

Charles P McClure

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

4,364
citations

304701
22
h-index

128286
60
g-index

67
all docs

67
docs citations

67
times ranked

9792
citing authors

#	ARTICLE	IF	CITATIONS
1	Real-World Outcomes of Direct-Acting Antiviral Treatment and Retreatment in United Kingdom-Based Patients Infected With Hepatitis C Virus Genotypes/Subtypes Endemic in Africa. <i>Journal of Infectious Diseases</i> , 2022, 226, 995-1004.	4.0	8
2	The Impact of Real-Time Whole-Genome Sequencing in Controlling Healthcare-Associated SARS-CoV-2 Outbreaks. <i>Journal of Infectious Diseases</i> , 2022, 225, 10-18.	4.0	25
3	Sero-reactivity to three distinct regions within the hepatitis C virus alternative reading frame protein (ARFP/core+1) in patients with chronic HCV genotype-3 infection. <i>Journal of General Virology</i> , 2022, 103, .	2.9	2
4	Simultaneous determination of HCV genotype and NS5B resistance associated substitutions using dried serum spots from São Paulo state, Brazil. <i>Access Microbiology</i> , 2022, 4, .	0.5	3
5	Enterovirus D68 epidemic, UK, 2018, was caused by subclades B3 and D1, predominantly in children and adults, respectively, with both subclades exhibiting extensive genetic diversity. <i>Microbial Genomics</i> , 2022, 8, .	2.0	2
6	Human parainfluenza 2 & 4: Clinical and genetic epidemiology in the UK, 2013–2017, reveals distinct disease features and co-circulating genomic subtypes. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 1122-1132.	3.4	3
7	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
8	Comparative effects of viral-transport-medium heat inactivation upon downstream SARS-CoV-2 detection in patient samples. <i>Journal of Medical Microbiology</i> , 2021, 70, .	1.8	4
9	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
10	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141.	27.8	648
11	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	10.0	269
12	Retrospective screening of routine respiratory samples revealed undetected community transmission and missed intervention opportunities for SARS-CoV-2 in the United Kingdom. <i>Journal of General Virology</i> , 2021, 102, .	2.9	10
13	Gold–Oligonucleotide Nanoconstructs Engineered to Detect Conserved Enteroviral Nucleic Acid Sequences. <i>Biosensors</i> , 2021, 11, 238.	4.7	5
14	The UK Leicester COVID-19 “exceedance” May–July 2020: An analysis of hospitalised cases. <i>Journal of Infection</i> , 2021, 83, e5-e7.	3.3	1
15	Challenges on the development of a pseudotyping assay for Zika glycoproteins. <i>Journal of Medical Microbiology</i> , 2021, 70, .	1.8	5
16	Perceptions and Experiences of the University of Nottingham Pilot SARS-CoV-2 Asymptomatic Testing Service: A Mixed-Methods Study. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 188.	2.6	34
17	Enterovirus subtyping in a routine UK laboratory setting between 2013 and 2017. <i>Journal of Clinical Virology</i> , 2020, 132, 104646.	3.1	2
18	Liver-expressed <i>Cd302</i> and <i>Cr1l</i> limit hepatitis C virus cross-species transmission to mice. <i>Science Advances</i> , 2020, 6, .	10.3	23

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19	Human Bocavirus infection and respiratory tract disease identified in a UK patient cohort. Journal of Clinical Virology, 2020, 129, 104453.	3.1	29
20	An integrated national scale SARS-CoV-2 genomic surveillance network. Lancet Microbe, The, 2020, 1, e99-e100.	7.3	232
21	Nanopore sequencing from extraction-free direct PCR of dried serum spots for portable hepatitis B virus drug-resistance typing. Journal of Clinical Virology, 2020, 129, 104483.	3.1	9
22	Discovery and Prevalence of Divergent RNA Viruses in European Field Voles and Rabbits. Viruses, 2020, 12, 47.	3.3	9
23	Retrieval of the Complete Coding Sequence of the UK-Endemic Tatenale Orthohantavirus Reveals Extensive Strain Variation and Supports Its Classification as a Novel Species. Viruses, 2020, 12, 454.	3.3	4
24	Elevated serum activity of MBL and ficolin-2 as biomarkers for progression to hepatocellular carcinoma in chronic HCV infection. Virology, 2019, 530, 99-106.	2.4	9
25	Shared Common Ancestry of Rodent Alphacoronaviruses Sampled Globally. Viruses, 2019, 11, 125.	3.3	35
26	Identification of Infectious Agents in High-Throughput Sequencing Data Sets Is Easily Achievable Using Free, Cloud-Based Bioinformatics Platforms. Journal of Clinical Microbiology, 2019, 57, .	3.9	3
27	InFusion Cloning for the Generation of Biologically Relevant HCV Chimeric Molecular Clones. Methods in Molecular Biology, 2019, 1911, 93-104.	0.9	1
28	Expression of human ficolin-2 in hepatocytes confers resistance to infection by diverse hepatotropic viruses. Journal of Medical Microbiology, 2019, 68, 642-648.	1.8	4
29	Discovery of novel highly divergent RNA viruses in European rodents and rabbits. Access Microbiology, 2019, 1, .	0.5	0
30	Trichodysplasia Spinulosa Polyomavirus in Respiratory Tract of Immunocompromised Child. Emerging Infectious Diseases, 2018, 24, 1744-1746.	4.3	6
31	Development and clinical validation of the Genedrive point-of-care test for qualitative detection of hepatitis C virus. Gut, 2018, 67, 2017-2024.	12.1	64
32	Immunization with a synthetic consensus hepatitis C virus E2 glycoprotein ectodomain elicits virus-neutralizing antibodies. Antiviral Research, 2018, 160, 25-37.	4.1	8
33	Tracking HCV protease population diversity during transmission and susceptibility of founder populations to antiviral therapy. Antiviral Research, 2017, 139, 129-137.	4.1	5
34	Discovery of Novel Alphacoronaviruses in European Rodents and Shrews. Viruses, 2016, 8, 84.	3.3	45
35	Hepatitis C virus quasispecies and pseudotype analysis from acute infection to chronicity in HIV-1 co-infected individuals. Virology, 2016, 492, 213-224.	2.4	3
36	Broad neutralization of hepatitis C virus-resistant variants by Civacir hepatitis C immunoglobulin. Hepatology, 2016, 64, 1495-1506.	7.3	8

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37	Human Adaptation of Ebola Virus during the West African Outbreak. <i>Cell</i> , 2016, 167, 1079-1087.e5.	28.9	180
38	A Diverse Panel of Hepatitis C Virus Glycoproteins for Use in Vaccine Research Reveals Extremes of Monoclonal Antibody Neutralization Resistance. <i>Journal of Virology</i> , 2016, 90, 3288-3301.	3.4	62
39	Targeting a host-cell entry factor barricades antiviral-resistant HCV variants from on-therapy breakthrough in human-liver mice. <i>Gut</i> , 2016, 65, 2029-2034.	12.1	21
40	Novel human anti-claudin 1 mAbs inhibit hepatitis C virus infection and may synergize with anti-SRB1 mAb. <i>Journal of General Virology</i> , 2016, 97, 82-94.	2.9	16
41	Flexible and rapid construction of viral chimeras applied to hepatitis C virus. <i>Journal of General Virology</i> , 2016, 97, 2187-2193.	2.9	11
42	Novel functional hepatitis C virus glycoprotein isolates identified using an optimized viral pseudotype entry assay. <i>Journal of General Virology</i> , 2016, 97, 2265-2279.	2.9	33
43	In silico and in vitro interrogation of a widely used HEV RT-qPCR assay for detection of the species <i>Orthohepevirus A</i> . <i>Journal of Virological Methods</i> , 2015, 214, 25-28.	2.1	13
44	Structural Flexibility of a Conserved Antigenic Region in Hepatitis C Virus Glycoprotein E2 Recognized by Broadly Neutralizing Antibodies. <i>Journal of Virology</i> , 2015, 89, 2170-2181.	3.4	96
45	Recombinant Human L-Ficolin Directly Neutralizes Hepatitis C Virus Entry. <i>Journal of Innate Immunity</i> , 2014, 6, 676-684.	3.8	28
46	Analysis of Serine Codon Conservation Reveals Diverse Phenotypic Constraints on Hepatitis C Virus Glycoprotein Evolution. <i>Journal of Virology</i> , 2014, 88, 667-678.	3.4	2
47	Development of a high-throughput pyrosequencing assay for monitoring temporal evolution and resistance associated variant emergence in the Hepatitis C virus protease coding-region. <i>Antiviral Research</i> , 2014, 110, 52-59.	4.1	12
48	Use of short tandem repeat fingerprinting to validate sample origins in hepatitis C virus molecular epidemiology studies. <i>Journal of General Virology</i> , 2014, 95, 66-70.	2.9	2
49	Mannan binding lectin-associated serine protease 1 is induced by hepatitis C virus infection and activates human hepatic stellate cells. <i>Clinical and Experimental Immunology</i> , 2013, 174, 265-273.	2.6	25
50	HIV-1 co-receptor expression and epithelial immune cells of the cervix in asymptomatic women attending a genitourinary medicine clinic. <i>HIV Medicine</i> , 2013, 14, 108-114.	2.2	5
51	Parvovirus 4 Infection and Clinical Outcome in High-Risk Populations. <i>Journal of Infectious Diseases</i> , 2012, 205, 1816-1820.	4.0	34
52	Identification of improved IL28B SNPs and haplotypes for prediction of drug response in treatment of hepatitis C using massively parallel sequencing in a cross-sectional European cohort. <i>Genome Medicine</i> , 2011, 3, 57.	8.2	62
53	Hepatitis C Patient-Derived Glycoproteins Exhibit Marked Differences in Susceptibility to Serum Neutralizing Antibodies: Genetic Subtype Defines Antigenic but Not Neutralization Serotype. <i>Journal of Virology</i> , 2011, 85, 4246-4257.	3.4	51
54	Intercompartmental Recombination of HIV-1 Contributes to <i>env</i> Intrahost Diversity and Modulates Viral Tropism and Sensitivity to Entry Inhibitors. <i>Journal of Virology</i> , 2011, 85, 6024-6037.	3.4	50

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55	Association of antibodies to hepatitis C virus glycoproteins 1 and 2 (anti-E1E2) with HCV disease. Journal of Viral Hepatitis, 2008, 15, 339-345.	2.0	5
56	Cross-genotype characterization of genetic diversity and molecular adaptation in hepatitis C virus envelope glycoprotein genes. Journal of General Virology, 2007, 88, 458-469.	2.9	25
57	Characterization of the hepatitis C virus E2 epitope defined by the broadly neutralizing monoclonal antibody AP33. Hepatology, 2006, 43, 592-601.	7.3	150
58	HIV coreceptor and chemokine ligand gene expression in the male urethra and female cervix. Aids, 2005, 19, 1257-1265.	2.2	19
59	A polymerase chain reaction method for the amplification of full-length envelope genes of HIV-1 from DNA samples containing single molecules of HIV-1 provirus. Journal of Virological Methods, 2000, 88, 73-80.	2.1	11
60	Use of Randomly Amplified Polymorphic Dna Markers as a Tool to Study Variation in Lichen-Forming Fungi. Lichenologist, 1999, 31, 257-267.	0.8	20
61	Identification, Mapping, and Phylogenomic Analysis of Four New Human Members of the T-box Gene Family: EOMES, TBX6, TBX18, and TBX19. Genomics, 1999, 55, 10-20.	2.9	57