

# Matthew Cotten

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4005166/publications.pdf>

Version: 2024-02-01

47  
papers

3,799  
citations

279487

23  
h-index

233125

45  
g-index

61  
all docs

61  
docs citations

61  
times ranked

6663  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hospital Outbreak of Middle East Respiratory Syndrome Coronavirus. <i>New England Journal of Medicine</i> , 2013, 369, 407-416.	13.9	1,044
2	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
3	Human Infection with MERS Coronavirus after Exposure to Infected Camels, Saudi Arabia, 2013. <i>Emerging Infectious Diseases</i> , 2014, 20, 1012-1015.	2.0	305
4	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet</i> , The, 2013, 382, 1993-2002.	6.3	282
5	Spread, Circulation, and Evolution of the Middle East Respiratory Syndrome Coronavirus. <i>MBio</i> , 2014, 5, .	1.8	235
6	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
7	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013, 19, 736-42B.	2.0	131
8	Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018, 217, 1728-1739.	1.9	116
9	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	2.2	105
10	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. <i>Nature Microbiology</i> , 2021, 6, 1094-1101.	5.9	82
11	Deep Sequencing of Norovirus Genomes Defines Evolutionary Patterns in an Urban Tropical Setting. <i>Journal of Virology</i> , 2014, 88, 11056-11069.	1.5	78
12	Local Evolutionary Patterns of Human Respiratory Syncytial Virus Derived from Whole-Genome Sequencing. <i>Journal of Virology</i> , 2015, 89, 3444-3454.	1.5	74
13	Full Genome Virus Detection in Fecal Samples Using Sensitive Nucleic Acid Preparation, Deep Sequencing, and a Novel Iterative Sequence Classification Algorithm. <i>PLoS ONE</i> , 2014, 9, e93269.	1.1	71
14	Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , 2018, 4, vey035.	2.2	56
15	Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation of multiple groups of rotaviruses and a putative zoonotic infection. <i>Virus Evolution</i> , 2016, 2, vew027.	2.2	52
16	Unexplained diarrhoea in HIV-1 infected individuals. <i>BMC Infectious Diseases</i> , 2014, 14, 22.	1.3	48
17	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. <i>EcoHealth</i> , 2015, 12, 726-735.	0.9	47
18	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39

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19	Whole-Genome Next-Generation Sequencing to Study Within-Host Evolution of Norovirus (NoV) Among Immunocompromised Patients With Chronic NoV Infection. <i>Journal of Infectious Diseases</i> , 2017, 216, 1513-1524.	1.9	36
20	Characterization of Norovirus and Other Human Enteric Viruses in Sewage and Stool Samples Through Next-Generation Sequencing. <i>Food and Environmental Virology</i> , 2019, 11, 400-409.	1.5	35
21	Infectious diseases epidemic threats and mass gatherings: refocusing global attention on the continuing spread of the Middle East Respiratory syndrome coronavirus (MERS-CoV). <i>BMC Medicine</i> , 2016, 14, 132.	2.3	34
22	Entamoeba and Giardia parasites implicated as hosts of CRESS viruses. <i>Nature Communications</i> , 2020, 11, 4620.	5.8	34
23	The COMPARE Data Hubs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	28
24	Whole genome analysis of local Kenyan and global sequences unravels the epidemiological and molecular evolutionary dynamics of RSV genotype ON1 strains. <i>Virus Evolution</i> , 2018, 4, vey027.	2.2	27
25	Transmission patterns and evolution of respiratory syncytial virus in a community outbreak identified by genomic analysis. <i>Virus Evolution</i> , 2017, 3, vex006.	2.2	26
26	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. <i>Frontiers in Microbiology</i> , 2019, 10, 2394.	1.5	26
27	Alternate primers for whole-genome SARS-CoV-2 sequencing. <i>Virus Evolution</i> , 2021, 7, veab006.	2.2	25
28	Main Routes of Entry and Genomic Diversity of SARS-CoV-2, Uganda. <i>Emerging Infectious Diseases</i> , 2020, 26, 2411-2415.	2.0	24
29	Nosocomial outbreak of the Middle East Respiratory Syndrome coronavirus: A phylogenetic, epidemiological, clinical and infection control analysis. <i>Travel Medicine and Infectious Disease</i> , 2020, 37, 101807.	1.5	21
30	Spike Protein Cleavage-Activation in the Context of the SARS-CoV-2 P681R Mutation: an Analysis from Its First Appearance in Lineage A.23.1 Identified in Uganda. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	20
31	Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , 2019, 9, 10076.	1.6	19
32	Complete Genome Sequences of Dengue Virus Type 2 Strains from Kilifi, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	14
33	Evaluating the performance of tools used to call minority variants from whole genome short-read data. <i>Wellcome Open Research</i> , 2018, 3, 21.	0.9	13
34	Virus discovery reveals frequent infection by diverse novel members of the Flaviviridae in wild lemurs. <i>Archives of Virology</i> , 2019, 164, 509-522.	0.9	11
35	Evaluating the performance of tools used to call minority variants from whole genome short-read data. <i>Wellcome Open Research</i> , 2018, 3, 21.	0.9	10
36	Genomic sequence of yellow fever virus from a Dutch traveller returning from the Gambia-Senegal region, the Netherlands, November 2018. <i>Eurosurveillance</i> , 2019, 24, .	3.9	9

#	ARTICLE	IF	CITATIONS
37	Next-generation sequencing and norovirus. <i>Future Virology</i> , 2016, 11, 719-722.	0.9	8
38	Complete Genome Sequences of Six Measles Virus Strains. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
39	Increased resolution of African swine fever virus genome patterns based on profile HMMs of protein domains. <i>Virus Evolution</i> , 2020, 6, veaa044.	2.2	7
40	Complete Genome Characterization of Eight Human Parainfluenza Viruses from the Netherlands. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
41	Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia. <i>BMC Genomics</i> , 2020, 21, 5.	1.2	4
42	SARS-CoV-2 Variants, South Sudan, Januaryâ€“March 2021. <i>Emerging Infectious Diseases</i> , 2021, 27, 3133-3136.	2.0	4
43	The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences. <i>Viruses</i> , 2019, 11, 394.	1.5	2
44	Shedding of Yellow Fever Virus From an Imported Case in the Netherlands After Travel to Brazil. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa020.	0.4	2
45	Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. <i>Virus Evolution</i> , 2021, 7, veab067.	2.2	2
46	139 HIV-2 Capsids Distinguishing High and Low Virus Load Patients in a West African Community Cohort. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2009, 51, .	0.9	0
47	Molecular epidemiology of endemic Human T-Lymphotropic virus 1 (HTLV-1) in a community in rural Guinea-Bissau. <i>Retrovirology</i> , 2011, 8, .	0.9	0