

# Brian T Foley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2915138/publications.pdf>

Version: 2024-02-01

105  
papers

9,435  
citations

117625  
34  
h-index

46799  
89  
g-index

113  
all docs

113  
docs citations

113  
times ranked

15706  
citing authors

#	ARTICLE	IF	CITATIONS
1	The emergence and transmission dynamics of HIV-1 CRF07_BC in Mainland China. <i>Virus Evolution</i> , 2022, 8, veac014.	4.9	5
2	Fast Evaluation of Viral Emerging Risks (FEVER): A computational tool for biosurveillance, diagnostics, and mutation typing of emerging viral pathogens. <i>PLOS Global Public Health</i> , 2022, 2, e0000207.	1.6	1
3	How Does Administrative Data Compare with Census Data for the Measurement of Internal Migration? The Case of Northern Ireland, 2001â€“2011. <i>Applied Spatial Analysis and Policy</i> , 2021, 14, 659-677.	2.0	3
4	Sequence Length of HIV-1 Subtype B Increases over Time: Analysis of a Cohort of Patients with Hemophilia over 30 Years. <i>Viruses</i> , 2021, 13, 806.	3.3	3
5	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	11.0	73
6	Prevalence of gp160 polymorphisms known to be related to decreased susceptibility to temsavir in different subtypes of HIV-1 in the Los Alamos National Laboratory HIV Sequence Database. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2958-2964.	3.0	8
7	Optical Biosensor Platforms Display Varying Sensitivity for the Direct Detection of Influenza RNA. <i>Biosensors</i> , 2021, 11, 367.	4.7	5
8	Updated HIV-1 Consensus Sequences Change but Stay Within Similar Distance From Worldwide Samples. <i>Frontiers in Microbiology</i> , 2021, 12, 828765.	3.5	8
9	Origin and evolution of HIV-1 subtype A6. <i>PLoS ONE</i> , 2021, 16, e0260604.	2.5	10
10	Emergence of SARS-CoV-2 through recombination and strong purifying selection. <i>Science Advances</i> , 2020, 6, .	10.3	307
11	Major Revisions in Arthropod Phylogeny Through Improved Supermatrix, With Support for Two Possible Waves of Land Invasion by Chelicerates. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090373.	1.2	19
12	Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus. <i>Cell</i> , 2020, 182, 812-827.e19.	28.9	3,551
13	Evolutionary history, potential intermediate animal host, and crossâ€“species analyses of SARSâ€“CoVâ€“2. <i>Journal of Medical Virology</i> , 2020, 92, 602-611.	5.0	350
14	HIV-1 recombinant forms in immigrants regularly residing in Milan, northern Italy. <i>Infection</i> , 2020, 48, 553-558.	4.7	8
15	Impact of HIV-1 subtype and Korean Red Ginseng on AIDS progression: comparison of subtype B and subtype D. <i>Journal of Ginseng Research</i> , 2019, 43, 312-318.	5.7	9
16	Characterization of HIV-1 Subtypes Among South Sudanese Patients. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 968-971.	1.1	4
17	Persistent Viral Reservoirs in Lymphoid Tissues in SIV-Infected Rhesus Macaques of Chinese-Origin on Suppressive Antiretroviral Therapy. <i>Viruses</i> , 2019, 11, 105.	3.3	22
18	Genetic Analysis of the Full-Length gag Gene from the Earliest Korean Subclade B of HIV-1: An Outbreak among Korean Hemophiliacs. <i>Viruses</i> , 2019, 11, 545.	3.3	2

#	ARTICLE	IF	CITATIONS
19	Detection of Human Immunodeficiency Virus Type 1 (HIV-1) Antisense Protein (ASP) RNA Transcripts in Patients by Strand-Specific RT-PCR. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	3
20	Detection of antisense protein (ASP) RNA transcripts in individuals infected with human immunodeficiency virus type 1 (HIV-1). <i>Journal of General Virology</i> , 2019, 100, 863-876.	2.9	15
21	Origin and Spread of HIV-1 Subtype B Among Heterosexual Individuals in Bulgaria. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 244-253.	1.1	6
22	High Prevalence of Non-B HIV-1 Subtypes in Overseas Sailors and Prostitutes in Korea. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 347-353.	1.1	7
23	Persistence of SIV in the brain of SIV-infected Chinese rhesus macaques with or without antiretroviral therapy. <i>Journal of NeuroVirology</i> , 2018, 24, 62-74.	2.1	19
24	HIV-2 Infection in a Migrant from Gambia: The History of the Disease Combined with Phylogenetic Analysis Revealed the Real Source of Infection. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 1090-1094.	1.1	3
25	Molecular epidemiology of HIV-1 subtype A in former Soviet Union countries. <i>PLoS ONE</i> , 2018, 13, e0191891.	2.5	25
26	Administrative Data Quality: Investigating Record-Level Address Accuracy in the Northern Ireland Health Register. <i>Journal of Official Statistics</i> , 2018, 34, 55-81.	0.4	3
27	HIV and SIV Evolution. , 2017, , 71-92.		2
28	Zika Virus and HIV/AIDS. , 2017, , 731-750.		0
29	Signature pattern analysis for the full-length env gene of the earliest Korean subclade B of HIV-1: outbreak among Korean hemophiliacs. <i>Virus Genes</i> , 2017, 53, 789-796.	1.6	4
30	Signature pattern and phylogenetic analysis of full-length env genes in 20 hemophiliacs infected with Korean subclade of HIV-1 subtype B. <i>Virus Evolution</i> , 2017, 3, vew036.	4.9	1
31	The HIV-1 late domain-2 S40A polymorphism in antiretroviral (or ART)-exposed individuals influences protease inhibitor susceptibility. <i>Retrovirology</i> , 2016, 13, 64.	2.0	4
32	Primate immunodeficiency virus classification and nomenclature: Review. <i>Infection, Genetics and Evolution</i> , 2016, 46, 150-158.	2.3	47
33	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. <i>BMC Genomics</i> , 2016, 17, 180.	2.8	71
34	Integrated sequence and immunology filovirus database at Los Alamos. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw047.	3.0	3
35	Genetic diversity within the botulinum neurotoxin-producing bacteria and their neurotoxins. <i>Toxicon</i> , 2015, 107, 2-8.	1.6	65
36	Genomic sequences of six botulinum neurotoxin-producing strains representing three clostridial species illustrate the mobility and diversity of botulinum neurotoxin genes. <i>Infection, Genetics and Evolution</i> , 2015, 30, 102-113.	2.3	70

#	ARTICLE	IF	CITATIONS
37	Genetic Characterization of Near Full Length SIVdrl Genomes from Four Captive Drills (Mandrillus Tj ETQq1 1 0.784314 rgBT /Overl	1.1	0
38	CATNAP: a tool to compile, analyze and tally neutralizing antibody panels. Nucleic Acids Research, 2015, 43, W213-W219.	14.5	118
39	Zika Virus. , 2015, , 477-500.		5
40	What Is the Epidemiology of Human Mammary Tumor Virus?. International Journal of Gynecological Cancer, 2014, 24, 382.1-382.	2.5	0
41	First Report on a T69-ins Insertion in CRF06_cpx HIV Type 1. AIDS Research and Human Retroviruses, 2013, 29, 1079-1084.	1.1	6
42	Laser Capture Microdissection Assessment of Virus Compartmentalization in the Central Nervous Systems of Macaques Infected with Neurovirulent Simian Immunodeficiency Virus. Journal of Virology, 2013, 87, 8896-8908.	3.4	26
43	An HIV Type 2 Case Series in Italy: A Phylogenetic Analysis. AIDS Research and Human Retroviruses, 2013, 29, 1254-1259.	1.1	6
44	Phylogenetic Analysis of Near Full-Length HIV Type 1 Genomic Sequences from 21 Korean Individuals. AIDS Research and Human Retroviruses, 2013, 29, 738-743.	1.1	8
45	Near Full-Length Sequence Analysis of HIV Type 1 BF Recombinants from Italy. AIDS Research and Human Retroviruses, 2012, 28, 299-303.	1.1	2
46	Phylogenetic Analysis of the Earliest nef Gene from Hemophiliacs and Local Controls in Korea. BioResearch Open Access, 2012, 1, 41-49.	2.6	9
47	Nonrandom Distribution of Cryptic Repeating Triplets of Purines and Pyrimidines (RNY) <sub>n</sub> in gp120 of HIV Type1. AIDS Research and Human Retroviruses, 2012, 28, 493-504.	1.1	0
48	Recombination Between Variants from Genital Tract and Plasma: Evolution of Multidrug-Resistant HIV Type 1. AIDS Research and Human Retroviruses, 2012, 28, 1766-1774.	1.1	10
49	Designing and Testing Broadly-Protective Filoviral Vaccines Optimized for Cytotoxic T-Lymphocyte Epitope Coverage. PLoS ONE, 2012, 7, e44769.	2.5	20
50	Molecular evidence of HIV-1 transmission in 20 Korean individuals with haemophilia: phylogenetic analysis of the vif gene. Haemophilia, 2012, 18, 291-299.	2.1	10
51	Characterization of full-length HIV-1 CRF17_BF genomes and comparison to the prototype CRF12_BF strains. Infection, Genetics and Evolution, 2012, 12, 443-447.	2.3	9
52	Diversity of HIV-1 subtype C strains isolated in Romania. Infection, Genetics and Evolution, 2011, 11, 270-275.	2.3	10
53	Analysis of Clostridium botulinum Serotype E Strains by Using Multilocus Sequence Typing, Amplified Fragment Length Polymorphism, Variable-Number Tandem-Repeat Analysis, and Botulinum Neurotoxin Gene Sequencing. Applied and Environmental Microbiology, 2011, 77, 8625-8634.	3.1	53
54	Phylogenetic Analysis of Full-Length pol Gene from Korean Hemophiliacs and Plasma Donors Infected with Korean Subclade B of HIV Type 1. AIDS Research and Human Retroviruses, 2011, 27, 613-621.	1.1	17

#	ARTICLE	IF	CITATIONS
55	AIDS Research Pioneer Gerry Myers Dies. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 453-454.	1.1	0
56	The role of recombination in the emergence of a complex and dynamic HIV epidemic. <i>Retrovirology</i> , 2010, 7, 25.	2.0	110
57	Evolution and recombination of genes encoding HIV-1 drug resistance and tropism during antiretroviral therapy. <i>Virology</i> , 2010, 404, 5-20.	2.4	29
58	Isolated norovirus GII.7 strain within an extended GII.4 outbreak. <i>Journal of Medical Virology</i> , 2010, 82, 1058-1064.	5.0	9
59	Comment on "The Origins of Sexually Transmitted HIV Among Men Who Have Sex with Men". <i>Science Translational Medicine</i> , 2010, 2, 50le1; author reply 50lr1.	12.4	6
60	HIV-1 subtype distribution in the Gambia and the significant presence of CRF49_cpx, a novel circulating recombinant form. <i>Retrovirology</i> , 2010, 7, 82.	2.0	11
61	The Polymorphic Nature of HIV Type 1envV4 Affects the Patterns of Potential N-Glycosylation Sites in Proviral DNA at the Intrahost Level. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 199-206.	1.1	10
62	Complex Mosaic Composition of Near Full-Length Genomes of Two NED (NIH-ENVA-DOD) Subtype Panel HIV Type 1 Strains, BCF-Dioum and BCF-Kita, Originating from the Democratic Republic of Congo (DRC). <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 1039-1043.	1.1	3
63	Recombination and insertion events involving the botulinum neurotoxin complex genes in <i>Clostridium botulinum</i> types A, B, E and F and <i>Clostridium butyricum</i> type E strains. <i>BMC Biology</i> , 2009, 7, 66.	3.8	141
64	Adaptive Evolution of Simian Immunodeficiency Viruses Isolated from 2 Conventionalâ€Progressor Macaques with Encephalitis. <i>Journal of Infectious Diseases</i> , 2008, 197, 1695-1700.	4.0	7
65	HIVâ€™ Drug Resistance in Variants from the Female Genital Tract and Plasma. <i>Journal of Infectious Diseases</i> , 2007, 195, 535-545.	4.0	34
66	Interaction of endosialin/TEM1 with extracellular matrix proteins mediates cell adhesion and migration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17965-17970.	7.1	122
67	Founder Effects in the Assessment of HIV Polymorphisms and HLA Allele Associations. <i>Science</i> , 2007, 315, 1583-1586.	12.6	234
68	Genetic Diversity among Botulinum Neurotoxin-Producing Clostridial Strains. <i>Journal of Bacteriology</i> , 2007, 189, 818-832.	2.2	352
69	Analysis of the Neurotoxin Complex Genes in <i>Clostridium botulinum</i> A1-A4 and B1 Strains: BoNT/A3, /Ba4 and /B1 Clusters Are Located within Plasmids. <i>PLoS ONE</i> , 2007, 2, e1271.	2.5	154
70	Molecular epidemiologic study of a human immunodeficiency virus 1 outbreak in haemophiliacs B infected through clotting factor 9 after 1990. <i>Vox Sanguinis</i> , 2007, 92, 113-120.	1.5	21
71	Complex patterns of the HIV-1 epidemic in Kuala Lumpur, Malaysia: Evidence for expansion of circulating recombinant form CRF33_01B and detection of multiple other recombinants. <i>Virology</i> , 2007, 367, 288-297.	2.4	20
72	Kinetic studies of HIV-1 and HIV-2 envelope glycoprotein-mediated fusion. <i>Retrovirology</i> , 2006, 3, 90.	2.0	29

#	ARTICLE	IF	CITATIONS
73	Potential for HIV transmission through unsafe injections. <i>Aids</i> , 2006, 20, 1074-1076.	2.2	19
74	A comprehensive system for consistent numbering of HCV sequences, proteins and epitopes. <i>Hepatology</i> , 2006, 44, 1355-1361.	7.3	105
75	Consistent Patterns of Change during the Divergence of Human Immunodeficiency Virus Type 1 Envelope from That of the Inoculated Virus in Simian/Human Immunodeficiency Virus-Infected Macaques. <i>Journal of Virology</i> , 2006, 80, 999-1014.	3.4	55
76	Sensitivity and Specificity of the ViroSeq Human Immunodeficiency Virus Type 1 (HIV-1) Genotyping System for Detection of HIV-1 Drug Resistance Mutations by Use of an ABI PRISM 3100 Genetic Analyzer. <i>Journal of Clinical Microbiology</i> , 2005, 43, 813-817.	3.9	37
77	Human Immunodeficiency Virus Type 1 Genomic RNA Sequences in the Female Genital Tract and Blood: Compartmentalization and Intrapatient Recombination. <i>Journal of Virology</i> , 2005, 79, 353-363.	3.4	89
78	Tracing Axons of Peripheral Nerves in Rats: A Potential Technique to Study the Equine Recurrent Laryngeal Nerve. <i>Journal of Investigative Surgery</i> , 2004, 17, 151-162.	1.3	4
79	First report of human immunodeficiency virus transmission via an RNA-screened blood donation. <i>Vox Sanguinis</i> , 2004, 86, 171-177.	1.5	93
80	Identification of regions in multiple sequence alignments thermodynamically suitable for targeting by consensus oligonucleotides: application to HIV genome. <i>BMC Bioinformatics</i> , 2004, 5, 44.	2.6	3
81	Tracking global patterns of N-linked glycosylation site variation in highly variable viral glycoproteins: HIV, SIV, and HCV envelopes and influenza hemagglutinin. <i>Glycobiology</i> , 2004, 14, 1229-1246.	2.5	409
82	HIV-1 in genital tract and plasma of women: Compartmentalization of viral sequences, coreceptor usage, and glycosylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12972-12977.	7.1	109
83	Natural Polymorphisms of Protease in Protease Inhibitor-Naive HIV-1 Infected Patients in Korea: A Novel L63M in Subtype B. <i>AIDS Research and Human Retroviruses</i> , 2003, 19, 525-530.	1.1	13
84	Characterization and Comparison of Recombinant Simian Immunodeficiency Virus from Drill ( <i>Trichoposus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 4867-4880.	3.4	51
85	Identification of a Novel Clade of Human Immunodeficiency Virus Type 1 in Democratic Republic of Congo. <i>AIDS Research and Human Retroviruses</i> , 2002, 18, 817-823.	1.1	30
86	Homogeneous quasispecies in 16 out of 17 individuals during very early HIV-1 primary infection. <i>Aids</i> , 2002, 16, 189-195.	2.2	90
87	Human Immunodeficiency Virus Type 1 Subtype C Molecular Phylogeny: Consensus Sequence for an AIDS Vaccine Design?. <i>Journal of Virology</i> , 2002, 76, 5435-5451.	3.4	143
88	Diversity Considerations in HIV-1 Vaccine Selection. <i>Science</i> , 2002, 296, 2354-2360.	12.6	731
89	Characterization of Novel Simian Immunodeficiency Viruses from Red-Capped Mangabeys from Nigeria (SIVrcmNG409 and -NG411). <i>Journal of Virology</i> , 2001, 75, 12014-12027.	3.4	96
90	Importation of Multiple HIV Type 1 Strains into West Papua, Indonesia (Irian Jaya). <i>AIDS Research and Human Retroviruses</i> , 2001, 17, 1655-1659.	1.1	14

#	ARTICLE	IF	CITATIONS
91	Molecular Characterization of a Highly Divergent HIV Type 1 Isolate Obtained Early in the AIDS Epidemic from the Democratic Republic of Congo. AIDS Research and Human Retroviruses, 2001, 17, 1217-1222.	1.1	14
92	Identification of Human Immunodeficiency Virus Type 1 Subtype C Gag-, Tat-, Rev-, and Nef-Specific Elispot-Based Cytotoxic T-Lymphocyte Responses for AIDS Vaccine Design. Journal of Virology, 2001, 75, 9210-9228.	3.4	107
93	Phylogenetic Analysis of Reverse Transcriptase in Antiretroviral Drug-Naïve Korean HIV Type 1 Patients. AIDS Research and Human Retroviruses, 2001, 17, 1549-1554.	1.1	22
94	Sequence Note: HIV Type 1 A/J Recombinant with a Pronounced pol Gene Mosaicism. AIDS Research and Human Retroviruses, 2000, 16, 1015-1020.	1.1	19
95	Apparent Founder Effect during the Early Years of the San Francisco HIV Type 1 Epidemic (1978-1979). AIDS Research and Human Retroviruses, 2000, 16, 1463-1469.	1.1	28
96	Molecular Cloning and Phylogenetic Analysis of Human Immunodeficiency Virus Type 1 Subtype C: a Set of 23 Full-Length Clones from Botswana. Journal of Virology, 1999, 73, 4427-4432.	3.4	114
97	Sequence Note: HIV Type 1 gagD/envG Recombinants in Russia. AIDS Research and Human Retroviruses, 1998, 14, 1597-1599.	1.1	9
98	Sequence Note: Analysis of Sequence Diversity in the C2-V3 Regions of the External Glycoproteins of HIV Type 1 in Singapore. AIDS Research and Human Retroviruses, 1998, 14, 1601-1604.	1.1	9
99	Maintaining the integrity of human immunodeficiency virus sequence databases. Journal of Virology, 1996, 70, 5720-5730.	3.4	126
100	Analysis of mutations in alleles of the fur gene from an endoprotease-deficient chinese hamster ovary cell strain. Somatic Cell and Molecular Genetics, 1995, 21, 1-18.	0.7	36
101	Mutations in the Elongation Factor 2 Gene Which Confer Resistance to Diphtheria Toxin and Pseudomonas Exotoxin A. Journal of Biological Chemistry, 1995, 270, 23218-23225.	3.4	48
102	RT-PCR with affinity-captured mRNA. Nucleic Acids Research, 1993, 21, 2281-2281.	14.5	4
103	A mutation in codon 717 of the CHO-K1 elongation factor 2 gene prevents the first step in the biosynthesis of diphthamide. Somatic Cell and Molecular Genetics, 1992, 18, 227-231.	0.7	19
104	Cross-sections of the GenBank® database. Trends in Genetics, 1986, 2, 233-238.	6.7	10
105	Epidemiological and Immunological Implications of the Global Variability of HIV-1. , 0, , 1-32.		5