

Damien C Tully

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6042422/publications.pdf>

Version: 2024-02-01

54
papers

6,693
citations

257450

24
h-index

161849

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. | 5.8 | 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. | 2.9 | 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. | 1.9 | 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. | 4.3 | 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. | 10.0 | 156 |
| 6 | Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. <i>Science</i> , 2021, 372, . | 12.6 | 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. | 2.1 | 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. | 14.5 | 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. | 9.1 | 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. | 14.5 | 63 |
| 11 | SARS-CoV-2 infection risk during delivery of childhood vaccination campaigns: a modelling study. <i>BMC Medicine</i> , 2021, 19, 198. | 5.5 | 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. | 5.5 | 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. | 3.3 | 15 |
| 14 | Response strategies for COVID-19 epidemics in African settings: a mathematical modelling study. <i>BMC Medicine</i> , 2020, 18, 324. | 5.5 | 66 |
| 15 | Using a real-world network to model localized COVID-19 control strategies. <i>Nature Medicine</i> , 2020, 26, 1616-1622. | 30.7 | 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. | 6.3 | 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. | 9.1 | 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. | 6.3 | 760 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Phylogenetic interpretation during outbreaks requires caution. <i>Nature Microbiology</i> , 2020, 5, 876-877. | 13.3 | 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. | 0.9 | 7 |
| 21 | Lower Broadly Neutralizing Antibody Responses in Female Versus Male HIV-1 Infected Injecting Drug Users. <i>Viruses</i> , 2019, 11, 384. | 3.3 | 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, . | 3.4 | 7 |
| 23 | Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168. | 17.5 | 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, . | 3.4 | 11 |
| 25 | Rare Control of SIVmac239 Infection in a Vaccinated Rhesus Macaque. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 843-858. | 1.1 | 15 |
| 26 | Interferon-I: The Piñce de Résistance of HIV-1 Transmission?. <i>Trends in Microbiology</i> , 2017, 25, 332-334. | 7.7 | 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. | 14.3 | 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. | 3.7 | 28 |
| 29 | The epigenetic landscape of T cell exhaustion. <i>Science</i> , 2016, 354, 1165-1169. | 12.6 | 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. | 2.4 | 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. | 3.9 | 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. | 4.7 | 97 |
| 33 | Use of Dried Blood Spots to Elucidate Full-Length Transmitted/Founder HIV-1 Genomes. <i>Pathogens and Immunity</i> , 2016, 1, 129. | 3.1 | 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. | 3.4 | 30 |
| 35 | Trace amounts of sporadically reappearing HCV RNA can cause infection. <i>Journal of Clinical Investigation</i> , 2014, 124, 3469-3478. | 8.2 | 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. | 2.5 | 6 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 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. | 0.5 | 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. | 0.5 | 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. | 0.5 | 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. | 4.7 | 306 |
| 41 | Vaccine-induced CD8+ T cells control AIDS virus replication. <i>Nature</i> , 2012, 491, 129-133. | 27.8 | 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. | 2.5 | 3 |
| 43 | Chronology and evolution of the HIV-1 subtype C epidemic in Ethiopia. <i>Aids</i> , 2010, 24, 1577-1582. | 2.2 | 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. | 2.4 | 41 |
| 45 | Molecular determinants of HIV-1 subtype C coreceptor transition from R5 to R5X4. <i>Virology</i> , 2010, 407, 68-79. | 2.4 | 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. | 2.2 | 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. | 1.1 | 16 |
| 48 | Restricted Genetic Diversity of HIV-1 Subtype C Envelope Glycoprotein from Perinatally Infected Zambian Infants. <i>PLoS ONE</i> , 2010, 5, e9294. | 2.5 | 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. | 3.4 | 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. | 2.2 | 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. | 2.4 | 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. | 8.9 | 41 |
| 53 | Unravelling selection shifts among foot-and-mouth disease virus (FMDV) serotypes. <i>Evolutionary Bioinformatics</i> , 2007, 2, 211-25. | 1.2 | 10 |
| 54 | Unravelling Selection Shifts among Foot-and-Mouth Disease virus (FMDV) Serotypes. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200. | 1.2 | 15 |