

Charles P McClure

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

4,364
citations

304602

22
h-index

128225

60
g-index

67
all docs

67
docs citations

67
times ranked

9792
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	13.7	1,001
2	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
3	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141.	13.7	648
4	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.	4.7	269
5	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	3.4	232
6	Human Adaptation of Ebola Virus during the West African Outbreak. <i>Cell</i> , 2016, 167, 1079-1087.e5.	13.5	180
7	Characterization of the hepatitis C virus E2 epitope defined by the broadly neutralizing monoclonal antibody AP33. <i>Hepatology</i> , 2006, 43, 592-601.	3.6	150
8	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.	1.5	96
9	Development and clinical validation of the Genedrive point-of-care test for qualitative detection of hepatitis C virus. <i>Gut</i> , 2018, 67, 2017-2024.	6.1	64
10	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.	3.6	62
11	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.	1.5	62
12	Identification, Mapping, and Phylogenomic Analysis of Four New Human Members of the T-box Gene Family: EOMES, TBX6, TBX18, and TBX19. <i>Genomics</i> , 1999, 55, 10-20.	1.3	57
13	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.	1.5	51
14	Intercompartmental Recombination of HIV-1 Contributes to <i>env</i> Intra-host Diversity and Modulates Viral Tropism and Sensitivity to Entry Inhibitors. <i>Journal of Virology</i> , 2011, 85, 6024-6037.	1.5	50
15	Discovery of Novel Alphacoronaviruses in European Rodents and Shrews. <i>Viruses</i> , 2016, 8, 84.	1.5	45
16	Shared Common Ancestry of Rodent Alphacoronaviruses Sampled Globally. <i>Viruses</i> , 2019, 11, 125.	1.5	35
17	Parvovirus 4 Infection and Clinical Outcome in High-Risk Populations. <i>Journal of Infectious Diseases</i> , 2012, 205, 1816-1820.	1.9	34
18	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.	1.2	34

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19	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.	1.3	33
20	Human Bocavirus infection and respiratory tract disease identified in a UK patient cohort. <i>Journal of Clinical Virology</i> , 2020, 129, 104453.	1.6	29
21	Recombinant Human L-Ficolin Directly Neutralizes Hepatitis C Virus Entry. <i>Journal of Innate Immunity</i> , 2014, 6, 676-684.	1.8	28
22	Cross-genotype characterization of genetic diversity and molecular adaptation in hepatitis C virus envelope glycoprotein genes. <i>Journal of General Virology</i> , 2007, 88, 458-469.	1.3	25
23	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.	1.1	25
24	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.	1.9	25
25	Liver-expressed <i>Cd302</i> and <i>Cr11</i> limit hepatitis C virus cross-species transmission to mice. <i>Science Advances</i> , 2020, 6, .	4.7	23
26	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.	6.1	21
27	Use of Randomly Amplified Polymorphic Dna Markers as a Tool to Study Variation in Lichen-Forming Fungi. <i>Lichenologist</i> , 1999, 31, 257-267.	0.5	20
28	HIV coreceptor and chemokine ligand gene expression in the male urethra and female cervix. <i>Aids</i> , 2005, 19, 1257-1265.	1.0	19
29	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.	1.3	16
30	In silico and in vitro interrogation of a widely used HEV RT-qPCR assay for detection of the species Orthohepevirus A. <i>Journal of Virological Methods</i> , 2015, 214, 25-28.	1.0	13
31	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.	1.9	12
32	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. <i>Journal of Virological Methods</i> , 2000, 88, 73-80.	1.0	11
33	Flexible and rapid construction of viral chimeras applied to hepatitis C virus. <i>Journal of General Virology</i> , 2016, 97, 2187-2193.	1.3	11
34	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, .	1.3	10
35	Elevated serum activity of MBL and ficolin-2 as biomarkers for progression to hepatocellular carcinoma in chronic HCV infection. <i>Virology</i> , 2019, 530, 99-106.	1.1	9
36	Nanopore sequencing from extraction-free direct PCR of dried serum spots for portable hepatitis B virus drug-resistance typing. <i>Journal of Clinical Virology</i> , 2020, 129, 104483.	1.6	9

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37	Discovery and Prevalence of Divergent RNA Viruses in European Field Voles and Rabbits. <i>Viruses</i> , 2020, 12, 47.	1.5	9
38	Broad neutralization of hepatitis C virus-resistant variants by Civacir hepatitis C immunoglobulin. <i>Hepatology</i> , 2016, 64, 1495-1506.	3.6	8
39	Immunization with a synthetic consensus hepatitis C virus E2 glycoprotein ectodomain elicits virus-neutralizing antibodies. <i>Antiviral Research</i> , 2018, 160, 25-37.	1.9	8
40	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.	1.9	8
41	Trichodysplasia Spinulosa Polyomavirus in Respiratory Tract of Immunocompromised Child. <i>Emerging Infectious Diseases</i> , 2018, 24, 1744-1746.	2.0	6
42	Association of antibodies to hepatitis C virus glycoproteins 1 and 2 (anti-E1E2) with HCV disease. <i>Journal of Viral Hepatitis</i> , 2008, 15, 339-345.	1.0	5
43	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.	1.0	5
44	Tracking HCV protease population diversity during transmission and susceptibility of founder populations to antiviral therapy. <i>Antiviral Research</i> , 2017, 139, 129-137.	1.9	5
45	Gold-Oligonucleotide Nanoconstructs Engineered to Detect Conserved Enteroviral Nucleic Acid Sequences. <i>Biosensors</i> , 2021, 11, 238.	2.3	5
46	Challenges on the development of a pseudotyping assay for Zika glycoproteins. <i>Journal of Medical Microbiology</i> , 2021, 70, .	0.7	5
47	Retrieval of the Complete Coding Sequence of the UK-Endemic Tatenale Orthohantavirus Reveals Extensive Strain Variation and Supports Its Classification as a Novel Species. <i>Viruses</i> , 2020, 12, 454.	1.5	4
48	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, .	0.7	4
49	Expression of human ficolin-2 in hepatocytes confers resistance to infection by diverse hepatotropic viruses. <i>Journal of Medical Microbiology</i> , 2019, 68, 642-648.	0.7	4
50	Hepatitis C virus quasispecies and pseudotype analysis from acute infection to chronicity in HIV-1 co-infected individuals. <i>Virology</i> , 2016, 492, 213-224.	1.1	3
51	Identification of Infectious Agents in High-Throughput Sequencing Data Sets Is Easily Achievable Using Free, Cloud-Based Bioinformatics Platforms. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	3
52	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, .	0.2	3
53	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.	1.5	3
54	Analysis of Serine Codon Conservation Reveals Diverse Phenotypic Constraints on Hepatitis C Virus Glycoprotein Evolution. <i>Journal of Virology</i> , 2014, 88, 667-678.	1.5	2

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55	Enterovirus subtyping in a routine UK laboratory setting between 2013 and 2017. <i>Journal of Clinical Virology</i> , 2020, 132, 104646.	1.6	2
56	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.	1.3	2
57	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, .	1.3	2
58	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, .	1.0	2
59	The UK Leicester COVID-19 "exceedance"™ May-July 2020: An analysis of hospitalised cases. <i>Journal of Infection</i> , 2021, 83, e5-e7.	1.7	1
60	InFusion Cloning for the Generation of Biologically Relevant HCV Chimeric Molecular Clones. <i>Methods in Molecular Biology</i> , 2019, 1911, 93-104.	0.4	1
61	Discovery of novel highly divergent RNA viruses in European rodents and rabbits. <i>Access Microbiology</i> , 2019, 1, .	0.2	0