

Rowena A Bull

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

4,258
citations

136740

32
h-index

118652

62
g-index

99
all docs

99
docs citations

99
times ranked

5853
citing authors

#	ARTICLE	IF	CITATIONS
1	Emergence of a New Norovirus Genotype GII.4 Variant Associated with Global Outbreaks of Gastroenteritis. <i>Journal of Clinical Microbiology</i> , 2006, 44, 327-333.	1.8	302
2	Norovirus recombination. <i>Journal of General Virology</i> , 2007, 88, 3347-3359.	1.3	294
3	Norovirus Recombination in ORF1/ORF2 Overlap. <i>Emerging Infectious Diseases</i> , 2005, 11, 1079-1085.	2.0	257
4	Rapid Evolution of Pandemic Noroviruses of the GII.4 Lineage. <i>PLoS Pathogens</i> , 2010, 6, e1000831.	2.1	252
5	Sequential Bottlenecks Drive Viral Evolution in Early Acute Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2011, 7, e1002243.	2.1	201
6	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. <i>Nature Communications</i> , 2020, 11, 6272.	5.8	183
7	Epidemics of Gastroenteritis during 2006 Were Associated with the Spread of Norovirus GII.4 Variants 2006a and 2006b. <i>Clinical Infectious Diseases</i> , 2008, 46, 413-420.	2.9	152
8	Mechanisms of GII.4 norovirus evolution. <i>Trends in Microbiology</i> , 2011, 19, 233-240.	3.5	135
9	The Interferon-induced Transmembrane Proteins, IFITM1, IFITM2, and IFITM3 Inhibit Hepatitis C Virus Entry. <i>Journal of Biological Chemistry</i> , 2015, 290, 25946-25959.	1.6	128
10	Linking the T cell receptor to the single cell transcriptome in antigen-specific human T cells. <i>Immunology and Cell Biology</i> , 2016, 94, 604-611.	1.0	118
11	Contribution of Intra- and Interhost Dynamics to Norovirus Evolution. <i>Journal of Virology</i> , 2012, 86, 3219-3229.	1.5	109
12	Clonally diverse CD38+HLA-DR+CD8+ T cells persist during fatal H7N9 disease. <i>Nature Communications</i> , 2018, 9, 824.	5.8	107
13	Inhibitors of the Hepatitis C Virus Polymerase; Mode of Action and Resistance. <i>Viruses</i> , 2015, 7, 5206-5224.	1.5	102
14	Viral Quasispecies Assembly via Maximal Clique Enumeration. <i>PLoS Computational Biology</i> , 2014, 10, e1003515.	1.5	93
15	Frequent multiple hepatitis C virus infections among injection drug users in a prison setting. <i>Hepatology</i> , 2010, 52, 1564-1572.	3.6	88
16	Norovirus Excretion in an Aged-Care Setting. <i>Journal of Clinical Microbiology</i> , 2008, 46, 2119-2121.	1.8	83
17	Hepatitis C virus reinfection and superinfection among treated and untreated participants with recent infection. <i>Hepatology</i> , 2012, 55, 1058-1069.	3.6	82
18	Norovirus GII.4 Strains and Outbreaks, Australia. <i>Emerging Infectious Diseases</i> , 2007, 13, 1128-1130.	2.0	80

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19	Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in Australia during 2007 and 2008. <i>Journal of Clinical Virology</i> , 2010, 49, 265-271.	1.6	77
20	Long-term persistence of RBD+ memory B cells encoding neutralizing antibodies in SARS-CoV-2 infection. <i>Cell Reports Medicine</i> , 2021, 2, 100228.	3.3	66
21	Broadly-Neutralizing Antibodies Against Emerging SARS-CoV-2 Variants. <i>Frontiers in Immunology</i> , 2021, 12, 752003.	2.2	62
22	Accurate single nucleotide variant detection in viral populations by combining probabilistic clustering with a statistical test of strand bias. <i>BMC Genomics</i> , 2013, 14, 501.	1.2	61
23	Impact of sequencing depth and read length on single cell RNA sequencing data of T cells. <i>Scientific Reports</i> , 2017, 7, 12781.	1.6	60
24	Next generation deep sequencing and vaccine design: today and tomorrow. <i>Trends in Biotechnology</i> , 2012, 30, 443-452.	4.9	59
25	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. <i>Scientific Reports</i> , 2021, 11, 3934.	1.6	55
26	A method for near full-length amplification and sequencing for six hepatitis C virus genotypes. <i>BMC Genomics</i> , 2016, 17, 247.	1.2	52
27	The Influence of Hepatitis C Virus Genetic Region on Phylogenetic Clustering Analysis. <i>PLoS ONE</i> , 2015, 10, e0131437.	1.1	48
28	Broadly neutralizing antibodies from an individual that naturally cleared multiple hepatitis C virus infections uncover molecular determinants for E2 targeting and vaccine design. <i>PLoS Pathogens</i> , 2019, 15, e1007772.	2.1	45
29	Graphene- and Nanoparticle-Embedded Antimicrobial and Biocompatible Cotton/Silk Fabrics for Protective Clothing. <i>ACS Applied Bio Materials</i> , 2021, 4, 6175-6185.	2.3	39
30	Transmission of Hepatitis C Virus among Prisoners, Australia, 2005–2012. <i>Emerging Infectious Diseases</i> , 2015, 21, 765-774.	2.0	37
31	Higher abundance of enterovirus A species in the gut of children with islet autoimmunity. <i>Scientific Reports</i> , 2019, 9, 1749.	1.6	37
32	Hepatitis C Virus Nonstructural Protein 5B Is Involved in Virus Morphogenesis. <i>Journal of Virology</i> , 2012, 86, 5080-5088.	1.5	35
33	Immunizations with diverse sarbecovirus receptor-binding domains elicit SARS-CoV-2 neutralizing antibodies against a conserved site of vulnerability. <i>Immunity</i> , 2021, 54, 2908-2921.e6.	6.6	35
34	Transmitted/Founder Viruses Rapidly Escape from CD8 ⁺ T Cell Responses in Acute Hepatitis C Virus Infection. <i>Journal of Virology</i> , 2015, 89, 5478-5490.	1.5	31
35	Maintenance of broad neutralizing antibodies and memory B cells 1 year post-infection is predicted by SARS-CoV-2-specific CD4 ⁺ T cell responses. <i>Cell Reports</i> , 2022, 38, 110345.	2.9	30
36	A Hepatitis C Virus DNA Vaccine Encoding a Secreted, Oligomerized Form of Envelope Proteins Is Highly Immunogenic and Elicits Neutralizing Antibodies in Vaccinated Mice. <i>Frontiers in Immunology</i> , 2019, 10, 1145.	2.2	29

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37	Clearance of hepatitis C virus is associated with early and potent but narrowly-directed, Envelope-specific antibodies. <i>Scientific Reports</i> , 2019, 9, 13300.	1.6	28
38	SARS Coronavirus-2 Microneutralisation and Commercial Serological Assays Correlated Closely for Some but Not All Enzyme Immunoassays. <i>Viruses</i> , 2021, 13, 247.	1.5	28
39	Comparison of the replication properties of murine and human calicivirus RNA-dependent RNA polymerases. <i>Virus Genes</i> , 2011, 42, 16-27.	0.7	26
40	Sequencing of hepatitis C virus for detection of resistance to direct-acting antiviral therapy: A systematic review. <i>Hepatology Communications</i> , 2017, 1, 379-390.	2.0	26
41	Genome-Wide Mutagenesis of Dengue Virus Reveals Plasticity of the NS1 Protein and Enables Generation of Infectious Tagged Reporter Viruses. <i>Journal of Virology</i> , 2017, 91, .	1.5	24
42	A molecular transmission network of recent hepatitis C infection in people with and without HIV: Implications for targeted treatment strategies. <i>Journal of Viral Hepatitis</i> , 2017, 24, 404-411.	1.0	23
43	Optimized cell systems for the investigation of hepatitis C virus E1E2 glycoproteins. <i>Journal of General Virology</i> , 2021, 102, .	1.3	23
44	Amplification and next generation sequencing of near full-length human enteroviruses for identification and characterisation from clinical samples. <i>Scientific Reports</i> , 2018, 8, 11889.	1.6	22
45	Potent SARS-CoV-2 binding and neutralization through maturation of iconic SARS-CoV-1 antibodies. <i>MAbs</i> , 2021, 13, 1922134.	2.6	22
46	Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. <i>Virus Evolution</i> , 2017, 3, vex018.	2.2	21
47	B cell immunodominance in primary hepatitis C virus infection. <i>Journal of Hepatology</i> , 2020, 72, 670-679.	1.8	21
48	Understanding the complex evolution of rapidly mutating viruses with deep sequencing: Beyond the analysis of viral diversity. <i>Virus Research</i> , 2017, 239, 43-54.	1.1	19
49	Envelope-Specific IgG3 and IgG1 Responses Are Associated with Clearance of Acute Hepatitis C Virus Infection. <i>Viruses</i> , 2020, 12, 75.	1.5	19
50	Resistance to hepatitis C virus: potential genetic and immunological determinants. <i>Lancet Infectious Diseases</i> , 2015, 15, 451-460.	4.6	17
51	Historical Trends in the Hepatitis C Virus Epidemics in North America and Australia. <i>Journal of Infectious Diseases</i> , 2016, 214, 1383-1389.	1.9	16
52	Understanding the Determinants of BnAb Induction in Acute HCV Infection. <i>Viruses</i> , 2018, 10, 659.	1.5	15
53	A method for detecting hepatitis C envelope specific memory B cells from multiple genotypes using cocktail E2 tetramers. <i>Journal of Immunological Methods</i> , 2019, 472, 65-74.	0.6	15
54	Phylogenetic analysis of full-length, early infection, hepatitis C virus genomes among people with intravenous drug use: the InC ³ Study. <i>Journal of Viral Hepatitis</i> , 2017, 24, 43-52.	1.0	14

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55	Genomic characterization of hepatitis C virus transmitted founder variants with deep sequencing. <i>Infection, Genetics and Evolution</i> , 2019, 71, 36-41.	1.0	14
56	Adaptation of Oxford Nanopore technology for hepatitis C whole genome sequencing and identification of within-host viral variants. <i>BMC Genomics</i> , 2021, 22, 148.	1.2	14
57	Occult infection with hepatitis C virus: friend or foe?. <i>Immunology and Cell Biology</i> , 2012, 90, 763-773.	1.0	13
58	Hepatitis C-specific effector and regulatory CD4 T cell responses are associated with the outcomes of primary infection. <i>Journal of Viral Hepatitis</i> , 2016, 23, 985-993.	1.0	13
59	HIV infection and hepatitis C virus genotype 1a are associated with phylogenetic clustering among people with recently acquired hepatitis C virus infection. <i>Infection, Genetics and Evolution</i> , 2016, 37, 252-258.	1.0	13
60	Incident Hepatitis C Virus Genotype Distribution and Multiple Infection in Australian Prisons. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1855-1861.	1.8	12
61	Dynamic evolution of hepatitis C virus resistance-associated substitutions in the absence of antiviral treatment. <i>Scientific Reports</i> , 2017, 7, 41719.	1.6	12
62	Analysis of resistance-associated substitutions in acute hepatitis C virus infection by deep sequencing across six genotypes and three continents. <i>Journal of Viral Hepatitis</i> , 2017, 24, 37-42.	1.0	11
63	Chemokine-Regulated Recruitment of Antigen-Specific T-Cell Subpopulations to the Liver in Acute and Chronic Hepatitis C Infection. <i>Journal of Infectious Diseases</i> , 2019, 219, 1430-1438.	1.9	11
64	Single molecule, near full-length genome sequencing of dengue virus. <i>Scientific Reports</i> , 2020, 10, 18196.	1.6	11
65	Toward DNA-Based T-Cell Mediated Vaccines to Target HIV-1 and Hepatitis C Virus: Approaches to Elicit Localized Immunity for Protection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 91.	1.8	10
66	Rare occurrence of occult hepatitis C virus in apparently uninfected injecting drug users: a two-centre, masked, case-control study. <i>Journal of Viral Hepatitis</i> , 2013, 20, 725-728.	1.0	9
67	A Bioinformatics Pipeline for the Analyses of Viral Escape Dynamics and Host Immune Responses during an Infection. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	9
68	Limited naturally occurring escape in broadly neutralizing antibody epitopes in hepatitis C glycoprotein E2 and constrained sequence usage in acute infection. <i>Infection, Genetics and Evolution</i> , 2017, 49, 88-96.	1.0	8
69	SARS-CoV-2 N-gene mutation leading to Xpert Xpress SARS-CoV-2 assay instability. <i>Pathology</i> , 2022, , .	0.3	8
70	Getting to the (germinal) center of humoral immune responses to SARS-CoV-2. <i>Cell</i> , 2022, 185, 945-948.	13.5	7
71	Correlation of polymerase replication fidelity with genetic evolution of influenza A/Fujian/411/02(H3N2) viruses. <i>Journal of Medical Virology</i> , 2011, 83, 510-516.	2.5	6
72	Genomic variability of within-host hepatitis C variants in acute infection. <i>Journal of Viral Hepatitis</i> , 2019, 26, 476-484.	1.0	6

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73	Optimisation and validation of a new method for antibody dependent cellular phagocytosis in hepatitis C virus infection. <i>Journal of Immunological Methods</i> , 2021, 495, 113087.	0.6	6
74	Viral Quasispecies Assembly via Maximal Clique Enumeration. <i>Lecture Notes in Computer Science</i> , 2014, , 309-310.	1.0	6
75	Conserved epitopes with high HLA-I population coverage are targets of CD8+ T cells associated with high IFN- γ responses against all dengue virus serotypes. <i>Scientific Reports</i> , 2020, 10, 20497.	1.6	5
76	Human CD8 T stem cell memory subsets phenotypic and functional characterization are defined by expression of CD122 or CXCR3. <i>European Journal of Immunology</i> , 2021, 51, 1732-1747.	1.6	5
77	Hepatitis C Virus Epitope Immunodominance and B Cell Repertoire Diversity. <i>Viruses</i> , 2021, 13, 983.	1.5	5
78	Effect of reassortment on the nucleotide and amino acid changes of human A/H3N2 RNP subunits during 1998-2009. <i>Journal of Clinical Virology</i> , 2011, 51, 270-275.	1.6	4
79	Evidence that hepatitis C virus genome partly controls infection outcome. <i>Evolutionary Applications</i> , 2014, 7, 533-547.	1.5	4
80	Impact of an Open Access Nationwide Treatment Model on Hepatitis C Virus Antiviral Drug Resistance. <i>Hepatology Communications</i> , 2020, 4, 904-915.	2.0	4
81	Assessment of Inter-Laboratory Differences in SARS-CoV-2 Consensus Genome Assemblies between Public Health Laboratories in Australia. <i>Viruses</i> , 2022, 14, 185.	1.5	4
82	Persistent high-level shedding of cultivable SARS-CoV-2 Delta virus 33 days after onset of COVID-19 in a hospitalized patient with pneumonia. <i>Journal of Medical Virology</i> , 2022, 94, 4043-4046.	2.5	4
83	Comparison of influenza virus replication fidelity in vitro using selection pressure with monoclonal antibodies. <i>Journal of Medical Virology</i> , 2013, 85, 1090-1094.	2.5	2
84	Erratum to "A Bioinformatics Pipeline for the Analyses of Viral Escape Dynamics and Host Immune Responses during an Infection". <i>BioMed Research International</i> , 2014, 2014, 1-2.	0.9	1
85	Anti-envelope antibody responses in highly exposed seronegative individuals may be associated with protection from HCV infection. <i>Journal of Viral Hepatitis</i> , 2020, 27, 1012-1021.	1.0	1
86	Co-evolving mutations in hepatitis C virus in the context of immune escape against neutralising antibody responses - A bioinformatic workflow for the analysis of co-evolving mutations in viral genomes. , 2015, , .		0
87	Unravelling the complexities of virus and host interactions in the Viral Immunology Systems Program, NHMRC, ACH2, National Institutes of Health. <i>Impact</i> , 2017, 2017, 34-36.	0.0	0
88	Evolution of within-host variants of the hepatitis C virus. <i>Infection, Genetics and Evolution</i> , 2022, 99, 105242.	1.0	0