Rowena A Bull

List of Publications by Citations

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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	Emergence of a new norovirus genotype II.4 variant associated with global outbreaks of gastroenteritis. *Journal of Clinical Microbiology*, **2006**, 44, 327-33	9.7	271
87	Norovirus recombination. *Journal of General Virology*, **2007**, 88, 3347-3359	4.9	265
86	Rapid evolution of pandemic noroviruses of the GII.4 lineage. *PLoS Pathogens*, **2010**, 6, e1000831	7.6	228
85	Norovirus recombination in ORF1/ORF2 overlap. *Emerging Infectious Diseases*, **2005**, 11, 1079-85	10.2	219
84	Sequential bottlenecks drive viral evolution in early acute hepatitis C virus infection. *PLoS Pathogens*, **2011**, 7, e1002243	7.6	179
83	Epidemics of gastroenteritis during 2006 were associated with the spread of norovirus GII.4 variants 2006a and 2006b. *Clinical Infectious Diseases*, **2008**, 46, 413-20	11.6	137
82	Mechanisms of GII.4 norovirus evolution. *Trends in Microbiology*, **2011**, 19, 233-40	12.4	125
81	Contribution of intra- and interhost dynamics to norovirus evolution. *Journal of Virology*, **2012**, 86, 3219-29	6.6	93
80	Linking the T cell receptor to the single cell transcriptome in antigen-specific human T cells. *Immunology and Cell Biology*, **2016**, 94, 604-11	5	91
79	The Interferon-induced Transmembrane Proteins, IFITM1, IFITM2, and IFITM3 Inhibit Hepatitis C Virus Entry. *Journal of Biological Chemistry*, **2015**, 290, 25946-59	5.4	82
78	Frequent multiple hepatitis C virus infections among injection drug users in a prison setting. *Hepatology*, **2010**, 52, 1564-72	11.2	82
77	Inhibitors of the Hepatitis C Virus Polymerase; Mode of Action and Resistance. *Viruses*, **2015**, 7, 5206-24	6.2	81
76	Norovirus excretion in an aged-care setting. *Journal of Clinical Microbiology*, **2008**, 46, 2119-21	9.7	74
75	Hepatitis C virus reinfection and superinfection among treated and untreated participants with recent infection. *Hepatology*, **2012**, 55, 1058-69	11.2	73
74	Norovirus GII.4 strains and outbreaks, Australia. *Emerging Infectious Diseases*, **2007**, 13, 1128-30	10.2	73
73	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. *Nature Communications*, **2020**, 11, 6272	17.4	70
72	Viral quasispecies assembly via maximal clique enumeration. *PLoS Computational Biology*, **2014**, 10, e1003515	5	70

71	Clonally diverse CD38HLA-DRCD8 T cells persist during fatal H7N9 disease. *Nature Communications*, **2018**, 9, 824	17.4	69
70	Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in Australia during 2007 and 2008. *Journal of Clinical Virology*, **2010**, 49, 265-71	14.5	69
69	Next generation deep sequencing and vaccine design: today and tomorrow. *Trends in Biotechnology* , **2012**, 30, 443-52	15.1	48
68	Impact of sequencing depth and read length on single cell RNA sequencing data of T cells. *Scientific Reports*, **2017**, 7, 12781	4.9	45
67	A method for near full-length amplification and sequencing for six hepatitis C virus genotypes. *BMC Genomics*, **2016**, 17, 247	4.5	43
66	The Influence of Hepatitis C Virus Genetic Region on Phylogenetic Clustering Analysis. *PLoS ONE*, **2015**, 10, e0131437	3.7	39
65	Transmission of Hepatitis C Virus among Prisoners, Australia, 2005-2012. *Emerging Infectious Diseases*, **2015**, 21, 765-74	10.2	35
64	Long-term persistence of RBD memory B cells encoding neutralizing antibodies in SARS-CoV-2 infection. *Cell Reports Medicine*, **2021**, 2, 100228	18	34
63	Accurate single nucleotide variant detection in viral populations by combining probabilistic clustering with a statistical test of strand bias. *BMC Genomics*, **2013**, 14, 501	4.5	33
62	Hepatitis C virus nonstructural protein 5B is involved in virus morphogenesis. *Journal of Virology*, **2012**, 86, 5080-8	6.6	30
61	Transmitted/Founder Viruses Rapidly Escape from CD8+ T Cell Responses in Acute Hepatitis C Virus Infection. *Journal of Virology*, **2015**, 89, 5478-90	6.6	26
60	Sequencing of hepatitis C virus for detection of resistance to direct-acting antiviral therapy: A systematic review. *Hepatology Communications*, **2017**, 1, 379-390	6	26
59	Broadly neutralizing antibodies from an individual that naturally cleared multiple hepatitis C virus infections uncover molecular determinants for E2 targeting and vaccine design. *PLoS Pathogens*, **2019**, 15, e1007772	7.6	24
58	Comparison of the replication properties of murine and human calicivirus RNA-dependent RNA polymerases. *Virus Genes*, **2011**, 42, 16-27	2.3	24
57	Higher abundance of enterovirus A species in the gut of children with islet autoimmunity. *Scientific Reports*, **2019**, 9, 1749	4.9	24
56	A Hepatitis C Virus DNA Vaccine Encoding a Secreted, Oligomerized Form of Envelope Proteins Is Highly Immunogenic and Elicits Neutralizing Antibodies in Vaccinated Mice. *Frontiers in Immunology* , **2019**, 10, 1145	8.4	20
55	Genome-Wide Mutagenesis of Dengue Virus Reveals Plasticity of the NS1 Protein and Enables Generation of Infectious Tagged Reporter Viruses. *Journal of Virology*, **2017**, 91,	6.6	17
54	Clearance of hepatitis C virus is associated with early and potent but narrowly-directed, Envelope-specific antibodies. *Scientific Reports*, **2019**, 9, 13300	4.9	17

53	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. *Scientific Reports*, **2021**, 11, 3934	4.9	17
52	Resistance to hepatitis C virus: potential genetic and immunological determinants. *Lancet Infectious Diseases, The*, **2015**, 15, 451-60	25.5	16
51	SARS Coronavirus-2 Microneutralisation and Commercial Serological Assays Correlated Closely for Some but Not All Enzyme Immunoassays. *Viruses*, **2021**, 13,	6.2	15
50	Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. *Virus Evolution*, **2017**, 3, vex018	3.7	14
49	Phylogenetic analysis of full-length, early infection, hepatitis C virus genomes among people with intravenous drug use: the InC Study. *Journal of Viral Hepatitis*, **2017**, 24, 43-52	3.4	14
48	A molecular transmission network of recent hepatitis C infection in people with and without HIV: Implications for targeted treatment strategies. *Journal of Viral Hepatitis*, **2017**, 24, 404-411	3.4	14
47	Understanding the complex evolution of rapidly mutating viruses with deep sequencing: Beyond the analysis of viral diversity. *Virus Research*, **2017**, 239, 43-54	6.4	14
46	Genomic characterization of hepatitis C virus transmitted founder variants with deep sequencing. *Infection, Genetics and Evolution*, **2019**, 71, 36-41	4.5	13
45	Hepatitis C-specific effector and regulatory CD4 T-cell responses are associated with the outcomes of primary infection. *Journal of Viral Hepatitis*, **2016**, 23, 985-993	3.4	12
44	Historical Trends in the Hepatitis C Virus Epidemics in North America and Australia. *Journal of Infectious Diseases*, **2016**, 214, 1383-1389	7	12
43	Envelope-Specific IgG3 and IgG1 Responses Are Associated with Clearance of Acute Hepatitis C Virus Infection. *Viruses*, **2020**, 12,	6.2	12
42	Dynamic evolution of hepatitis C virus resistance-associated substitutions in the absence of antiviral treatment. *Scientific Reports*, **2017**, 7, 41719	4.9	11
41	Analysis of resistance-associated substitutions in acute hepatitis C virus infection by deep sequencing across six genotypes and three continents. *Journal of Viral Hepatitis*, **2017**, 24, 37-42	3.4	11
40	Occult infection with hepatitis C virus: friend or foe?. *Immunology and Cell Biology*, **2012**, 90, 763-73	5	11
39	Graphene- and Nanoparticle-Embedded Antimicrobial and Biocompatible Cotton/Silk Fabrics for Protective Clothing.. *ACS Applied Bio Materials*, **2021**, 4, 6175-6185	4.1	11
38	Amplification and next generation sequencing of near full-length human enteroviruses for identification and characterisation from clinical samples. *Scientific Reports*, **2018**, 8, 11889	4.9	10
37	HIV infection and hepatitis C virus genotype 1a are associated with phylogenetic clustering among people with recently acquired hepatitis C virus infection. *Infection, Genetics and Evolution*, **2016**, 37, 252-8	4.5	9
36	Optimized cell systems for the investigation of hepatitis C virus E1E2 glycoproteins. *Journal of General Virology*, **2021**, 102,	4.9	9

35	Potent SARS-CoV-2 binding and neutralization through maturation of iconic SARS-CoV-1 antibodies. *MAbs*, **2021**, 13, 1922134	6.6	9
34	A method for detecting hepatitis C envelope specific memory B cells from multiple genotypes using cocktail E2 tetramers. *Journal of Immunological Methods*, **2019**, 472, 65-74	2.5	8
33	Immunizations with diverse sarbecovirus receptor-binding domains elicit SARS-CoV-2 neutralizing antibodies against a conserved site of vulnerability. *Immunity*, **2021**,	32.3	8
32	B cell immunodominance in primary hepatitis C virus infection. *Journal of Hepatology*, **2020**, 72, 670-679	13.4	8
31	Incident Hepatitis C Virus Genotype Distribution and Multiple Infection in Australian Prisons. *Journal of Clinical Microbiology*, **2016**, 54, 1855-1861	9.7	8
30	Understanding the Determinants of BnAb Induction in Acute HCV Infection. *Viruses*, **2018**, 10,	6.2	8
29	Broadly-Neutralizing Antibodies Against Emerging SARS-CoV-2 Variants. *Frontiers in Immunology*, **2021**, 12, 752003	8.4	8
28	Rare occurrence of occult hepatitis C virus in apparently uninfected injecting drug users: a two-centre, masked, case-control study. *Journal of Viral Hepatitis*, **2013**, 20, 725-8	3.4	7
27	Adaptation of Oxford Nanopore technology for hepatitis C whole genome sequencing and identification of within-host viral variants. *BMC Genomics*, **2021**, 22, 148	4.5	7
26	Chemokine-Regulated Recruitment of Antigen-Specific T-Cell Subpopulations to the Liver in Acute and Chronic Hepatitis C Infection. *Journal of Infectious Diseases*, **2019**, 219, 1430-1438	7	7
25	Limited naturally occurring escape in broadly neutralizing antibody epitopes in hepatitis C glycoprotein E2 and constrained sequence usage in acute infection. *Infection, Genetics and Evolution*, **2017**, 49, 88-96	4.5	6
24	A bioinformatics pipeline for the analyses of viral escape dynamics and host immune responses during an infection. *BioMed Research International*, **2014**, 2014, 264519	3	6
23	Correlation of polymerase replication fidelity with genetic evolution of influenza A/Fujian/411/02(H3N2) viruses. *Journal of Medical Virology*, **2011**, 83, 510-6	19.7	6
22	Genomic variability of within-host hepatitis C variants in acute infection. *Journal of Viral Hepatitis*, **2019**, 26, 476-484	3.4	6
21	Toward DNA-Based T-Cell Mediated Vaccines to Target HIV-1 and Hepatitis C Virus: Approaches to Elicit Localized Immunity for Protection. *Frontiers in Cellular and Infection Microbiology*, **2019**, 9, 91	5.9	5
20	Evidence that hepatitis C virus genome partly controls infection outcome. *Evolutionary Applications*, **2014**, 7, 533-47	4.8	4
19	Effect of reassortment on the nucleotide and amino acid changes of human A/H3N2 RNP subunits during 1998-2009. *Journal of Clinical Virology*, **2011**, 51, 270-5	14.5	4
18	Viral Quasispecies Assembly via Maximal Clique Enumeration. *Lecture Notes in Computer Science*, **2014**, 309-310	0.9	4

17	Single molecule, near full-length genome sequencing of dengue virus. *Scientific Reports*, **2020**, 10, 18196	4.9	4
16	Maintenance of broad neutralizing antibodies and memory B cells 1 year post-infection is predicted by SARS-CoV-2-specific CD4+ T‑cell responses.. *Cell Reports*, **2022**, 110345	10.6	3
15	Human CD8 T-stem cell memory subsets phenotypic and functional characterization are defined by expression of CD122 or CXCR3. *European Journal of Immunology*, **2021**, 51, 1732-1747	6.1	3
14	Impact of an Open Access Nationwide Treatment Model on Hepatitis C Virus Antiviral Drug Resistance. *Hepatology Communications*, **2020**, 4, 904-915	6	2
13	Comparison of influenza virus replication fidelity in vitro using selection pressure with monoclonal antibodies. *Journal of Medical Virology*, **2013**, 85, 1090-4	19.7	2
12	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis		2
11	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. *Scientific Reports*, **2020**, 10, 20497	4.9	2
10	Ageing impairs the airway epithelium defence response to SARS-CoV-2		2
9	Optimisation and validation of a new method for antibody dependent cellular phagocytosis in hepatitis C virus infection. *Journal of Immunological Methods*, **2021**, 495, 113087	2.5	2
8	Erratum to “A Bioinformatics Pipeline for the Analyses of Viral Escape Dynamics and Host Immune Responses during an Infection” *BioMed Research International*, **2014**, 2014, 1-2	3	1
7	Impact of sequencing depth and read length on single cell RNA sequencing data: lessons from T cells		1
6	Hepatitis C Virus Epitope Immunodominance and B Cell Repertoire Diversity. *Viruses*, **2021**, 13,	6.2	1
5	SARS-CoV-2 N-gene mutation leading to Xpert Xpress SARS-CoV-2 assay instability.. *Pathology*, **2022**,	1.6	1
4	Getting to the (germinal) center of humoral immune responses to SARS-CoV-2.. *Cell*, **2022**, 185, 945-948	56.2	0
3	Anti-envelope antibody responses in highly exposed seronegative individuals may be associated with protection from HCV infection. *Journal of Viral Hepatitis*, **2020**, 27, 1012-1021	3.4	
2	Evolution of within-host variants of the hepatitis C virus.. *Infection, Genetics and Evolution*, **2022**, 105242	4.5	
1	Persistent high-level shedding of cultivable SARS-CoV-2 Delta virus 33 days after onset of COVID-19 in a hospitalized patient with pneumonia.. *Journal of Medical Virology*, **2022**,	19.7	