

# Michael J Carr

## List of Publications by Year in descending order

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98  
papers

2,476  
citations

186265  
28  
h-index

254184  
43  
g-index

101  
all docs

101  
docs citations

101  
times ranked

4285  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	1.8	115
2	A Consensus on Fungal Polymerase Chain Reaction Diagnosis?. Journal of Molecular Diagnostics, 2006, 8, 376-384.	2.8	99
3	Hepatitis B virus subgenotyping: History, effects of recombination, misclassifications, and corrections. Infection, Genetics and Evolution, 2013, 16, 355-361.	2.3	89
4	Development of a real-time RT-PCR for the detection of Swine-lineage Influenza A (H1N1) virus infections. Journal of Clinical Virology, 2009, 45, 196-199.	3.1	85
5	Host-directed editing of the SARS-CoV-2 genome. Biochemical and Biophysical Research Communications, 2021, 538, 35-39.	2.1	80
6	Radiation Therapy is Associated with Improved Outcomes in Merkel Cell Carcinoma. Annals of Surgical Oncology, 2016, 23, 3572-3578.	1.5	77
7	Deaths Associated with Human Adenovirus-14p1 Infections, Europe, 2009â€“2010. Emerging Infectious Diseases, 2011, 17, 1402-1408.	4.3	70
8	Human Polyomavirus Reactivation: Disease Pathogenesis and Treatment Approaches. Clinical and Developmental Immunology, 2013, 2013, 1-27.	3.3	66
9	Enterovirus-Associated Hand-Foot and Mouth Disease and Neurological Complications in Japan and the Rest of the World. International Journal of Molecular Sciences, 2019, 20, 5201.	4.1	66
10	Spread of Measles Virus D4-Hamburg, Europe, 2008â€“2011. Emerging Infectious Diseases, 2011, 17, 1396-1401.	4.3	65
11	Identification of a genomic subgroup of BK polyomavirus spread in European populations. Journal of General Virology, 2006, 87, 3201-3208.	2.9	60
12	A Multicentre Molecular Analysis of Hepatitis B and Blood-Borne Virus Coinfections in Viet Nam. PLoS ONE, 2012, 7, e39027.	2.5	56
13	The Role of Heparan Sulfate Proteoglycans as an Attachment Factor for Rabies Virus Entry and Infection. Journal of Infectious Diseases, 2018, 217, 1740-1749.	4.0	50
14	Hepatitis C Virus in Vietnam: High Prevalence of Infection in Dialysis and Multi-Transfused Patients Involving Diverse and Novel Virus Variants. PLoS ONE, 2012, 7, e41266.	2.5	50
15	Global and Local Persistence of Influenza A(H5N1) Virus. Emerging Infectious Diseases, 2014, 20, 1287-1295.	4.3	49
16	REE inverse modeling of HSDP2 basalts: Evidence for multiple sources in the Hawaiian plume. Geochemistry, Geophysics, Geosystems, 2003, 4, .	2.5	48
17	Unique BK virus non-coding control region (NCCR) variants in hematopoietic stem cell transplant recipients with and without hemorrhagic cystitis. Journal of Medical Virology, 2006, 78, 485-493.	5.0	44
18	Identification of novel inter-genotypic recombinants of human hepatitis B viruses by large-scale phylogenetic analysis. Virology, 2012, 427, 51-59.	2.4	44

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19	A genetic barcode of SARS-CoV-2 for monitoring global distribution of different clades during the COVID-19 pandemic. <i>International Journal of Infectious Diseases</i> , 2020, 100, 216-223.	3.3	43
20	Deaths Associated with Human Adenovirus-14p1 Infections, Europe, 2009-2010. <i>Emerging Infectious Diseases</i> , 2011, 17, 1402-8.	4.3	41
21	Long noncoding RNAs: Novel regulators of virus-host interactions. <i>Reviews in Medical Virology</i> , 2019, 29, e2046.	8.3	38
22	Rapid molecular detection of the H275Y oseltamivir resistance gene mutation in circulating influenza A (H1N1) viruses. <i>Journal of Virological Methods</i> , 2008, 153, 257-262.	2.1	36
23	Epidemiological characteristics of hand, foot, and mouth disease in Shandong, China, 2009-2016. <i>Scientific Reports</i> , 2017, 7, 8900.	3.3	35
24	Development of a rapid and quantitative method for the analysis of viral entry and release using a NanoLuc luciferase complementation assay. <i>Virus Research</i> , 2018, 243, 69-74.	2.2	34
25	Molecular Epidemiological Evaluation of the Recent Resurgence in Mumps Virus Infections in Ireland. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3288-3294.	3.9	32
26	Discovery of a novel antiviral agent targeting the nonstructural protein 4 (nsP4) of chikungunya virus. <i>Virology</i> , 2017, 505, 102-112.	2.4	32
27	A Neonatal Murine Model of Coxsackievirus A6 Infection for Evaluation of Antiviral and Vaccine Efficacy. <i>Journal of Virology</i> , 2017, 91, .	3.4	32
28	Valosin-containing protein (VCP/p97) plays a role in the replication of West Nile virus. <i>Virus Research</i> , 2017, 228, 114-123.	2.2	32
29	First Report of Sudden Death Due to Myocarditis Caused by Adenovirus Serotype 3. <i>Journal of Clinical Microbiology</i> , 2010, 48, 642-645.	3.9	30
30	Protective Efficacies of Formaldehyde-Inactivated Whole-Virus Vaccine and Antivirals in a Murine Model of Coxsackievirus A10 Infection. <i>Journal of Virology</i> , 2017, 91, .	3.4	30
31	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. <i>Virologica Sinica</i> , 2019, 34, 1-8.	3.0	30
32	Prevalence of HIV Type 1 Antiretroviral Drug Resistance Mutations in Vietnam: A Multicenter Study. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 797-801.	1.1	29
33	A low density oligonucleotide microarray for the detection of viral and atypical bacterial respiratory pathogens. <i>Journal of Virological Methods</i> , 2010, 163, 17-24.	2.1	28
34	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	6.5	28
35	Subgenotyping of Genotype C Hepatitis B Virus: Correcting Misclassifications and Identifying a Novel Subgenotype. <i>PLoS ONE</i> , 2012, 7, e47271.	2.5	26
36	Genetic variation in clinical varicella-zoster virus isolates collected in Ireland between 2002 and 2003. <i>Journal of Medical Virology</i> , 2004, 73, 131-136.	5.0	25

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37	Discovery of Mwinilunga alphavirus: A novel alphavirus in Culex mosquitoes in Zambia. <i>Virus Research</i> , 2018, 250, 31-36.	2.2	25
38	SARS-CoV-2 variant trends in Ireland: Wastewater-based epidemiology and clinical surveillance. <i>Science of the Total Environment</i> , 2022, 838, 155828.	8.0	25
39	First Reported Case of Endocarditis Caused by <i>Candida dubliniensis</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 3023-3026.	3.9	23
40	The Role of Hepatitis C Virus Core Antigen Testing in the Era of Direct Acting Antiviral Therapies: What We Can Learn from the Protease Inhibitors. <i>PLoS ONE</i> , 2016, 11, e0163900.	2.5	21
41	Generation of recombinant rabies viruses encoding NanoLuc luciferase for antiviral activity assays. <i>Virus Research</i> , 2016, 215, 121-128.	2.2	21
42	Epstein-Barr Virus Gene Expression, Human Leukocyte Antigen Alleles and Chronic High Viral Loads in Pediatric Renal Transplant Patients. <i>Transplantation</i> , 2011, 92, 328-333.	1.0	20
43	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012, 12, 116.	2.0	20
44	Rapid, highly sensitive detection of herpes simplex virus-1 using multiple antigenic peptide-coated superparamagnetic beads. <i>Analyst</i> , 2014, 139, 6126-6134.	3.5	19
45	Baseline Prevalence and Emergence of Protease Inhibitor Resistance Mutations following Treatment in Chronic HCV Genotype-1-Infected Individuals. <i>Antiviral Therapy</i> , 2015, 20, 865-869.	1.0	19
46	Interleukin-15 is associated with disease severity in viral bronchiolitis. <i>European Respiratory Journal</i> , 2016, 47, 212-222.	6.7	19
47	Reactivation of BK polyomavirus in patients with multiple sclerosis receiving natalizumab therapy. <i>Journal of NeuroVirology</i> , 2009, 15, 351-359.	2.1	18
48	Hepatitis C Virus Core Mutations Associated with False-Negative Serological Results for Genotype 3a Core Antigen. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2697-2700.	3.9	18
49	High genetic diversity and frequent genetic reassortment of avian influenza A(H9N2) viruses along the East Asian–Australian migratory flyway. <i>Infection, Genetics and Evolution</i> , 2016, 39, 325-329.	2.3	18
50	Novel sub-lineages, recombinants and reassortants of severe fever with thrombocytopenia syndrome virus. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 385-390.	2.7	18
51	Molecular epidemiology of human metapneumovirus in Ireland. <i>Journal of Medical Virology</i> , 2008, 80, 510-516.	5.0	17
52	Characterization of an inactivated whole-virus bivalent vaccine that induces balanced protective immunity against coxsackievirus A6 and A10 in mice. <i>Vaccine</i> , 2018, 36, 7095-7104.	3.8	17
53	Rapid detection of hand, foot and mouth disease enterovirus genotypes by multiplex PCR. <i>Journal of Virological Methods</i> , 2018, 258, 7-12.	2.1	16
54	Serological evidence of Zika virus infection in non-human primates in Zambia. <i>Archives of Virology</i> , 2019, 164, 2165-2170.	2.1	16

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55	Naturally Occurring HCV NS5A/B Inhibitor Resistance-Associated Mutations to Direct-Acting Antivirals. <i>Antiviral Therapy</i> , 2016, 21, 447-453.	1.0	15
56	Seroepidemiology of the recent mumps virus outbreaks in Ireland. <i>Journal of Clinical Virology</i> , 2012, 53, 320-324.	3.1	14
57	Upregulated expression of the antioxidant sestrin 2 identified by transcriptomic analysis of Japanese encephalitis virus-infected SH-SY5Y neuroblastoma cells. <i>Virus Genes</i> , 2019, 55, 630-642.	1.6	14
58	Evidence for exposure of asymptomatic domestic pigs to African swine fever virus during an inter-epidemic period in Zambia. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2741-2752.	3.0	14
59	Discovery of African bat polyomaviruses and infrequent recombination in the large T antigen in the Polyomaviridae. <i>Journal of General Virology</i> , 2017, 98, 726-738.	2.9	14
60	Identification of group A rotaviruses from Zambian fruit bats provides evidence for long-distance dispersal events in Africa. <i>Infection, Genetics and Evolution</i> , 2018, 63, 104-109.	2.3	13
61	Spontaneous clearance of hepatitis C infection after liver transplantation from IL28B rs12979860 CC donors. <i>European Journal of Gastroenterology and Hepatology</i> , 2012, 24, 1110-1112.	1.6	12
62	Seroepidemiology and phylogenetic characterisation of measles virus in Ireland, 2004-2013. <i>Journal of Clinical Virology</i> , 2014, 60, 374-380.	3.1	12
63	Self-collected buccal swabs and rapid, real-time PCR during a large measles outbreak in Wales: Evidence for the protective effect of prior MMR immunisation. <i>Journal of Clinical Virology</i> , 2015, 67, 1-7.	3.1	12
64	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019, 10, 1001.	3.5	12
65	Host ESCRT factors are recruited during chikungunya virus infection and are required for the intracellular viral replication cycle. <i>Journal of Biological Chemistry</i> , 2020, 295, 7941-7957.	3.4	12
66	Extensive Genetic Diversity of Polyomaviruses in Sympatric Bat Communities: Host Switching versus Coevolution. <i>Journal of Virology</i> , 2020, 94, .	3.4	12
67	A neonatal murine model of coxsackievirus A4 infection for evaluation of vaccines and antiviral drugs. <i>Emerging Microbes and Infections</i> , 2019, 8, 1445-1455.	6.5	11
68	Identification of the same polyomavirus species in different African horseshoe bat species is indicative of short-range host-switching events. <i>Journal of General Virology</i> , 2017, 98, 2771-2785.	2.9	11
69	Molecular epidemiology of circulating measles virus in Ireland 2002-2007. <i>Journal of Medical Virology</i> , 2009, 81, 125-129.	5.0	10
70	Genomic characterization of human adenovirus type 4 strains isolated worldwide since 1953 identifies two separable phylogroups evolving at different rates from their most recent common ancestor. <i>Virology</i> , 2019, 538, 11-23.	2.4	10
71	Seroepidemiological and phylogenetic characterization of neurotropic enteroviruses in Ireland, 2005-2014. <i>Journal of Medical Virology</i> , 2017, 89, 1550-1558.	5.0	9
72	Direct identification of the herpes simplex virus <i>UL27</i> gene through single particle manipulation and optical detection using a micromagnetic array. <i>Nanoscale</i> , 2020, 12, 3482-3490.	5.6	9

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73	Isolation of a simian immunodeficiency virus from a malbrouck ( <i>Chlorocebus cynosuros</i> ). <i>Archives of Virology</i> , 2017, 162, 543-548.	2.1	8
74	Discovery and genetic characterization of diverse smacoviruses in Zambian non-human primates. <i>Scientific Reports</i> , 2019, 9, 5045.	3.3	8
75	Design of micromagnetic arrays for on-chip separation of superparamagnetic bead aggregates and detection of a model protein and double-stranded DNA analytes. <i>Scientific Reports</i> , 2021, 11, 5302.	3.3	8
76	Prevalence and genetic diversity of Dabieshan tick virus in Shandong Province, China. <i>Journal of Infection</i> , 2022, 85, 90-122.	3.3	8
77	Effects of Acetylshikonin on the Infection and Replication of Coxsackievirus A16 in Vitro and in Vivo. <i>Journal of Natural Products</i> , 2019, 82, 1089-1097.	3.0	7
78	HIV Type 1 Coreceptor Tropism, CCR5 Genotype, and Integrase Inhibitor Resistance Profiles in Vietnam: Implications for the Introduction of New Antiretroviral Regimens. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1344-1348.	1.1	6
79	Influence of viral transport media and freeze-thaw cycling on the sensitivity of qRT-PCR detection of SARS-CoV-2 nucleic acids. <i>Nanoscale</i> , 2021, 13, 15659-15667.	5.6	6
80	Pediatric Infections by Human mastadenovirus C Types 2, 89, and a Recombinant Type Detected in Japan between 2011 and 2018. <i>Viruses</i> , 2019, 11, 1131.	3.3	5
81	Recombinant expression and immunological characterisation of proteins derived from human metapneumovirus. <i>Journal of Clinical Virology</i> , 2011, 52, 236-243.	3.1	4
82	High Prevalence of Hepatitis Delta Virus among Persons Who Inject Drugs, Vietnam. <i>Emerging Infectious Diseases</i> , 2015, 21, 540-543.	4.3	4
83	Homozygosity for HLA Group 2 Alleles Predicts Treatment Failure with Interferon- $\alpha$ and Ribavirin in Chronic Hepatitis C Virus Genotype 1 Infection. <i>Journal of Interferon and Cytokine Research</i> , 2015, 35, 126-133.	1.2	4
84	Single Amino Acid Mutation in Dengue Virus NS4B Protein Has Opposing Effects on Viral Proliferation in Mammalian and Mosquito Cells. <i>Japanese Journal of Infectious Diseases</i> , 2018, 71, 448-454.	1.2	4
85	Genomic epidemiological analysis of SARS-CoV-2 household transmission. <i>Access Microbiology</i> , 2021, 3, 000252.	0.5	4
86	Bat-borne polyomaviruses in Europe reveal an evolutionary history of intrahost divergence with horseshoe bats distributed across the African and Eurasian continents. <i>Journal of General Virology</i> , 2020, 101, 1119-1130.	2.9	4
87	Non-coding regions of the Ebola virus genome contain indispensable phylogenetic and evolutionary information. <i>Science China Life Sciences</i> , 2015, 58, 682-686.	4.9	3
88	Rapid humoral immune responses are required for recovery from haemorrhagic fever with renal syndrome patients. <i>Emerging Microbes and Infections</i> , 2020, 9, 2303-2314.	6.5	3
89	Co-Circulation of Multiple Serotypes of Bluetongue Virus in Zambia. <i>Viruses</i> , 2020, 12, 963.	3.3	3
90	Interferon lambda rs368234815 G/G is associated with higher CD4 <sup>+</sup> :CD8 <sup>+</sup> T-cell ratio in treated HIV-1 infection. <i>AIDS Research and Therapy</i> , 2020, 17, 13.	1.7	3

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91	Clinical and Epidemiological Aspects of the Emerging Adenovirus 14p1, Part II. Clinical Microbiology Newsletter, 2011, 33, 153-158.	0.7	2
92	Viral Bronchiolitis is Associated With Altered Cytokine Gene Expression and Lymphocyte Activation Status. Pediatric Infectious Disease Journal, 2016, 35, e326-e338.	2.0	2
93	Association of interferon lambda polymorphisms with elevated baseline viral loads in chronic hepatitis C virus genotype 6 infection. Archives of Virology, 2018, 163, 115-124.	2.1	2
94	Influenza viruses. , 2010, , 1590-1597.		2
95	Clinical and Epidemiological Aspects of the Emerging Adenovirus 14p1, Part I. Clinical Microbiology Newsletter, 2011, 33, 145-150.	0.7	1
96	Bat Polyomaviruses: A Challenge to the Strict Host-Restriction Paradigm within the Mammalian Polyomaviridae. , 2020, , .		1
97	æŸ`è`â¥‡ç—...æ`B4è`±â`¼æ€¥æ€\$â¿fè,CEç,Žâ`CEâ\$è,,çš®â±,ç¥žç»â...fæ°`è,¿â°é¼æ`jâžçš,,â»°ç««. Zoological Research, 2018, 39, 52-55.		
98	Rapid detection of the emerging tick-borne Tamdy virus by TaqMan-based real-time reverse transcription PCR. Journal of Virological Methods, 2022, 305, 114538.	2.1	0