John M Coffin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

5,011
papers

5,011
papers

6,000
ext. papers

5,011
papers

6,000
ext. citations

33
papers

70
g-index

5.49
ext. citations

avg, IF

L-index

#	Paper	IF	Citations
67	Clonal Expansion of Infected CD4+ T Cells in People Living with HIV. Viruses, 2021 , 13,	6.2	3
66	CpG Methylation Profiles of HIV-1 Pro-Viral DNA in Individuals on ART. Viruses, 2021, 13,	6.2	4
65	Integration in oncogenes plays only a minor role in determining the in vivo distribution of HIV integration sites before or during suppressive antiretroviral therapy. <i>PLoS Pathogens</i> , 2021 , 17, e10091	47.6	10
64	Early Emergence and Long-Term Persistence of HIV-Infected T-Cell Clones in Children. <i>MBio</i> , 2021 , 12,	7.8	5
63	Tracking HIV-1-Infected Cell Clones Using Integration Site-Specific qPCR. Viruses, 2021 , 13,	6.2	2
62	HIVIntact: a python-based tool for HIV-1 genome intactness inference. <i>Retrovirology</i> , 2021 , 18, 16	3.6	O
61	50th anniversary of the discovery of reverse transcriptase. <i>Molecular Biology of the Cell</i> , 2021 , 32, 91-97	3.5	1
60	An analytical pipeline for identifying and mapping the integration sites of HIV and other retroviruses. <i>BMC Genomics</i> , 2020 , 21, 216	4.5	8
59	HIV-1 viremia not suppressible by antiretroviral therapy can originate from large T cell clones producing infectious virus. <i>Journal of Clinical Investigation</i> , 2020 , 130, 5847-5857	15.9	31
58	Short Communication: HIV-DRLink: A Tool for Reporting Linked HIV-1 Drug Resistance Mutations in Large Single-Genome Data Sets Using the Stanford HIV Database. <i>AIDS Research and Human Retroviruses</i> , 2020 , 36, 942-947	1.6	1
57	HIV Proviral Sequence Database: A New Public Database for Near Full-Length HIV Proviral Sequences and Their Meta-Analyses. <i>AIDS Research and Human Retroviruses</i> , 2020 , 36, 1-3	1.6	8
56	Clonal expansion of SIV-infected cells in macaques on antiretroviral therapy is similar to that of HIV-infected cells in humans. <i>PLoS Pathogens</i> , 2019 , 15, e1007869	7.6	18
55	A9 A method to obtain full-length HIV proviral sequences and their sites of integration. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
54	A12 Modeling residual HIV replication and the emergence of drug resistance on ART. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
53	HIV Infected T Cells Can Proliferate Without Inducing Expression of the Integrated Provirus. <i>Frontiers in Microbiology</i> , 2019 , 10, 2204	5.7	21
52	Clones of infected cells arise early in HIV-infected individuals. JCI Insight, 2019, 4,	9.9	35
51	Linked dual-class HIV resistance mutations are associated with treatment failure. <i>JCI Insight</i> , 2019 , 4,	9.9	4

(2016-2019)

50	HIV-1 in lymph nodes is maintained by cellular proliferation during antiretroviral therapy. <i>Journal of Clinical Investigation</i> , 2019 , 129, 4629-4642	15.9	44
49	Combined HIV-1 sequence and integration site analysis informs viral dynamics and allows reconstruction of replicating viral ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 25891-25899	11.5	41
48	Gorillas have been infected with the HERV-K (HML-2) endogenous retrovirus much more recently than humans and chimpanzees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1337-1346	11.5	9
47	Ortervirales: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses. <i>Journal of Virology</i> , 2018 , 92,	6.6	56
46	Mechanisms of HERV-K (HML-2) Transcription during Human Mammary Epithelial Cell Transformation. <i>Journal of Virology</i> , 2018 , 92,	6.6	19
45	Promoter expression of HERV-K (HML-2) provirus-derived sequences is related to LTR sequence variation and polymorphic transcription factor binding sites. <i>Retrovirology</i> , 2018 , 15, 57	3.6	18
44	Lower pre-ART intra-participant HIV-1 pol diversity may not be associated with virologic failure in adults. <i>PLoS ONE</i> , 2018 , 13, e0190438	3.7	3
43	Nomenclature for endogenous retrovirus (ERV) loci. <i>Retrovirology</i> , 2018 , 15, 59	3.6	47
42	Single-cell analysis of HIV-1 transcriptional activity reveals expression of proviruses in expanded clones during ART. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E3659-E3668	11.5	87
41	Clinical Trial of the Anti-PD-L1 Antibody BMS-936559 in HIV-1 Infected Participants on Suppressive Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2017 , 215, 1725-1733	7	146
40	Proviruses with identical sequences comprise a large fraction of the replication-competent HIV reservoir. <i>PLoS Pathogens</i> , 2017 , 13, e1006283	7.6	137
39	Ongoing HIV Replication During ART Reconsidered. <i>Open Forum Infectious Diseases</i> , 2017 , 4, ofx173	1	38
38	No evidence of HIV replication in children on antiretroviral therapy. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3827-3834	15.9	44
37	Origin of Rebound Plasma HIV Includes Cells with Identical Proviruses That Are Transcriptionally Active before Stopping of Antiretroviral Therapy. <i>Journal of Virology</i> , 2016 , 90, 1369-76	6.6	92
36	Discovery of unfixed endogenous retrovirus insertions in diverse human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E2326-34	11.5	151
35	Clonally expanded CD4+ T cells can produce infectious HIV-1 in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 1883-8	11.5	225
34	Retrovirus Integration Database (RID): a public database for retroviral insertion sites into host genomes. <i>Retrovirology</i> , 2016 , 13, 47	3.6	25
33	Ultrasensitive single-genome sequencing: accurate, targeted, next generation sequencing of HIV-1 RNA. <i>Retrovirology</i> , 2016 , 13, 87	3.6	30

32	What Integration Sites Tell Us about HIV Persistence. <i>Cell Host and Microbe</i> , 2016 , 19, 588-98	23.4	47
31	The Discovery of Reverse Transcriptase. <i>Annual Review of Virology</i> , 2016 , 3, 29-51	14.6	23
30	Differential expression of HERV-K (HML-2) proviruses in cells and virions of the teratocarcinoma cell line Tera-1. <i>Viruses</i> , 2015 , 7, 939-68	6.2	43
29	Well-mixed plasma and tissue viral populations in RT-SHIV-infected macaques implies a lack of viral replication in the tissues during antiretroviral therapy. <i>Retrovirology</i> , 2015 , 12, 93	3.6	16
28	The discovery of HTLV-1, the first pathogenic human retrovirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 15525-9	11.5	22
27	The distribution of insertionally polymorphic endogenous retroviruses in breast cancer patients and cancer-free controls. <i>Retrovirology</i> , 2014 , 11, 62	3.6	26
26	Quantification of HIV-1 latency reversal in resting CD4+ T cells from patients on suppressive antiretroviral therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 7078-83	11.5	169
25	PAPNC, a novel method to calculate nucleotide diversity from large scale next generation sequencing data. <i>Journal of Virological Methods</i> , 2014 , 203, 73-80	2.6	12
24	Endogenous retroviruses and human cancer: is there anything to the rumors?. <i>Cell Host and Microbe</i> , 2014 , 15, 255-9	23.4	12
23	Improved single-copy assays for quantification of persistent HIV-1 viremia in patients on suppressive antiretroviral therapy. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 3944-51	9.7	70
22	False-positive HIV PCR test following ex vivo lentiviral gene transfer treatment of X-linked severe combined immunodeficiency vector. <i>Molecular Therapy</i> , 2014 , 22, 244-245	11.7	12
21	Lack of detectable HIV-1 molecular evolution during suppressive antiretroviral therapy. <i>PLoS Pathogens</i> , 2014 , 10, e1004010	7.6	156
20	HIV-1 expression within resting CD4+ T cells after multiple doses of vorinostat. <i>Journal of Infectious Diseases</i> , 2014 , 210, 728-35	7	191
19	Low-frequency nevirapine (NVP)-resistant HIV-1 variants are not associated with failure of antiretroviral therapy in women without prior exposure to single-dose NVP. <i>Journal of Infectious Diseases</i> , 2014 , 209, 703-10	7	27
18	Virions at the gates: receptors and the host-virus arms race. <i>PLoS Biology</i> , 2013 , 11, e1001574	9.7	20
17	HIV pathogenesis: dynamics and genetics of viral populations and infected cells. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2013 , 3, a012526	5.4	76
16	Role of low-frequency HIV-1 variants in failure of nevirapine-containing antiviral therapy in women previously exposed to single-dose nevirapine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 9202-7	11.5	47
15	The effect of raltegravir intensification on low-level residual viremia in HIV-infected patients on antiretroviral therapy: a randomized controlled trial. <i>PLoS Medicine</i> , 2010 , 7, e1000321	11.6	222

LIST OF PUBLICATIONS

14	Flexible use of nuclear import pathways by HIV-1. <i>Cell Host and Microbe</i> , 2010 , 7, 221-33	23.4	322
13	Attenuation by a thousand cuts. New England Journal of Medicine, 2008, 359, 2283-5	59.2	12
12	Effects of retroviruses on host genome function. Annual Review of Genetics, 2008, 42, 709-32	14.5	337
11	Retroviruses and AIDS: evolution and drug resistance. <i>Future HIV Therapy</i> , 2007 , 1, 243-245		
10	Multiple, linked human immunodeficiency virus type 1 drug resistance mutations in treatment-experienced patients are missed by standard genotype analysis. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 406-13	9.7	398
9	New real-time reverse transcriptase-initiated PCR assay with single-copy sensitivity for human immunodeficiency virus type 1 RNA in plasma. <i>Journal of Clinical Microbiology</i> , 2003 , 41, 4531-6	9.7	485
8	Evidence for genomic rearrangements mediated by human endogenous retroviruses during primate evolution. <i>Nature Genetics</i> , 2001 , 29, 487-9	36.3	165
7	The dangers of xenotransplantation. <i>Nature Medicine</i> , 1995 , 1, 1100	50.5	57
6	Multifactorial inheritance of neural tube defects: localization of the major gene and recognition of modifiers in ct mutant mice. <i>Nature Genetics</i> , 1994 , 6, 357-62	36.3	109
5			109 297
	Linkage of Mls genes to endogenous mammary tumour viruses of inbred mice. <i>Nature</i> , 1991 , 349, 526-8		
5	modifiers in ct mutant mice. <i>Nature Genetics</i> , 1994 , 6, 357-62 Linkage of Mls genes to endogenous mammary tumour viruses of inbred mice. <i>Nature</i> , 1991 , 349, 526-8 Molecular mechanisms of nucleic acid integration. <i>Journal of Medical Virology</i> , 1990 , 31, 43-9	50.4	297
5	Linkage of Mls genes to endogenous mammary tumour viruses of inbred mice. <i>Nature</i> , 1991 , 349, 526-8 Molecular mechanisms of nucleic acid integration. <i>Journal of Medical Virology</i> , 1990 , 31, 43-9 Too high a price. <i>Nature</i> , 1989 , 340, 259-259 Microbiology: The Microbe 1984. Cambridge University Press, New York, 1984. In two volumes.	50.4	297