Martine Peeters

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Origin of HIV-1 in the chimpanzee Pan troglodytes troglodytes. Nature, 1999, 397, 436-441.	27.8	1,405
2	Chimpanzee Reservoirs of Pandemic and Nonpandemic HIV-1. Science, 2006, 313, 523-526.	12.6	723
3	The early spread and epidemic ignition of HIV-1 in human populations. Science, 2014, 346, 56-61.	12.6	515
4	Tetherin-Driven Adaptation of Vpu and Nef Function and the Evolution of Pandemic and Nonpandemic HIV-1 Strains. Cell Host and Microbe, 2009, 6, 409-421.	11.0	391
5	Nef-Mediated Suppression of T Cell Activation Was Lost in a Lentiviral Lineage that Gave Rise to HIV-1. Cell, 2006, 125, 1055-1067.	28.9	359
6	Hybrid Origin of SIV in Chimpanzees. Science, 2003, 300, 1713-1713.	12.6	337
7	SIV infection in wild gorillas. Nature, 2006, 444, 164-164.	27.8	315
8	Unprecedented Degree of Human Immunodeficiency Virus Type 1 (HIV-1) Group M Genetic Diversity in the Democratic Republic of Congo Suggests that the HIV-1 Pandemic Originated in Central Africa. Journal of Virology, 2000, 74, 10498-10507.	3.4	295
9	Simian Immunodeficiency Virus Infection in Free-Ranging Sooty Mangabeys (Cercocebus atys atys) from the Tail`Forest, Col,te d'Ivoire: Implications for the Origin of Epidemic Human Immunodeficiency Virus Type 2. Journal of Virology, 2005, 79, 12515-12527.	3.4	274
10	Risk to Human Health from a Plethora of Simian Immunodeficiency Viruses in Primate Bushmeat. Emerging Infectious Diseases, 2002, 8, 451-457.	4.3	240
11	Isolation and partial characterization of an HIV-related virus occurring naturally in chimpanzees in Gabon. Aids, 1989, 3, 625-630.	2.2	217
12	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.	8.4	188
13	Genetic Diversity of Protease and Reverse Transcriptase Sequences in Non-Subtype-B Human Immunodeficiency Virus Type 1 Strains: Evidence of Many Minor Drug Resistance Mutations in Treatment-Naive Patients. Journal of Clinical Microbiology, 2000, 38, 3919-3925.	3.9	169
14	Impact of HIV-1 Genetic Diversity on Plasma HIV-1 RNA Quantification. Journal of Acquired Immune Deficiency Syndromes (1999), 2007, 45, 380-388.	2.1	145
15	Phylogeny and the origin of HIV-1. Nature, 2001, 410, 1047-1048.	27.8	143
16	Origin of the HIV-1 group O epidemic in western lowland gorillas. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1343-52.	7.1	136
17	Geographical distribution of HIV-1 group O viruses in Africa. Aids, 1997, 11, 493-498.	2.2	135
18	Characterization of a Novel Simian Immunodeficiency Virus with a vpu Gene from Greater Spot-Nosed Monkeys (Cercopithecus nictitans) Provides New Insights into Simian/Human Immunodeficiency Virus Phylogeny. Journal of Virology, 2002, 76, 8298-8309.	3.4	124

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19	New Simian Immunodeficiency Virus Infecting De Brazza's Monkeys (Cercopithecus neglectus): Evidence for a Cercopithecus Monkey Virus Clade. Journal of Virology, 2004, 78, 7748-7762.	3.4	121
20	Cross-species transmission of simian retroviruses. Aids, 2012, 26, 659-673.	2.2	120
21	Genetic diversity and phylogeographic clustering of SIVcpzPtt in wild chimpanzees in Cameroon. Virology, 2007, 368, 155-171.	2.4	118
22	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. Nature, 2021, 597, 539-543.	27.8	113
23	Origin and Biology of Simian Immunodeficiency Virus in Wild-Living Western Gorillas. Journal of Virology, 2009, 83, 1635-1648.	3.4	106
24	Characterization of a Novel Simian Immunodeficiency Virus from Guereza Colobus Monkeys (Colobus) Tj ETQq0 0 2001, 75, 857-866.	0 rgBT /0 3.4	Overlock 10 7 102
25	Adaptation of HIV-1 to Its Human Host. Molecular Biology and Evolution, 2007, 24, 1853-1860.	8.9	100
26	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.	2.3	100
27	Characterization of a Highly Replicative Intergroup M/O Human Immunodeficiency Virus Type 1 Recombinant Isolated from a Cameroonian Patient. Journal of Virology, 1999, 73, 7368-7375.	3.4	99
28	Evaluation of Different RNA Extraction Methods and Storage Conditions of Dried Plasma or Blood Spots for Human Immunodeficiency Virus Type 1 RNA Quantification and PCR Amplification for Drug Resistance Testing. Journal of Clinical Microbiology, 2009, 47, 1107-1118.	3.9	98
29	Multidisciplinary assessment of post-Ebola sequelae in Guinea (Postebogui): an observational cohort study. Lancet Infectious Diseases, The, 2017, 17, 545-552.	9.1	96
30	Biological and genetic characteristics of HIV infections in Cameroon reveals dual group M and O infections and a correlation between SI-inducing phenotype of the predominant CRF02_AG variant and disease stage. Virology, 2003, 310, 254-266.	2.4	95
31	Sequence Analysis of a Highly Divergent HIV-1-Related Lentivirus Isolated from a Wild Captured Chimpanzee. Virology, 1996, 221, 346-350.	2.4	94
32	The Potency of Nef-Mediated SERINC5 Antagonism Correlates with the Prevalence of Primate Lentiviruses in the Wild. Cell Host and Microbe, 2016, 20, 381-391.	11.0	88
33	Identification of a New Simian Immunodeficiency Virus Lineage with a vpu Gene Present among Different Cercopithecus Monkeys (C. mona , C. cephus , and C. nictitans) from Cameroon. Journal of Virology, 2003, 77, 12523-12534.	3.4	85
34	Recombination Confounds the Early Evolutionary History of Human Immunodeficiency Virus Type 1: Subtype G Is a Circulating Recombinant Form. Journal of Virology, 2007, 81, 8543-8551.	3.4	84
35	Extraordinary Heterogeneity of Virological Outcomes in Patients Receiving Highly Antiretroviral Therapy and Monitored With the World Health Organization Public Health Approach in Sub-Saharan Africa and Southeast Asia. Clinical Infectious Diseases, 2014, 58, 99-109.	5.8	83
36	Molecular Epidemiology of Simian Immunodeficiency Virus Infection in Wild-Living Gorillas. Journal of Virology, 2010, 84, 1464-1476.	3.4	78

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37	Nef Proteins of Epidemic HIV-1 Group O Strains Antagonize Human Tetherin. Cell Host and Microbe, 2014, 16, 639-650.	11.0	77
38	Eastern Chimpanzees, but Not Bonobos, Represent a Simian Immunodeficiency Virus Reservoir. Journal of Virology, 2012, 86, 10776-10791.	3.4	73
39	Inaccurate Diagnosis of HIV-1 Group M and O Is a Key Challenge for Ongoing Universal Access to Antiretroviral Treatment and HIV Prevention in Cameroon. PLoS ONE, 2009, 4, e7702.	2.5	72
40	Multiplex detection and dynamics of IgG antibodies to SARS-CoV2 and the highly pathogenic human coronaviruses SARS-CoV and MERS-CoV. Journal of Clinical Virology, 2020, 129, 104521.	3.1	68
41	Evidence for continuing cross-species transmission of SIVsmm to humans. Aids, 2013, 27, 2488-2491.	2.2	66
42	Survey of Ebola Viruses in Frugivorous and Insectivorous Bats in Guinea, Cameroon, and the Democratic Republic of the Congo, 2015–2017. Emerging Infectious Diseases, 2018, 24, 2228-2240.	4.3	66
43	Anthrax in Western and Central African great apes. American Journal of Primatology, 2006, 68, 928-933.	1.7	65
44	High rates of virological failure and drug resistance in perinatally HIVâ€1â€infected children and adolescents receiving lifelong antiretroviral therapy in routine clinics in Togo. Journal of the International AIDS Society, 2016, 19, 20683.	3.0	64
45	Low Levels of Antiretroviralâ€Resistant HIV Infection in a Routine Clinic in Cameroon that Uses the World Health Organization (WHO) Public Health Approach to Monitor Antiretroviral Treatment and Adequacy with the WHO Recommendation for Secondâ€Line Treatment. Clinical Infectious Diseases, 2009. 48. 1318-1322.	5.8	62
46	Medical countermeasures during the 2018 Ebola virus disease outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo: a rapid genomic assessment. Lancet Infectious Diseases, The, 2019, 19, 648-657.	9.1	62
47	Field Evaluation of Dried Blood Spots for Routine HIV-1 Viral Load and Drug Resistance Monitoring in Patients Receiving Antiretroviral Therapy in Africa and Asia. Journal of Clinical Microbiology, 2014, 52, 578-586.	3.9	60
48	Characterization of a new simian immunodeficiency virus strain in a naturally infected Pan troglodytes troglodyteschimpanzee with AIDS related symptoms. Retrovirology, 2011, 8, 4.	2.0	58
49	Challenges in interpreting SARS-CoV-2 serological results in African countries. The Lancet Global Health, 2021, 9, e588-e589.	6.3	57
50	Widely varying SIV prevalence rates in naturally infected primate species from Cameroon. Virology, 2006, 345, 174-189.	2.4	52
51	Virological failure rates and HIVâ€1 drug resistance patterns in patients on firstâ€line antiretroviral treatment in semirural and rural Gabon. Journal of the International AIDS Society, 2012, 15, 17985.	3.0	52
52	Novel simian foamy virus infections from multiple monkey species in women from the Democratic Republic of Congo. Retrovirology, 2012, 9, 100.	2.0	51
53	Primate immunodeficiency virus classification and nomenclature: Review. Infection, Genetics and Evolution, 2016, 46, 150-158.	2.3	47
54	Development of a Sensitive and Specific Serological Assay Based on Luminex Technology for Detection of Antibodies to Zaire Ebola Virus. Journal of Clinical Microbiology, 2017, 55, 165-176.	3.9	47

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55	High prevalence of HIV-1 drug resistance among patients on first-line antiretroviral treatment in Lomé, Togo. Journal of the International AIDS Society, 2011, 14, 30.	3.0	45
56	The origin and molecular epidemiology of HIV. Expert Review of Anti-Infective Therapy, 2013, 11, 885-896.	4.4	45
57	Wild bonobos host geographically restricted malaria parasites including a putative new Laverania species. Nature Communications, 2017, 8, 1635.	12.8	45
58	Full-length sequence analysis of SIVmus in wild populations of mustached monkeys (Cercopithecus) Tj ETQq0 0 407-418.	0 rgBT /Ov 2.4	verlock 10 Tf 5 43
59	Genetic diversity among human immunodeficiency virus-1 non-B subtypes in viral load and drug resistance assays. Clinical Microbiology and Infection, 2010, 16, 1525-1531.	6.0	38
60	Multigenomic Delineation of <i>Plasmodium</i> Species of the <i>Laverania</i> Subgenus Infecting Wild-Living Chimpanzees and Gorillas. Genome Biology and Evolution, 2016, 8, 1929-1939.	2.5	38
61	High Prevalence of Anti–Severe Acute Respiratory Syndrome Coronavirus 2 (Anti–SARS-CoV-2) Antibodies After the First Wave of Coronavirus Disease 2019 (COVID-19) in Kinshasa, Democratic Republic of the Congo: Results of a Cross-sectional Household-Based Survey. Clinical Infectious Diseases. 2022. 74. 882-890.	5.8	38
62	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. PLoS Pathogens, 2019, 15, e1007976.	4.7	37
63	Prevalence of infection among asymptomatic and paucisymptomatic contact persons exposed to Ebola virus in Guinea: a retrospective, cross-sectional observational study. Lancet Infectious Diseases, The, 2019, 19, 308-316.	9.1	36
64	Virological outcome and patterns of HIVâ€1 drug resistance in patients with 36 months' antiretroviral therapy experience in Cameroon. Journal of the International AIDS Society, 2013, 16, 18004.	3.0	32
65	Full-Length Genome Characterization of a Novel Simian Immunodeficiency Virus Lineage (SIVolc) from Olive Colobus (Procolobus verus) and New SIVwrcPbb Strains from Western Red Colobus (Piliocolobus badius badius) from the Tail^ Forest in Ivory Coast. Journal of Virology, 2009, 83, 428-439.	3.4	30
66	Simian retroviruses in African apes. Clinical Microbiology and Infection, 2012, 18, 514-520.	6.0	30
67	The genetic population structure of wild western lowland gorillas (<i>Gorilla gorilla gorilla</i>) living in continuous rain forest. American Journal of Primatology, 2014, 76, 868-878.	1.7	30
68	Novel Multiplexed HIV/Simian Immunodeficiency Virus Antibody Detection Assay. Emerging Infectious Diseases, 2011, 17, 2277-2286.	4.3	29
69	New STLV-3 strains and a divergent SIVmus strain identified in non-human primate bushmeat in Gabon. Retrovirology, 2012, 9, 28.	2.0	28
70	Short Communication: High Viral Load and Multidrug Resistance Due to Late Switch to Second-Line Regimens Could Be a Major Obstacle to Reach the 90-90-90 UNAIDS Objectives in Sub-Saharan Africa. AIDS Research and Human Retroviruses, 2016, 32, 1159-1162.	1.1	28
71	2018 Ebola virus disease outbreak in Équateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. Lancet Infectious Diseases, The, 2019, 19, 641-647.	9.1	27
72	High level of treatment failure and drug resistance to first-line antiretroviral therapies among HIV-infected children receiving decentralized care in Senegal. BMC Pediatrics, 2019, 19, 47.	1.7	27

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73	Surprisingly High Prevalence of Subtype C and Specific HIV-1 Subtype/CRF Distribution in Men Having Sex With Men in Senegal. Journal of Acquired Immune Deficiency Syndromes (1999), 2009, 52, 249-252.	2.1	26
74	Noninvasive Follow-Up of Simian Immunodeficiency Virus Infection in Wild-Living Nonhabituated Western Lowland Gorillas in Cameroon. Journal of Virology, 2012, 86, 9760-9772.	3.4	26
75	A 40 months follow-up of Ebola virus disease survivors in Guinea (Postebogui)Âreveals longterm detection of Ebola viral RNA in semen and breast milk. Open Forum Infectious Diseases, 2019, 6, ofz482.	0.9	26
76	Antiretroviral Drug Resistance and Routine Therapy, Cameroon. Emerging Infectious Diseases, 2006, 12, 1001-1004.	4.3	25
77	In-depth analysis of HIV-1 drug resistance mutations in HIV-infected individuals failing first-line regimens in West and Central Africa. Aids, 2016, 30, 2577-2589.	2.2	24
78	Phylodynamics of the major HIV-1 CRF02_AG African lineages and its global dissemination. Infection, Genetics and Evolution, 2016, 46, 190-199.	2.3	24
79	Full molecular characterization of a simian immunodeficiency virus, SIVwrcpbt from Temminck's red colobus (Piliocolobus badius temminckii) from Abuko Nature Reserve, The Gambia. Virology, 2008, 376, 90-100.	2.4	23
80	Implementation and Operational Research. Journal of Acquired Immune Deficiency Syndromes (1999), 2016, 71, e9-e15.	2.1	23
81	Comparison of different nucleic acid preparation methods to improve specific HIV-1 RNA isolation for viral load testing on dried blood spots. Journal of Virological Methods, 2018, 251, 75-79.	2.1	23
82	Extensive Serological Survey of Multiple African Nonhuman Primate Species Reveals Low Prevalence of Immunoglobulin G Antibodies to 4 Ebola Virus Species. Journal of Infectious Diseases, 2019, 220, 1599-1608.	4.0	23
83	Complete Genome Analysis of One of the Earliest SIVcpzPtt Strains from Gabon (SIVcpzGAB2). AIDS Research and Human Retroviruses, 2004, 20, 1377-1381.	1.1	22
84	HIV-1 group O infection in Cameroon from 2006 to 2013: Prevalence, genetic diversity, evolution and public health challenges. Infection, Genetics and Evolution, 2015, 36, 210-216.	2.3	22
85	Molecular characterization of a novel simian immunodeficiency virus lineage (SIVtal) from northern talapoins (Miopithecus ogouensis). Virology, 2006, 349, 55-65.	2.4	21
86	Successful Integrase Inhibitor-Based Highly Active Antiretroviral Therapy for a Multidrug-Class-Resistant HIV Type 1 Group O-Infected Patient in Cameroon. AIDS Research and Human Retroviruses, 2013, 29, 1-3.	1.1	21
87	Assessing Host-Virus Codivergence for Close Relatives of Merkel Cell Polyomavirus Infecting African Great Apes. Journal of Virology, 2016, 90, 8531-8541.	3.4	21
88	Assessment of the gorilla gut virome in association with natural simian immunodeficiency virus infection. Retrovirology, 2018, 15, 19.	2.0	21
89	CD4 receptor diversity in chimpanzees protects against SIV infection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3229-3238.	7.1	21
90	The Origin and Evolutionary History of HIV-1 Subtype C in Senegal. PLoS ONE, 2012, 7, e33579.	2.5	20

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91	Understanding Ebola virus and other zoonotic transmission risks through human–bat contacts: Exploratory study on knowledge, attitudes and practices in Southern Cameroon. Zoonoses and Public Health, 2019, 66, 288-295.	2.2	20
92	Multiplex detection of antibodies to Chikungunya, O'nyong-nyong, Zika, Dengue, West Nile and Usutu viruses in diverse non-human primate species from Cameroon and the Democratic Republic of Congo. PLoS Neglected Tropical Diseases, 2021, 15, e0009028.	3.0	18
93	HIV-1 drug-resistance mutations among newly diagnosed patients before scaling-up programmes in Burkina Faso and Cameroon. Antiviral Therapy, 2006, 11, 575-9.	1.0	17
94	Alarming rates of virological failure and drug resistance in patients on long-term antiretroviral treatment in routine HIV clinics in Togo. Aids, 2015, 29, 2527-2530.	2.2	16
95	Rapid Increase of Community SARS-CoV-2 Seroprevalence during Second Wave of COVID-19, Yaoundé, Cameroon. Emerging Infectious Diseases, 2022, 28, .	4.3	16
96	High frequency of HIV-1 infections with multiple HIV-1 strains in men having sex with men (MSM) in Senegal. Infection, Genetics and Evolution, 2013, 20, 206-214.	2.3	14
97	High Rates of Drug Resistance Among Newly Diagnosed HIV-infected Children in the National Prevention of Mother-to-child Transmission Program in Togo. Pediatric Infectious Disease Journal, 2016, 35, 879-885.	2.0	14
98	Investigating the Circulation of Ebola Viruses in Bats during the Ebola Virus Disease Outbreaks in the Equateur and North Kivu Provinces of the Democratic Republic of Congo from 2018. Pathogens, 2021, 10, 557.	2.8	13
99	Dried blood spots for HIVâ€1 drug resistance genotyping in decentralized settings in Senegal. Journal of Medical Virology, 2014, 86, 45-51.	5.0	12
100	Virologic Failure and Human Immunodeficiency Virus Drug Resistance in Rural Cameroon With Regard to the UNAIDS 90-90-90 Treatment Targets. Open Forum Infectious Diseases, 2016, 3, ofw233.	0.9	12
101	Loss of CXCR6 coreceptor usage characterizes pathogenic lentiviruses. PLoS Pathogens, 2018, 14, e1007003.	4.7	12
102	Understanding Long-term Evolution and Predictors of Sequelae of Ebola Virus Disease Survivors in Guinea: A 48-Month Prospective, Longitudinal Cohort Study (PostEboGui). Clinical Infectious Diseases, 2021, 73, 2166-2174.	5.8	12
103	Full-Length Genome Analyses of Two New Simian Immunodeficiency Virus (SIV) Strains from Mustached Monkeys (C. Cephus) in Gabon Illustrate a Complex Evolutionary History among the SIVmus/mon/gsn Lineage. Viruses, 2014, 6, 2880-2898.	3.3	11
104	Current challenges to viral load testing in the context of emerging genetic diversity of HIV-1. Expert Opinion on Medical Diagnostics, 2011, 5, 183-202.	1.6	10
105	Single Real-Time Reverse Transcription-PCR Assay for Detection and Quantification of Genetically Diverse HIV-1, SIVcpz, and SIVgor Strains. Journal of Clinical Microbiology, 2013, 51, 787-798.	3.9	10
106	Temporal evolution of the humoral antibody response after Ebola virus disease in Guinea: a 60-month observational prospective cohort study. Lancet Microbe, The, 2021, 2, e676-e684.	7.3	10
107	Molecular characterization of a new mosaic Simian Immunodeficiency Virus in a naturally infected tantalus monkey (Chlorocebus tantalus) from Cameroon: A challenge to the virus–host co-evolution of SIVagm in African green monkeys. Infection, Genetics and Evolution, 2015, 30, 65-73.	2.3	9
108	CD4 receptor diversity represents an ancient protection mechanism against primate lentiviruses. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9

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109	High and Rapid Increase in Seroprevalence for SARS-CoV-2 in Conakry, Guinea: Results From 3 Successive Cross-Sectional Surveys (ANRS COV16-ARIACOV). Open Forum Infectious Diseases, 2022, 9, ofac152.	0.9	8
110	Challenges of Antiretroviral Treatment Monitoring in Rural and Remote-Access Regions in Africa. AIDS Research and Human Retroviruses, 2014, 30, 623-625.	1.1	7
111	Phyloepidemiological Analysis Reveals that Viral Divergence Led to the Paucity of Simian Immunodeficiency Virus SIVmus/gsn/mon Infections in Wild Populations. Journal of Virology, 2017, 91, .	3.4	7
112	Dynamics of Antibodies to Ebolaviruses in an Eidolon helvum Bat Colony in Cameroon. Viruses, 2022, 14, 560.	3.3	7
113	Virological outcome among HIV-1 infected patients on first-line antiretroviral treatment in semi-rural HIV clinics in Togo. AIDS Research and Therapy, 2015, 12, 38.	1.7	6
114	Genetic diversity and transmission networks of HIV-1 strains among men having sex with men (MSM) in Lomé, Togo. Infection, Genetics and Evolution, 2016, 46, 279-285.	2.3	6
115	Serological Evidence of Ebola Virus Infection in Rural Guinea before the 2014 West African Epidemic Outbreak. American Journal of Tropical Medicine and Hygiene, 2018, 99, 425-427.	1.4	6
116	Added Value of an Anti-Ebola Serology for the Management of Clinically Suspected Ebola Virus Disease Patients Discharged as Negative in an Epidemic Context. Journal of Infectious Diseases, 2022, 226, 352-356.	4.0	5
117	Full-Length Genome Sequence of a Simian Immunodeficiency Virus from a Wild-Captured Sun-Tailed Monkey in Gabon Provides Evidence for a Species-Specific Monophyletic SIVsun Lineage. AIDS Research and Human Retroviruses, 2011, 27, 1237-1241.	1.1	4
118	Field evaluation of an open and polyvalent universal HIV-1/SIVcpz/SIVgor quantitative RT-PCR assay for HIV-1 viral load monitoring in comparison to Abbott RealTime HIV-1 in Cameroon. Journal of Virological Methods, 2016, 237, 121-126.	2.1	3
119	ldentification of a Novel Simian Immunodeficiency Virus-Infected African Green Monkey (<i>Chlorocebus tantalus</i>) Confirms that Tantalus Monkeys in Cameroon Are Infected with a Mosaic SIVagm Lineage. AIDS Research and Human Retroviruses, 2020, 36, 167-170.	1.1	2
120	Seroprevalence of IgG Antibodies Against Multiple Arboviruses in Bats from Cameroon, Guinea, and the Democratic Republic of Congo. Vector-Borne and Zoonotic Diseases, 2022, , .	1.5	2
121	Simian Immunodeficiency Virus Infections in the Wild. , 2014, , 37-67.		1
122	Full Genome Characterization of a New Simian Immune Deficiency Virus Lineage in a Naturally Infected <i>Cercopithecus ascanius whitesidei</i> in the Democratic Republic of Congo Reveals High Genetic Diversity Among Red-Tailed Monkeys in Central and Eastern Africa. AIDS Research and Human Retroviruses, 2017, 33, 735-739.	1.1	1
123	Reply to Zhang et al. Journal of Infectious Diseases, 2020, 222, 1065-1066.	4.0	1
124	High HIV burden and recent transmission chains in rural forest areas in southern Cameroon, where ancestors of HIV-1 have been identified in ape populations. Infection, Genetics and Evolution, 2020, 84, 104358.	2.3	1
125	Noninvasive western lowland gorilla's health monitoring: A decade of simian immunodeficiency virus surveillance in southern Cameroon. Ecology and Evolution, 2018, 8, 10698-10710.	1.9	0