

Rowena A Bull

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88

papers

3,206

citations

27

h-index

55

g-index

99

ext. papers

3,833

ext. citations

7.8

avg, IF

5.14

L-index

#	Paper	IF	Citations
88	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 , 110345	10.6	3
87	Evolution of within-host variants of the hepatitis C virus.. <i>Infection, Genetics and Evolution</i> , 2022 , 1052424.5		
86	Getting to the (germinal) center of humoral immune responses to SARS-CoV-2.. <i>Cell</i> , 2022 , 185, 945-948	56.2	0
85	SARS-CoV-2 N-gene mutation leading to Xpert Xpress SARS-CoV-2 assay instability.. <i>Pathology</i> , 2022 ,	1.6	1
84	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 ,	19.7	
83	Immunizations with diverse sarbecovirus receptor-binding domains elicit SARS-CoV-2 neutralizing antibodies against a conserved site of vulnerability. <i>Immunity</i> , 2021 ,	32.3	8
82	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	4.5	7
81	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	6.1	3
80	Long-term persistence of RBD memory B cells encoding neutralizing antibodies in SARS-CoV-2 infection. <i>Cell Reports Medicine</i> , 2021 , 2, 100228	18	34
79	Hepatitis C Virus Epitope Immunodominance and B Cell Repertoire Diversity. <i>Viruses</i> , 2021 , 13,	6.2	1
78	Optimized cell systems for the investigation of hepatitis C virus E1E2 glycoproteins. <i>Journal of General Virology</i> , 2021 , 102,	4.9	9
77	Potent SARS-CoV-2 binding and neutralization through maturation of iconic SARS-CoV-1 antibodies. <i>MAbs</i> , 2021 , 13, 1922134	6.6	9
76	SARS Coronavirus-2 Microneutralisation and Commercial Serological Assays Correlated Closely for Some but Not All Enzyme Immunoassays. <i>Viruses</i> , 2021 , 13,	6.2	15
75	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. <i>Scientific Reports</i> , 2021 , 11, 3934	4.9	17
74	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	2.5	2
73	Graphene- and Nanoparticle-Embedded Antimicrobial and Biocompatible Cotton/Silk Fabrics for Protective Clothing.. <i>ACS Applied Bio Materials</i> , 2021 , 4, 6175-6185	4.1	11
72	Broadly-Neutralizing Antibodies Against Emerging SARS-CoV-2 Variants. <i>Frontiers in Immunology</i> , 2021 , 12, 752003	8.4	8

71	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. <i>Nature Communications</i> , 2020 , 11, 6272	17.4	70
70	Impact of an Open Access Nationwide Treatment Model on Hepatitis C Virus Antiviral Drug Resistance. <i>Hepatology Communications</i> , 2020 , 4, 904-915	6	2
69	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	3.4	
68	Envelope-Specific IgG3 and IgG1 Responses Are Associated with Clearance of Acute Hepatitis C Virus Infection. <i>Viruses</i> , 2020 , 12,	6.2	12
67	B cell immunodominance in primary hepatitis C virus infection. <i>Journal of Hepatology</i> , 2020 , 72, 670-679	13.4	8
66	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	4.9	2
65	Single molecule, near full-length genome sequencing of dengue virus. <i>Scientific Reports</i> , 2020 , 10, 18196	4.9	4
64	Clearance of hepatitis C virus is associated with early and potent but narrowly-directed, Envelope-specific antibodies. <i>Scientific Reports</i> , 2019 , 9, 13300	4.9	17
63	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	2.5	8
62	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	8.4	20
61	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	7.6	24
60	Genomic characterization of hepatitis C virus transmitted founder variants with deep sequencing. <i>Infection, Genetics and Evolution</i> , 2019 , 71, 36-41	4.5	13
59	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	5.9	5
58	Higher abundance of enterovirus A species in the gut of children with islet autoimmunity. <i>Scientific Reports</i> , 2019 , 9, 1749	4.9	24
57	Genomic variability of within-host hepatitis C variants in acute infection. <i>Journal of Viral Hepatitis</i> , 2019 , 26, 476-484	3.4	6
56	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	7	7
55	Clonally diverse CD38HLA-DRCD8 T cells persist during fatal H7N9 disease. <i>Nature Communications</i> , 2018 , 9, 824	17.4	69
54	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	4.9	10

53	Understanding the Determinants of BnAb Induction in Acute HCV Infection. <i>Viruses</i> , 2018 , 10,	6.2	8
52	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	4.5	6
51	Dynamic evolution of hepatitis C virus resistance-associated substitutions in the absence of antiviral treatment. <i>Scientific Reports</i> , 2017 , 7, 41719	4.9	11
50	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,	6.6	17
49	Impact of sequencing depth and read length on single cell RNA sequencing data of T cells. <i>Scientific Reports</i> , 2017 , 7, 12781	4.9	45
48	Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. <i>Virus Evolution</i> , 2017 , 3, vex018	3.7	14
47	Phylogenetic analysis of full-length, early infection, hepatitis C virus genomes among people with intravenous drug use: the InC Study. <i>Journal of Viral Hepatitis</i> , 2017 , 24, 43-52	3.4	14
46	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	3.4	11
45	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	3.4	14
44	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	6.4	14
43	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	6	26
42	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	3.4	12
41	Historical Trends in the Hepatitis C Virus Epidemics in North America and Australia. <i>Journal of Infectious Diseases</i> , 2016 , 214, 1383-1389	7	12
40	Linking the T cell receptor to the single cell transcriptome in antigen-specific human T cells. <i>Immunology and Cell Biology</i> , 2016 , 94, 604-11	5	91
39	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, 252-8	4.5	9
38	Incident Hepatitis C Virus Genotype Distribution and Multiple Infection in Australian Prisons. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1855-1861	9.7	8
37	A method for near full-length amplification and sequencing for six hepatitis C virus genotypes. <i>BMC Genomics</i> , 2016 , 17, 247	4.5	43
36	Resistance to hepatitis C virus: potential genetic and immunological determinants. <i>Lancet Infectious Diseases, The</i> , 2015 , 15, 451-60	25.5	16

35	The Interferon-induced Transmembrane Proteins, IFITM1, IFITM2, and IFITM3 Inhibit Hepatitis C Virus Entry. <i>Journal of Biological Chemistry</i> , 2015 , 290, 25946-59	5.4	82
34	Transmission of Hepatitis C Virus among Prisoners, Australia, 2005-2012. <i>Emerging Infectious Diseases</i> , 2015 , 21, 765-74	10.2	35
33	Inhibitors of the Hepatitis C Virus Polymerase; Mode of Action and Resistance. <i>Viruses</i> , 2015 , 7, 5206-24	6.2	81
32	Transmitted/Founder Viruses Rapidly Escape from CD8+ T Cell Responses in Acute Hepatitis C Virus Infection. <i>Journal of Virology</i> , 2015 , 89, 5478-90	6.6	26
31	The Influence of Hepatitis C Virus Genetic Region on Phylogenetic Clustering Analysis. <i>PLoS ONE</i> , 2015 , 10, e0131437	3.7	39
30	Evidence that hepatitis C virus genome partly controls infection outcome. <i>Evolutionary Applications</i> , 2014 , 7, 533-47	4.8	4
29	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	3	1
28	A bioinformatics pipeline for the analyses of viral escape dynamics and host immune responses during an infection. <i>BioMed Research International</i> , 2014 , 2014, 264519	3	6
27	Viral quasispecies assembly via maximal clique enumeration. <i>PLoS Computational Biology</i> , 2014 , 10, e1003515	5.5	70
26	Viral Quasispecies Assembly via Maximal Clique Enumeration. <i>Lecture Notes in Computer Science</i> , 2014 , 309-310	0.9	4
25	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	4.5	33
24	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, 725-8	3.4	7
23	Comparison of influenza virus replication fidelity in vitro using selection pressure with monoclonal antibodies. <i>Journal of Medical Virology</i> , 2013 , 85, 1090-4	19.7	2
22	Next generation deep sequencing and vaccine design: today and tomorrow. <i>Trends in Biotechnology</i> , 2012 , 30, 443-52	15.1	48
21	Contribution of intra- and interhost dynamics to norovirus evolution. <i>Journal of Virology</i> , 2012 , 86, 3219-28	10.5	93
20	Occult infection with hepatitis C virus: friend or foe?. <i>Immunology and Cell Biology</i> , 2012 , 90, 763-73	5	11
19	Hepatitis C virus reinfection and superinfection among treated and untreated participants with recent infection. <i>Hepatology</i> , 2012 , 55, 1058-69	11.2	73
18	Hepatitis C virus nonstructural protein 5B is involved in virus morphogenesis. <i>Journal of Virology</i> , 2012 , 86, 5080-8	6.6	30

17	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, 270-5	14.5	4
16	Mechanisms of GII.4 norovirus evolution. <i>Trends in Microbiology</i> , 2011 , 19, 233-40	12.4	125
15	Comparison of the replication properties of murine and human calicivirus RNA-dependent RNA polymerases. <i>Virus Genes</i> , 2011 , 42, 16-27	2.3	24
14	Correlation of polymerase replication fidelity with genetic evolution of influenza A/Fujian/411/02(H3N2) viruses. <i>Journal of Medical Virology</i> , 2011 , 83, 510-6	19.7	6
13	Sequential bottlenecks drive viral evolution in early acute hepatitis C virus infection. <i>PLoS Pathogens</i> , 2011 , 7, e1002243	7.6	179
12	Rapid evolution of pandemic noroviruses of the GII.4 lineage. <i>PLoS Pathogens</i> , 2010 , 6, e1000831	7.6	228
11	Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in Australia during 2007 and 2008. <i>Journal of Clinical Virology</i> , 2010 , 49, 265-71	14.5	69
10	Frequent multiple hepatitis C virus infections among injection drug users in a prison setting. <i>Hepatology</i> , 2010 , 52, 1564-72	11.2	82
9	Norovirus excretion in an aged-care setting. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 2119-21	9.7	74
8	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, 413-20	11.6	137
7	Norovirus GII.4 strains and outbreaks, Australia. <i>Emerging Infectious Diseases</i> , 2007 , 13, 1128-30	10.2	73
6	Norovirus recombination. <i>Journal of General Virology</i> , 2007 , 88, 3347-3359	4.9	265
5	Emergence of a new norovirus genotype II.4 variant associated with global outbreaks of gastroenteritis. <i>Journal of Clinical Microbiology</i> , 2006 , 44, 327-33	9.7	271
4	Norovirus recombination in ORF1/ORF2 overlap. <i>Emerging Infectious Diseases</i> , 2005 , 11, 1079-85	10.2	219
3	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis		2
2	Impact of sequencing depth and read length on single cell RNA sequencing data: lessons from T cells		1
1	Ageing impairs the airway epithelium defence response to SARS-CoV-2		2