

Andrew J Leigh Brown

List of Publications by Year in descending order

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83
papers

5,757
citations

81900

39
h-index

79698

73
g-index

86
all docs

86
docs citations

86
times ranked

5937
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular evidence for genetic mixing of Arctic and Antarctic subpolar populations of planktonic foraminifers. <i>Nature</i> , 2000, 405, 43-47.	27.8	330
2	Episodic Sexual Transmission of HIV Revealed by Molecular Phylodynamics. <i>PLoS Medicine</i> , 2008, 5, e50.	8.4	326
3	Automated analysis of phylogenetic clusters. <i>BMC Bioinformatics</i> , 2013, 14, 317.	2.6	305
4	Heterogeneous clearance rates of long-lived lymphocytes infected with HIV: Intrinsic stability predicts lifelong persistence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4819-4824.	7.1	224
5	Adaptation to Different Human Populations by HIV-1 Revealed by Codon-Based Analyses. <i>PLoS Computational Biology</i> , 2006, 2, e62.	3.2	209
6	HIV-TRACE (TRANSMISSION Cluster Engine): a Tool for Large Scale Molecular Epidemiology of HIV-1 and Other Rapidly Evolving Pathogens. <i>Molecular Biology and Evolution</i> , 2018, 35, 1812-1819.	8.9	206
7	Phylodynamics of Infectious Disease Epidemics. <i>Genetics</i> , 2009, 183, 1421-1430.	2.9	200
8	The Global Transmission Network of HIV-1. <i>Journal of Infectious Diseases</i> , 2014, 209, 304-313.	4.0	194
9	Transmission Network Parameters Estimated From HIV Sequences for a Nationwide Epidemic. <i>Journal of Infectious Diseases</i> , 2011, 204, 1463-1469.	4.0	184
10	Transmission Fitness of Drug-Resistant Human Immunodeficiency Virus and the Prevalence of Resistance in the Antiretroviral-Treated Population. <i>Journal of Infectious Diseases</i> , 2003, 187, 683-686.	4.0	162
11	Multiple sites in HIV-1 reverse transcriptase associated with virological response to combination therapy. <i>Aids</i> , 2000, 14, 31-36.	2.2	160
12	Molecular Phylodynamics of the Heterosexual HIV Epidemic in the United Kingdom. <i>PLoS Pathogens</i> , 2009, 5, e1000590.	4.7	155
13	Evolution of Lamivudine Resistance in Human Immunodeficiency Virus Type 1-Infected Individuals: the Relative Roles of Drift and Selection. <i>Journal of Virology</i> , 2000, 74, 6262-6268.	3.4	152
14	An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009, 5, e1000581.	3.2	151
15	Planktic foraminiferal molecular evolution and their polyphyletic origins from benthic taxa. <i>Marine Micropaleontology</i> , 1997, 30, 251-266.	1.2	117
16	Dynamics of the Emergence and Establishment of a Newly Dominant Genotype of Japanese Encephalitis Virus throughout Asia. <i>Journal of Virology</i> , 2014, 88, 4522-4532.	3.4	110
17	A Maximum Likelihood Method for Detecting Directional Evolution in Protein Sequences and Its Application to Influenza A Virus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1809-1824.	8.9	106
18	Detection, quantification and sequencing of HIV-1 from the plasma of seropositive individuals and from factor VIII concentrates. <i>Aids</i> , 1991, 5, 675-682.	2.2	105

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19	HIV-1: Gambling on the evolution of drug resistance?. <i>Nature Medicine</i> , 1997, 3, 268-271.	30.7	100
20	Molecular Investigation of Human Immunodeficiency Virus (HIV) Infection in a Patient of an HIV-Infected Surgeon. <i>Journal of Infectious Diseases</i> , 1993, 167, 1411-1414.	4.0	96
21	Phylogeography of Japanese Encephalitis Virus: Genotype Is Associated with Climate. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2411.	3.0	96
22	Simple Epidemiological Dynamics Explain Phylogenetic Clustering of HIV from Patients with Recent Infection. <i>PLoS Computational Biology</i> , 2012, 8, e1002552.	3.2	89
23	Phylogenetic Studies of Transmission Dynamics in Generalized HIV Epidemics. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 67, 181-195.	2.1	80
24	Human Immunodeficiency Virus Type 1 Clade B Superinfection: Evidence for Differential Immune Containment of Distinct Clade B Strains. <i>Journal of Virology</i> , 2005, 79, 860-868.	3.4	79
25	Reassortment patterns of avian influenza virus internal segments among different subtypes. <i>BMC Evolutionary Biology</i> , 2014, 14, 16.	3.2	77
26	Detection of Mammalian Virulence Determinants in Highly Pathogenic Avian Influenza H5N1 Viruses: Multivariate Analysis of Published Data. <i>Journal of Virology</i> , 2009, 83, 9901-9910.	3.4	76
27	Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions. <i>Aids</i> , 2014, 28, 1967-1975.	2.2	69
28	Transmission of Non-B HIV Subtypes in the United Kingdom Is Increasingly Driven by Large Non-Heterosexual Transmission Clusters. <i>Journal of Infectious Diseases</i> , 2016, 213, 1410-1418.	4.0	67
29	Reduced Susceptibility of Human Immunodeficiency Virus Type 1 (HIV-1) from Patients with Primary HIV Infection to Nonnucleoside Reverse Transcriptase Inhibitors Is Associated with Variation at Novel Amino Acid Sites. <i>Journal of Virology</i> , 2000, 74, 10269-10273.	3.4	66
30	Differences in HIV-1 pol Sequences From Female Genital Tract and Blood During Antiretroviral Therapy. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2003, 34, 37-44.	2.1	57
31	Evolution of the Structural Proteins of Human Immunodeficiency Virus: Selective Constraints on Nucleotide Substitution. <i>AIDS Research and Human Retroviruses</i> , 1988, 4, 399-407.	1.1	56
32	Transposition of the I element and <i>copia</i> in a natural population of <i>Drosophila melanogaster</i> . <i>Genetical Research</i> , 1987, 49, 121-128.	0.9	55
33	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	8.9	53
34	Viral Dynamics during Structured Treatment Interruptions of Chronic Human Immunodeficiency Virus Type 1 Infection. <i>Journal of Virology</i> , 2002, 76, 968-979.	3.4	52
35	Adaptation to Human Populations Is Revealed by Within-Host Polymorphisms in HIV-1 and Hepatitis C Virus. <i>PLoS Pathogens</i> , 2007, 3, e45.	4.7	51
36	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 259-261.	9.1	51

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37	Recent and Rapid Transmission of HIV Among People Who Inject Drugs in Scotland Revealed Through Phylogenetic Analysis. <i>Journal of Infectious Diseases</i> , 2018, 217, 1875-1882.	4.0	50
38	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411.	12.8	50
39	Time trends in drug resistant HIV-1 infections in the United Kingdom up to 2009: multicentre observational study. <i>BMJ</i> , The, 2012, 345, e5253-e5253.	6.0	44
40	Evidence for Positive Selection Driving the Evolution of HIV-1 env under Potent Antiviral Therapy. <i>Virology</i> , 2001, 284, 250-258.	2.4	42
41	Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , 2012, 93, 2326-2336.	2.9	42
42	The Contribution of Viral Genotype to Plasma Viral Set-Point in HIV Infection. <i>PLoS Pathogens</i> , 2014, 10, e1004112.	4.7	42
43	The polymerase chain reaction in the diagnosis of vertically transmitted HIV infection. <i>Aids</i> , 1990, 4, 393-398.	2.2	40
44	The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120382.	4.0	40
45	Molecular epidemiological analysis of HIV in sexual networks in Uganda. <i>Aids</i> , 1998, 12, 285-290.	2.2	39
46	Non-disclosed men who have sex with men in UK HIV transmission networks: phylogenetic analysis of surveillance data. <i>Lancet HIV</i> , the, 2018, 5, e309-e316.	4.7	38
47	Insertion-deletion variation at the yellow-achaete-scute region in two natural populations of <i>Drosophila melanogaster</i> . <i>Genetical Research</i> , 1989, 53, 7-15.	0.9	34
48	Analysis of the history and spread of HIV-1 in Uganda using phylodynamics. <i>Journal of General Virology</i> , 2015, 96, 1890-1898.	2.9	34
49	The HIV Epidemic: High-Income Countries. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2012, 2, a007195-a007195.	6.2	33
50	Quantifying predictors for the spatial diffusion of avian influenza virus in China. <i>BMC Evolutionary Biology</i> , 2017, 17, 16.	3.2	31
51	HIV phylogenetics. <i>BMJ: British Medical Journal</i> , 2007, 335, 460-461.	2.3	30
52	Evolution of Zidovudine Resistance-Associated Genotypes in Human Immunodeficiency Virus Type 1-Infected Patients. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1996, 12, 6-18.	0.3	29
53	Mismatched Human Leukocyte Antigen Alleles Protect Against Heterosexual HIV Transmission. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2001, 27, 277-280.	2.1	28
54	Mismatched Human Leukocyte Antigen Alleles Protect Against Heterosexual HIV Transmission. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2001, 27, 277-280.	2.1	28

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55	Associations between Amino Acids in the Evolution of HIV Type 1 Protease Sequences under Indinavir Therapy. <i>AIDS Research and Human Retroviruses</i> , 1999, 15, 247-253.	1.1	27
56	Determining the Phylogenetic and Phylogeographic Origin of Highly Pathogenic Avian Influenza (H7N3) in Mexico. <i>PLoS ONE</i> , 2014, 9, e107330.	2.5	25
57	A high HIV-1 strain variability in London, UK, revealed by full-genome analysis: Results from the ICONIC project. <i>PLoS ONE</i> , 2018, 13, e0192081.	2.5	25
58	Evolutionary interactions between haemagglutinin and neuraminidase in avian influenza. <i>BMC Evolutionary Biology</i> , 2013, 13, 222.	3.2	24
59	Estimating the Rate of Intersubtype Recombination in Early HIV-1 Group M Strains. <i>Journal of Virology</i> , 2013, 87, 1967-1973.	3.4	24
60	Genetic Basis of Hypersusceptibility to Protease Inhibitors and Low Replicative Capacity of Human Immunodeficiency Virus Type 1 Strains in Primary Infection. <i>Journal of Virology</i> , 2004, 78, 2242-2246.	3.4	23
61	Novel HIV-1 Recombinants Spreading across Multiple Risk Groups in the United Kingdom: The Identification and Phylogeography of Circulating Recombinant Form (CRF) 50_A1D. <i>PLoS ONE</i> , 2014, 9, e83337.	2.5	23
62	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016, 6, 39489.	3.3	23
63	Sequence data as evidence. <i>Nature</i> , 1993, 364, 766-766.	27.8	21
64	Early evolutionary origin of the planktic foraminifera inferred from small subunit rDNA sequence comparisons. <i>Journal of Molecular Evolution</i> , 1996, 43, 672-677.	1.8	20
65	Estimating selection pressures on HIV using phylogenetic likelihood models. <i>Statistics in Medicine</i> , 2008, 27, 4779-4789.	1.6	19
66	Intercontinental Dispersal of HIV-1 Subtype B Associated with Transmission among Men Who Have Sex with Men in Japan. <i>Journal of Virology</i> , 2014, 88, 9864-9876.	3.4	18
67	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	1.1	18
68	A Direct Comparison of Two Densely Sampled HIV Epidemics: The UK and Switzerland. <i>Scientific Reports</i> , 2016, 6, 32251.	3.3	17
69	HIV-1 DNA Is Maintained in Antigen-Specific CD4+ T Cell Subsets in Patients on Long-Term Antiretroviral Therapy Regardless of Recurrent Antigen Exposure. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 112-120.	1.1	16
70	Phenotypic Hypersusceptibility to Multiple Protease Inhibitors and Low Replicative Capacity in Patients Who Are Chronically Infected with Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2005, 79, 5907-5913.	3.4	14
71	Origin and fate of A/H1N1 influenza in Scotland during 2009. <i>Journal of General Virology</i> , 2012, 93, 1253-1260.	2.9	14
72	Molecular evolution: On the origin of the Alu family of repeated sequences. <i>Nature</i> , 1984, 312, 106-106.	27.8	11

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73	Sero-Prevalence and Incidence of A/H1N1 2009 Influenza Infection in Scotland in Winter 2009â€“2010. PLoS ONE, 2011, 6, e20358.	2.5	11
74	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. Virus Evolution, 2020, 6, veaa004.	4.9	9
75	Genetic basis of variation in tenofovir drug susceptibility in HIV-1. Aids, 2008, 22, 1113-1123.	2.2	7
76	Reconstructing the HIV-1 CRF02_AG and CRF06_cpx epidemics in Burkina Faso and West Africa using early samples. Infection, Genetics and Evolution, 2016, 46, 209-218.	2.3	6
77	Evolutionary relationships of the human immunodeficiency viruses. Trends in Ecology and Evolution, 1990, 5, 177-181.	8.7	5
78	Phylogenetic Networks and Parameters Inferred from HIV Nucleotide Sequences of High-Risk and General Population Groups in Uganda: Implications for Epidemic Control. Viruses, 2021, 13, 970.	3.3	5
79	The Molecular Epidemiology and Transmission Dynamics of HIV Type 1 in a General Population Cohort in Uganda. Viruses, 2020, 12, 1283.	3.3	4
80	Employing phylogenetic tree shape statistics to resolve the underlying host population structure. BMC Bioinformatics, 2021, 22, 546.	2.6	3
81	Relationships among isolates of HIV. Nature, 1988, 335, 675-675.	27.8	2
82	Gut reactions of lysozyme. Nature, 1987, 330, 315-316.	27.8	1
83	Association of antiretroviral resistance genotypes with response to therapy--comparison of three models. Antiviral Therapy, 2002, 7, 151-7.	1.0	1