

Damien C Tully

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

6,693
citations

257101

24
h-index

161609

54
g-index

63
all docs

63
docs citations

63
times ranked

14949
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Genetically Related HCV Infections Among Self-Described Injecting Partnerships. <i>Clinical Infectious Diseases</i> , 2022, 74, 993-1003.	2.9	3
2	The impact of COVID-19 vaccination in prisons in England and Wales: a metapopulation model. <i>BMC Public Health</i> , 2022, 22, 1003.	1.2	4
3	Early prediction of mortality risk among patients with severe COVID-19, using machine learning. <i>International Journal of Epidemiology</i> , 2021, 49, 1918-1929.	0.9	92
4	Hepatitis C Virus Transmission Clusters in Public Health and Correctional Settings, Wisconsin, USA, 2016–2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 480-489.	2.0	3
5	Quarantine and testing strategies in contact tracing for SARS-CoV-2: a modelling study. <i>Lancet Public Health</i> , The, 2021, 6, e175-e183.	4.7	156
6	Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. <i>Science</i> , 2021, 372, .	6.0	2,103
7	Prevalence of transmitted HIV-1 drug resistance among treatment-naïve individuals in China, 2000-2016. <i>Archives of Virology</i> , 2021, 166, 2451-2460.	0.9	10
8	Epigenetic scars of CD8+ T cell exhaustion persist after cure of chronic infection in humans. <i>Nature Immunology</i> , 2021, 22, 1020-1029.	7.0	124
9	The potential health and economic value of SARS-CoV-2 vaccination alongside physical distancing in the UK: a transmission model-based future scenario analysis and economic evaluation. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 962-974.	4.6	117
10	Differentiation of exhausted CD8+ T cells after termination of chronic antigen stimulation stops short of achieving functional T cell memory. <i>Nature Immunology</i> , 2021, 22, 1030-1041.	7.0	63
11	SARS-CoV-2 infection risk during delivery of childhood vaccination campaigns: a modelling study. <i>BMC Medicine</i> , 2021, 19, 198.	2.3	8
12	Estimating the impact of reopening schools on the reproduction number of SARS-CoV-2 in England, using weekly contact survey data. <i>BMC Medicine</i> , 2021, 19, 233.	2.3	24
13	Evolutionary characteristics and genetic transmission patterns of predominant HIV-1 subtypes among men who have sex with men in China. <i>International Journal of Infectious Diseases</i> , 2020, 90, 125-131.	1.5	15
14	Response strategies for COVID-19 epidemics in African settings: a mathematical modelling study. <i>BMC Medicine</i> , 2020, 18, 324.	2.3	66
15	Using a real-world network to model localized COVID-19 control strategies. <i>Nature Medicine</i> , 2020, 26, 1616-1622.	15.2	191
16	Routine childhood immunisation during the COVID-19 pandemic in Africa: a benefit–risk analysis of health benefits versus excess risk of SARS-CoV-2 infection. <i>The Lancet Global Health</i> , 2020, 8, e1264-e1272.	2.9	265
17	Effectiveness of isolation, testing, contact tracing, and physical distancing on reducing transmission of SARS-CoV-2 in different settings: a mathematical modelling study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1151-1160.	4.6	710
18	Global, regional, and national estimates of the population at increased risk of severe COVID-19 due to underlying health conditions in 2020: a modelling study. <i>The Lancet Global Health</i> , 2020, 8, e1003-e1017.	2.9	760

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19	Phylogenetic interpretation during outbreaks requires caution. <i>Nature Microbiology</i> , 2020, 5, 876-877.	5.9	64
20	Role of HCV Viremia in Corroborated HCV Transmission Events Within Young Adult Injecting Partnerships. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz125.	0.4	7
21	Lower Broadly Neutralizing Antibody Responses in Female Versus Male HIV-1 Infected Injecting Drug Users. <i>Viruses</i> , 2019, 11, 384.	1.5	6
22	Metagenomic Sequencing of HIV-1 in the Blood and Female Genital Tract Reveals Little Quasispecies Diversity during Acute Infection. <i>Journal of Virology</i> , 2019, 93, .	1.5	7
23	Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168.	9.4	96
24	<i>Mamu-B*17</i> ⁺ Rhesus Macaques Vaccinated with <i>env</i> , <i>vif</i> , and <i>nef</i> Manifest Early Control of SIVmac239 Replication. <i>Journal of Virology</i> , 2018, 92, .	1.5	11
25	Rare Control of SIVmac239 Infection in a Vaccinated Rhesus Macaque. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 843-858.	0.5	15
26	Interferon-I: The Piñce de Résistance of HIV-1 Transmission?. <i>Trends in Microbiology</i> , 2017, 25, 332-334.	3.5	0
27	Early Transcriptional Divergence Marks Virus-Specific Primary Human CD8+ T Cells in Chronic versus Acute Infection. <i>Immunity</i> , 2017, 47, 648-663.e8.	6.6	50
28	High resolution sequencing of hepatitis C virus reveals limited intra-hepatic compartmentalization in end-stage liver disease. <i>Journal of Hepatology</i> , 2017, 66, 28-38.	1.8	28
29	The epigenetic landscape of T cell exhaustion. <i>Science</i> , 2016, 354, 1165-1169.	6.0	694
30	Effect of scavenger receptor class B type I antagonist ITX5061 in patients with hepatitis C virus infection undergoing liver transplantation. <i>Liver Transplantation</i> , 2016, 22, 287-297.	1.3	30
31	Deep sequencing of hepatitis C virus reveals genetic compartmentalization in cerebrospinal fluid from cognitively impaired patients. <i>Liver International</i> , 2016, 36, 1418-1424.	1.9	22
32	Differences in the Selection Bottleneck between Modes of Sexual Transmission Influence the Genetic Composition of the HIV-1 Founder Virus. <i>PLoS Pathogens</i> , 2016, 12, e1005619.	2.1	97
33	Use of Dried Blood Spots to Elucidate Full-Length Transmitted/Founder HIV-1 Genomes. <i>Pathogens and Immunity</i> , 2016, 1, 129.	1.4	9
34	Vaccine-Induced Simian Immunodeficiency Virus-Specific CD8 ⁺ T-Cell Responses Focused on a Single Nef Epitope Select for Escape Variants Shortly after Infection. <i>Journal of Virology</i> , 2015, 89, 10802-10820.	1.5	30
35	Trace amounts of sporadically reappearing HCV RNA can cause infection. <i>Journal of Clinical Investigation</i> , 2014, 124, 3469-3478.	3.9	23
36	Characteristics of HCV Co-Infection among HIV Infected Individuals from an Area with High Risk of Blood-Borne Infections in Central China. <i>PLoS ONE</i> , 2014, 9, e94219.	1.1	6

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37	Low-Abundance Resistant Mutations in HIV-1 Subtype C Antiretroviral Therapy-Naive Individuals as Revealed by Pyrosequencing. <i>Current HIV Research</i> , 2013, 11, 43-49.	0.2	0
38	Low-Abundance Resistant Mutations in HIV-1 Subtype C Antiretroviral Therapy-Naive Individuals as Revealed by Pyrosequencing. <i>Current HIV Research</i> , 2013, 11, 43-49.	0.2	7
39	Low-abundance resistant mutations in HIV-1 subtype C antiretroviral therapy-naive individuals as revealed by pyrosequencing. <i>Current HIV Research</i> , 2013, 11, 43-49.	0.2	8
40	Whole Genome Deep Sequencing of HIV-1 Reveals the Impact of Early Minor Variants Upon Immune Recognition During Acute Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002529.	2.1	306
41	Vaccine-induced CD8+ T cells control AIDS virus replication. <i>Nature</i> , 2012, 491, 129-133.	13.7	165
42	Dynamics of Envelope Evolution in Clade C SHIV-Infected Pig-Tailed Macaques during Disease Progression Analyzed by Ultra-Deep Pyrosequencing. <i>PLoS ONE</i> , 2012, 7, e32827.	1.1	3
43	Chronology and evolution of the HIV-1 subtype C epidemic in Ethiopia. <i>Aids</i> , 2010, 24, 1577-1582.	1.0	26
44	Functional properties of the HIV-1 subtype C envelope glycoprotein associated with mother-to-child transmission. <i>Virology</i> , 2010, 400, 164-174.	1.1	41
45	Molecular determinants of HIV-1 subtype C coreceptor transition from R5 to R5X4. <i>Virology</i> , 2010, 407, 68-79.	1.1	19
46	Sequence diversity of hepatitis C virus 6a within the extended interferon sensitivity-determining region correlates with interferon-alpha/ribavirin treatment outcomes. <i>Virus Research</i> , 2010, 153, 44-49.	1.1	5
47	Short Communication: Antiretroviral Therapy Resistance Mutations Present in the HIV Type 1 Subtype C pol and env Regions from Therapy-Naive Patients in Zambia. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 795-803.	0.5	16
48	Restricted Genetic Diversity of HIV-1 Subtype C Envelope Glycoprotein from Perinatally Infected Zambian Infants. <i>PLoS ONE</i> , 2010, 5, e9294.	1.1	36
49	Shifts in the Selection-Drift Balance Drive the Evolution and Epidemiology of Foot-and-Mouth Disease Virus. <i>Journal of Virology</i> , 2009, 83, 781-790.	1.5	23
50	A comparative study of HIV-1 clade C env evolution in a Zambian infant with an infected rhesus macaque during disease progression. <i>Aids</i> , 2009, 23, 1817-1828.	1.0	8
51	The tale of a modern animal plague: Tracing the evolutionary history and determining the time-scale for foot and mouth disease virus. <i>Virology</i> , 2008, 382, 250-256.	1.1	50
52	A Study of the Coevolutionary Patterns Operating within the env Gene of the HIV-1 Group M Subtypes. <i>Molecular Biology and Evolution</i> , 2007, 24, 2787-2801.	3.5	41
53	Unravelling selection shifts among foot-and-mouth disease virus (FMDV) serotypes. <i>Evolutionary Bioinformatics</i> , 2007, 2, 211-25.	0.6	10
54	Unravelling Selection Shifts among Foot-and-Mouth Disease virus (FMDV) Serotypes. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	15