectious Diseases</i> , 2021, 105, 217-223.	1.5	6
4	Quality Control of Next-Generation Sequencing-Based HIV-1 Drug Resistance Data in Clinical Laboratory Information Systems Framework. <i>Viruses</i> , 2020, 12, 645.	1.5	7
5	Chronic and Early Antiretroviral Therapy Impact Human Immunodeficiency Virus (HIV) Serological Assay Sensitivity, Leading to More False-Negative Test Results in HIV Diagnosis. <i>Journal of Infectious Diseases</i> , 2020, 222, 1660-1669.	1.9	5
6	High frequency of new recombinant forms in HIV-1 transmission networks demonstrated by full genome sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104365.	1.0	1
7	Stable level of HIV transmitted drug resistance in Estonia despite significant scale-up of antiretroviral therapy. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103901.	1.0	1
8	An Evolutionary Model-Based Approach To Quantify the Genetic Barrier to Drug Resistance in Fast-Evolving Viruses and Its Application to HIV-1 Subtypes and Integrase Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	10
9	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. <i>Frontiers in Microbiology</i> , 2019, 10, 613.	1.5	21
10	Exploring HIV-1 Transmission Dynamics by Combining Phylogenetic Analysis and Infection Timing. <i>Viruses</i> , 2019, 11, 1096.	1.5	9
11	Global and regional molecular epidemiology of HIV-1, 1990–2015: a systematic review, global survey, and trend analysis. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 143-155.	4.6	255
12	Phylogenetic analysis of the Belgian HIV-1 epidemic reveals that local transmission is almost exclusively driven by men having sex with men despite presence of large African migrant communities. <i>Infection, Genetics and Evolution</i> , 2018, 61, 36-44.	1.0	26
13	Analysis of ex vivo HIV-1 infection in a controller-discordant couple. <i>Journal of Virus Eradication</i> , 2018, 4, 170-173.	0.3	3
14	Analysis of HIV-1 infection in a controller-discordant couple. <i>Journal of Virus Eradication</i> , 2018, 4, 170-173.	0.3	2
15	Exploring resistance pathways for first-generation NS3/4A protease inhibitors boceprevir and telaprevir using Bayesian network learning. <i>Infection, Genetics and Evolution</i> , 2017, 53, 15-23.	1.0	14
16	Phylogenetic evidence for underreporting of male-to-male sex among human immunodeficiency virus-infected donors in the Netherlands and Flanders. <i>Transfusion</i> , 2017, 57, 1235-1247.	0.8	11
17	Implications of hepatitis C virus subtype 1a migration patterns for virus genetic sequencing policies in Italy. <i>BMC Evolutionary Biology</i> , 2017, 17, 70.	3.2	21
18	A21 HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017, 3, .	2.2	6

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19	Decision tree for accurate infection timing in individuals newly diagnosed with HIV-1 infection. <i>BMC Infectious Diseases</i> , 2017, 17, 738.	1.3	13
20	A18â€fRandom amplification with next-generation sequencing to cover HIV and HCV full-length genomes. <i>Virus Evolution</i> , 2017, 3, .	2.2	1
21	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	1.5	13
22	Impact of HCV genotype on treatment regimens and drug resistance: a snapshot in time. <i>Reviews in Medical Virology</i> , 2016, 26, 408-434.	3.9	34
23	Mapping the genomic diversity of HCV subtypes 1a and 1b: Implications of structural and immunological constraints for vaccine and drug development. <i>Virus Evolution</i> , 2016, 2, vew024.	2.2	17
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	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, 427-433.	0.5	19
26	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015, 29, 1549-1556.	1.0	16
27	Lack of evidence for the selection of E138 mutations by first-generation non-nucleoside reverse transcriptase inhibitors in patients infected with HIV-1 non-B subtypes. <i>Aids</i> , 2015, 29, 987-988.	1.0	1
28	Performance of an In-House Human Immunodeficiency Virus Type 1 Genotyping System for Assessment of Drug Resistance in Cuba. <i>PLoS ONE</i> , 2015, 10, e0117176.	1.1	4
29	HIV-1 genotypic drug resistance testing: digging deep, reaching wide?. <i>Current Opinion in Virology</i> , 2015, 14, 16-23.	2.6	36
30	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
31	Discordant predictions of residual activity could impact dolutegravir prescription upon raltegravir failure. <i>Journal of Clinical Virology</i> , 2015, 70, 120-127.	1.6	6
32	Trends and Predictors of Transmitted Drug Resistance (TDR) and Clusters with TDR in a Local Belgian HIV-1 Epidemic. <i>PLoS ONE</i> , 2014, 9, e101738.	1.1	36
33	High frequency of antiviral drug resistance and non-b subtypes in HIV-1 patients failing antiviral therapy in Cuba. <i>Journal of the International AIDS Society</i> , 2014, 17, 19754.	1.2	6
34	HIV-1 Gag C-terminal amino acid substitutions emerging under selective pressure of protease inhibitors in patient populations infected with different HIV-1 subtypes. <i>Retrovirology</i> , 2014, 11, 79.	0.9	11
35	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
36	Comparative Performances of HIV-1 RNA Load Assays at Low Viral Load Levels: Results of an International Collaboration. <i>Journal of Clinical Microbiology</i> , 2014, 52, 517-523.	1.8	47

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37	Possible Footprints of APOBEC3F and/or Other APOBEC3 Deaminases, but Not APOBEC3G, on HIV-1 from Patients with Acute/Early and Chronic Infections. <i>Journal of Virology</i> , 2014, 88, 12882-12894.	1.5	21
38	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
39	Horizontal gene transfer from human host to HIV-1 reverse transcriptase confers drug resistance and partly compensates for replication deficits. <i>Virology</i> , 2014, 456-457, 310-318.	1.1	5
40	Characterization of amino acids Arg, Ser and Thr at position 70 within HIV-1 reverse transcriptase. <i>Acta Clinica Belgica</i> , 2014, 69, 348-357.	0.5	3
41	Patterns of Transmitted HIV Drug Resistance in Europe Vary by Risk Group. <i>PLoS ONE</i> , 2014, 9, e94495.	1.1	32
42	Limited cross-border infections in patients newly diagnosed with HIV in Europe. <i>Retrovirology</i> , 2013, 10, 36.	0.9	52
43	HIV-1 fitness landscape models for indinavir treatment pressure using observed evolution in longitudinal sequence data are predictive for treatment failure. <i>Infection, Genetics and Evolution</i> , 2013, 19, 349-360.	1.0	4
44	Antiretroviral drug resistance in HIV-1 therapy-naive patients in Cuba. <i>Infection, Genetics and Evolution</i> , 2013, 16, 144-150.	1.0	23
45	Mutations selected in HIV-2-infected patients failing a regimen including atazanavir. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 190-192.	1.3	17
46	Evaluation of the automatic editing tool RECall for HIV-1 pol and V3 loop sequences. <i>Journal of Virological Methods</i> , 2013, 193, 135-139.	1.0	1
47	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013, 29, 1477-1480.	1.8	29
48	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
49	HIV-1 genetic variation and drug resistance development. <i>Expert Review of Anti-Infective Therapy</i> , 2013, 11, 1159-1178.	2.0	17
50	Superinfection with drug-resistant HIV is rare and does not contribute substantially to therapy failure in a large European cohort. <i>BMC Infectious Diseases</i> , 2013, 13, 537.	1.3	8
51	Clinical Evaluation of Rega 8: An Updated Genotypic Interpretation System That Significantly Predicts HIV-Therapy Response. <i>PLoS ONE</i> , 2013, 8, e61436.	1.1	17
52	HIV-1 protease mutation 82M contributes to phenotypic resistance to protease inhibitors in subtype G. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1075-1079.	1.3	8
53	Treatment-associated polymorphisms in protease are significantly associated with higher viral load and lower CD4 count in newly diagnosed drug-naive HIV-1 infected patients. <i>Retrovirology</i> , 2012, 9, 81.	0.9	23
54	High frequency of antiviral drug resistance and non-B subtypes in HIV-1 patients failing antiviral therapy in Cuba. <i>Journal of Clinical Virology</i> , 2012, 55, 348-355.	1.6	10

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55	European guidelines on the clinical management of HIV-1 tropism testing. <i>Lancet Infectious Diseases</i> , 2011, 11, 394-407.	4.6	218
56	Appearance of a Single Amino Acid Insertion at Position 33 in HIV Type 1 Protease Under a Lopinavir-Containing Regimen, Associated with Reduced Protease Inhibitor Susceptibility. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 1223-1229.	0.5	0
57	Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study). <i>HIV Medicine</i> , 2011, 12, 211-218.	1.0	32
58	Differences in the mannose oligomer specificities of the closely related lectins from <i>Galanthus nivalis</i> and <i>Zea mays</i> strongly determine their eventual anti-HIV activity. <i>Retrovirology</i> , 2011, 8, 10.	0.9	24
59	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
60	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. <i>BMC Bioinformatics</i> , 2010, 11, 409.	1.2	12
61	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, 253-260.	1.9	9
62	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
63	Pradimicin S, a Highly Soluble Nonpeptidic Small-Size Carbohydrate-Binding Antibiotic, Is an Anti-HIV Drug Lead for both Microbicidal and Systemic Use. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 1425-1435.	1.4	46
64	Actinohivin, a Broadly Neutralizing Prokaryotic Lectin, Inhibits HIV-1 Infection by Specifically Targeting High-Mannose-Type Glycans on the gp120 Envelope. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 3287-3301.	1.4	54
65	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.	1.3	16
66	Different Evolution of Genotypic Resistance Profiles to Emtricitabine Versus Lamivudine in Tenofovir-Containing Regimens. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010, 55, 336-344.	0.9	32
67	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.	1.1	10
68	Human Immunodeficiency Virus Type 1 Escape from Cyclotriazadisulfonamide-Induced CD4-Targeted Entry Inhibition Is Associated with Increased Neutralizing Antibody Susceptibility. <i>Journal of Virology</i> , 2009, 83, 9577-9583.	1.5	10
69	Predictive Value of HIV-1 Genotypic Resistance Test Interpretation Algorithms. <i>Journal of Infectious Diseases</i> , 2009, 200, 453-463.	1.9	39
70	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, 2232-2242.	1.8	13
71	Capture and transmission of HIV-1 by the C-type lectin L-SIGN (DC-SIGNR) is inhibited by carbohydrate-binding agents and polyanions. <i>Antiviral Research</i> , 2009, 83, 61-70.	1.9	10
72	Evolution of genotypic resistance to enfuvirtide in HIV-1 isolates from different group M subtypes. <i>Journal of Clinical Virology</i> , 2009, 44, 325-328.	1.6	11

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73	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , 2009, 6, 49.	0.9	114
74	Clinical Implications of Reverse Transcriptase Inhibitor Resistance. , 2009, , 589-619.		0
75	Transmitted drug resistance, selection of resistance mutations and moderate antiretroviral efficacy in HIV-2: Analysis of the HIV-2 Belgium and Luxembourg database. <i>BMC Infectious Diseases</i> , 2008, 8, 21.	1.3	38
76	Glycan deletions in the HIV-1 gp120 V1/V2 domain compromise viral infectivity, sensitize the mutant virus strains to carbohydrate-binding agents and represent a specific target for therapeutic intervention. <i>Virology</i> , 2008, 382, 10-19.	1.1	31
77	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
78	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, 355-362.	0.5	33
79	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, 1201-1204.	1.3	18
80	Bayesian network analyses of resistance pathways against efavirenz and nevirapine. <i>Aids</i> , 2008, 22, 2107-2115.	1.0	21
81	Impact on Replicative Fitness of the G48E Substitution in the Protease of HIV-1. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008, 48, 255-262.	0.9	6
82	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.	0.6	7
83	Estimating the Relative Contribution of dNTP Pool Imbalance and APOBEC3G/3F Editing to HIV Evolution <i>In Vivo</i> . <i>Journal of Computational Biology</i> , 2007, 14, 1105-1114.	0.8	26
84	Pradimicin A, a Carbohydrate-Binding Nonpeptidic Lead Compound for Treatment of Infections with Viruses with Highly Glycosylated Envelopes, Such as Human Immunodeficiency Virus. <i>Journal of Virology</i> , 2007, 81, 362-373.	1.5	99
85	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, 43-47.	1.6	38
86	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, 600-603.	1.0	7
87	Resistance of HIV-1 to the broadly HIV-1-neutralizing, anti-carbohydrate antibody 2G12. <i>Virology</i> , 2007, 360, 294-304.	1.1	40
88	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
89	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.	2.7	41
90	Discovery of TSAO derivatives with an unusual HIV-1 activity/resistance profile. <i>Antiviral Research</i> , 2006, 71, 15-23.	1.9	7

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91	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, 181-186.	1.0	16
92	Mutational Pathways, Resistance Profile, and Side Effects of Cyanovirin Relative to Human Immunodeficiency Virus Type 1 Strains with N-Glycan Deletions in Their gp120 Envelopes. <i>Journal of Virology</i> , 2006, 80, 8411-8421.	1.5	93
93	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
94	Pronounced in vitro and in vivo antiretroviral activity of 5-substituted 2,4-diamino-6-[2-(phosphonomethoxy)ethoxy] pyrimidines. <i>Journal of Antimicrobial Chemotherapy</i> , 2006, 59, 80-86.	1.3	27
95	Interpreting resistance data for HIV-1 therapy management—know the limitations. <i>AIDS Reviews</i> , 2006, 8, 37-43.	0.5	18
96	Molecular testing of multiple HIV-1 transmissions in a criminal case. <i>Aids</i> , 2005, 19, 1649-1658.	1.0	43
97	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.	1.0	39
98	Prevalence of Drug-Resistant HIV-1 Variants in Untreated Individuals in Europe: Implications for Clinical Management. <i>Journal of Infectious Diseases</i> , 2005, 192, 958-966.	1.9	385
99	Carbohydrate-binding Agents Cause Deletions of Highly Conserved Glycosylation Sites in HIV GP120. <i>Journal of Biological Chemistry</i> , 2005, 280, 41005-41014.	1.6	108
100	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
101	Marked Depletion of Glycosylation Sites in HIV-1 gp120 under Selection Pressure by the Mannose-Specific Plant Lectins of <i>Hippeastrum Hybrid</i> and <i>Galanthus nivalis</i> . <i>Molecular Pharmacology</i> , 2005, 67, 1556-1565.	1.0	62
102	Fatal brain necrosis in primary HIV infection. <i>Lancet, The</i> , 2005, 366, 866.	6.3	12
103	Profile of Resistance of Human Immunodeficiency Virus to Mannose-Specific Plant Lectins. <i>Journal of Virology</i> , 2004, 78, 10617-10627.	1.5	94
104	Rising Prevalence of HIV-1 Non-B Subtypes in Belgium: 1983-2001. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2004, 35, 279-285.	0.9	48
105	Performance of ViroSeq HIV-1 Genotyping System in routine practice at a Belgian clinical laboratory. <i>Journal of Virological Methods</i> , 2004, 119, 45-49.	1.0	26
106	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, 7-15.	1.6	1
107	Current Levels of Drug Resistance Among Therapy-Naive HIV-Infected Patients Have Significant Impact on Treatment Response. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2004, 37, 1664-1666.	0.9	25
108	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, 119-124.	2.7	10

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109	HIV-1 Protease and Reverse Transcriptase Mutation Patterns Responsible for Discordances Between Genotypic Drug Resistance Interpretation Algorithms. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2003, 33, 8-14.	0.9	86
110	env Chimeric Virus Technology for Evaluating Human Immunodeficiency Virus Susceptibility to Entry Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 3954-3962.	1.4	39
111	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.	1.1	37
112	Complete genome sequence of Montana Myotis leukoencephalitis virus, phylogenetic analysis and comparative study of the 3' untranslated region of flaviviruses with no known vector. <i>Journal of General Virology</i> , 2002, 83, 1875-1885.	1.3	40
113	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
114	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
115	Mutations in the non-nucleoside binding-pocket interfere with the multi-nucleoside resistance phenotype. <i>Aids</i> , 2001, 15, 553-561.	1.0	16
116	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</i> (1999), 2001, 28, 254-258.	0.9	41
117	Site-Directed Mutagenesis of Human Immunodeficiency Virus Type 1 Reverse Transcriptase at Amino Acid Position 138. <i>Virology</i> , 2001, 280, 97-106.	1.1	22
118	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</i> (1999), 2001, 28, 254-258.	0.9	1
119	Evaluating Clinical Isolates for Their Phenotypic and Genotypic Resistance Against Anti-HIV Drugs. , 2000, 24, 223-258.		27
120	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
121	Patient HIV-1 strains carrying the multiple nucleoside resistance mutations are cross-resistant to abacavir. <i>Aids</i> , 2000, 14, 469.	1.0	28
122	Full-Length Genomic Sequence of an HIV Type 1 Subtype G from Kinshasa. <i>AIDS Research and Human Retroviruses</i> , 1999, 15, 585-589.	0.5	7
123	Managing Resistance to Anti-HIV Drugs. <i>Drugs</i> , 1999, 57, 337-361.	4.9	95
124	Activity of non-nucleoside reverse transcriptase inhibitors against HIV-2 and SIV. <i>Aids</i> , 1999, 13, 1477-1483.	1.0	77
125	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, 153-166.	1.0	7
126	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.	1.0	34

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127	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
128	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
129	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
130	African Origin of Human T-Lymphotropic Virus Type 2 (HTLV-2) Supported by a Potential New HTLV-2d Subtype in Congolese Bambuti Efe Pygmies. <i>Journal of Virology</i> , 1998, 72, 4327-4340.	1.5	78
131	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.	0.6	10
132	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
133	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.		77
134	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