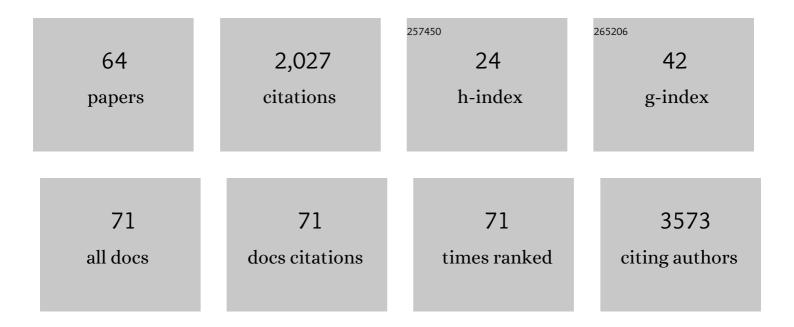
Samuel Cordey

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	External Quality Assessment of SARS-CoV-2 Sequencing: an ESGMD-SSM Pilot Trial across 15 European Laboratories. Journal of Clinical Microbiology, 2022, 60, JCM0169821.	3.9	13
2	Occupational and community risk of SARS-CoV-2 infection among employees of a long-term care facility: an observational study. Antimicrobial Resistance and Infection Control, 2022, 11, 51.	4.1	8
3	Blood virosphere in febrile Tanzanian children. Emerging Microbes and Infections, 2021, 10, 982-993.	6.5	9
4	Puumala Virus Infection in Family, Switzerland. Emerging Infectious Diseases, 2021, 27, 658-660.	4.3	7
5	Clinical, virologic and immunologic features of a mild case of SARS-CoV-2 reinfection. Clinical Microbiology and Infection, 2021, 27, 791.e1-791.e4.	6.0	22
6	Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples. Journal of Clinical Virology, 2021, 141, 104908.	3.1	28
7	Explosive nosocomial outbreak of SARS-CoV-2 in a rehabilitation clinic: the limits of genomics for outbreak reconstruction. Journal of Hospital Infection, 2021, 117, 124-134.	2.9	29
8	SARS-CoV-2 Evolution among Oncological Population: In-Depth Virological Analysis of a Clinical Cohort. Microorganisms, 2021, 9, 2145.	3.6	2
9	Sustained Trichodysplasia Spinulosa Polyomavirus Viremia Illustrating a Primary Disseminated Infection in a Kidney Transplant Recipient. Microorganisms, 2021, 9, 2298.	3.6	1
10	Daily Viral Kinetics and Innate and Adaptive Immune Response Assessment in COVID-19: a Case Series. MSphere, 2020, 5, .	2.9	52
11	Beyond Cytomegalovirus and Epstein-Barr Virus: a Review of Viruses Composing the Blood Virome of Solid Organ Transplant and Hematopoietic Stem Cell Transplant Recipients. Clinical Microbiology Reviews, 2020, 33, .	13.6	32
12	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. Viruses, 2020, 12, 1248.	3.3	9
13	Unbiased metagenomic next-generation sequencing of blood from hospitalized febrile children in Gabon. Emerging Microbes and Infections, 2020, 9, 1242-1244.	6.5	8
14	Human pegivirus persistence in human blood virome after allogeneic haematopoietic stem-cell transplantation. Clinical Microbiology and Infection, 2019, 25, 225-232.	6.0	28
15	Sequencing and analysis of globally obtained human parainfluenza viruses 1 and 3 genomes. PLoS ONE, 2019, 14, e0220057.	2.5	9
16	Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. Genes, 2019, 10, 655.	2.4	34
17	Viral Sequences Detection by High-Throughput Sequencing in Cerebrospinal Fluid of Individuals with and without Central Nervous System Disease. Genes, 2019, 10, 625.	2.4	11
18	Detection of dicistroviruses RNA in blood of febrile Tanzanian children. Emerging Microbes and Infections, 2019, 8, 613-623.	6.5	14

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#	Article	IF	CITATIONS
19	High-throughput sequencing for the aetiologic identification of viral encephalitis, meningoencephalitis, and meningitis. A narrative review and clinical appraisal. Clinical Microbiology and Infection, 2019, 25, 422-430.	6.0	24
20	Enterovirus, parechovirus, adenovirus and herpes virus type 6 viraemia in fever without source. Archives of Disease in Childhood, 2019, 105, archdischild-2019-317382.	1.9	13
21	Identification of Viral Signatures Using High-Throughput Sequencing on Blood of Patients With Kawasaki Disease. Frontiers in Pediatrics, 2019, 7, 524.	1.9	20
22	Nearly Complete Genome Sequence of a Novel Phlebovirus-Like Virus Detected in a Human Plasma Sample by High-Throughput Sequencing. Microbiology Resource Announcements, 2019, 8, .	0.6	4
23	Detection of novel astroviruses MLB1 and MLB2 in the sera of febrile Tanzanian children. Emerging Microbes and Infections, 2018, 7, 1-3.	6.5	12
24	Usutu virus in cerebrospinal fluid: A 2â€year survey in a Tertiary Care Hospital, Geneva, Switzerland. Journal of Medical Virology, 2018, 90, 609-611.	5.0	4
25	2569. High Incidence of Enterovirus, HHV6, Parechovirus and Adenovirus Blood Viremia in Children 0 to 3 Years Old Presenting With Fever Without Source. Open Forum Infectious Diseases, 2018, 5, S74-S74.	0.9	Ο
26	Metagenomics analysis of the virome of 300 concentrates from a Swiss platelet bank. Vox Sanguinis, 2018, 113, 601-604.	1.5	9
27	Investigation of the Plasma Virome from Cases of Unexplained Febrile Illness in Tanzania from 2013 to 2014: a Comparative Analysis between Unbiased and VirCapSeq-VERT High-Throughput Sequencing Approaches. MSphere, 2018, 3, .	2.9	21
28	Influenza A Virus Genetic Tools: From Clinical Sample to Molecular Clone. Methods in Molecular Biology, 2018, 1836, 33-58.	0.9	9
29	Novel human astroviruses in pediatric respiratory samples: A oneâ€year survey in a Swiss tertiary care hospital. Journal of Medical Virology, 2018, 90, 1775-1778.	5.0	12
30	Hospital surveillance of influenza strains: a concordant image of viruses identified by the Swiss Sentinel system?. Influenza and Other Respiratory Viruses, 2017, 11, 41-47.	3.4	3
31	Comparative analysis of viral shedding in pediatric and adult subjects with central nervous system-associated enterovirus infections from 2013 to 2015 in Switzerland. Journal of Clinical Virology, 2017, 89, 22-29.	3.1	24
32	Metagenomics analysis of red blood cell and freshâ€frozen plasma units. Transfusion, 2017, 57, 1787-1800.	1.6	24
33	Severe viral respiratory infections in children with <i>IFIH1</i> loss-of-function mutations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8342-8347.	7.1	111
34	Novel and classical human astroviruses in stool and cerebrospinal fluid: comprehensive screening in a tertiary care hospital, Switzerland. Emerging Microbes and Infections, 2017, 6, 1-7.	6.5	13
35	Astrovirus MLB2, a New Gastroenteric Virus Associated with Meningitis and Disseminated Infection. Emerging Infectious Diseases, 2016, 22, 846-853.	4.3	107
36	Astrovirus VA1 identified by next-generation sequencing in a nasopharyngeal specimen of a febrile Tanzanian child with acute respiratory disease of unknown etiology. Emerging Microbes and Infections, 2016, 5, 1-3.	6.5	24

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#	Article	IF	CITATIONS
37	Novel human astroviruses: Novel human diseases?. Journal of Clinical Virology, 2016, 82, 56-63.	3.1	81
38	Ebola virus disease diagnosis by real-time RT-PCR: A comparative study of 11 different procedures. Journal of Clinical Virology, 2016, 77, 9-14.	3.1	64
39	Predominance of influenza A(H1N1)pdm09 virus genetic subclade 6B.1 and influenza B/Victoria lineage viruses at the start of the 2015/16 influenza season in Europe. Eurosurveillance, 2016, 21, .	7.0	37
40	Astrovirus MLB2, a New Gastroenteric Virus Associated with Meningitis and Disseminated Infection. Emerging Infectious Diseases, 2016, 22, 846-853.	4.3	33
41	E119D Neuraminidase Mutation Conferring Pan-Resistance to Neuraminidase Inhibitors in an A(H1N1)pdm09 Isolate From a Stem-Cell Transplant Recipient. Journal of Infectious Diseases, 2015, 212, 1726-1734.	4.0	54
42	Toscana virus meningitis case in Switzerland: an example of the ezVIR bioinformatics pipeline utility for the identification of emerging viruses. Clinical Microbiology and Infection, 2015, 21, 387.e1-387.e4.	6.0	17
43	Enterovirus and Parechovirus viraemia in young children presenting to the emergency room: Unrecognised and frequent. Journal of Clinical Virology, 2015, 68, 69-72.	3.1	20
44	Human three-dimensional engineered neural tissue reveals cellular and molecular events following cytomegalovirus infection. Biomaterials, 2015, 53, 296-308.	11.4	18
45	Clinical features and viral kinetics in a rapidly cured patient with Ebola virus disease: a case report. Lancet Infectious Diseases, The, 2015, 15, 1034-1040.	9.1	46
46	Comprehensive metagenomic analysis of glioblastoma reveals absence of known virus despite antiviralâ€like type I interferon gene response. International Journal of Cancer, 2014, 135, 1381-1389.	5.1	35
47	Comprehensive Human Virus Screening Using High-Throughput Sequencing with a User-Friendly Representation of Bioinformatics Analysis: a Pilot Study. Journal of Clinical Microbiology, 2014, 52, 3351-3361.	3.9	60
48	Identification of Site-Specific Adaptations Conferring Increased Neural Cell Tropism during Human Enterovirus 71 Infection. PLoS Pathogens, 2012, 8, e1002826.	4.7	91
49	Pilot Evaluation of RT-PCR/Electrospray Ionization Mass Spectrometry (PLEX-ID/Flu assay) on Influenza-Positive Specimens. The Open Virology Journal, 2012, 6, 64-67.	1.8	11
50	Astrovirus Infection in Hospitalized Infants with Severe Combined Immunodeficiency after Allogeneic Hematopoietic Stem Cell Transplantation. PLoS ONE, 2011, 6, e27483.	2.5	110
51	Rhinovirus Genome Variation during Chronic Upper and Lower Respiratory Tract Infections. PLoS ONE, 2011, 6, e21163.	2.5	52
52	Analytical validation of a lymphocytic choriomeningitis virus real-time RT-PCR assay. Journal of Virological Methods, 2011, 177, 118-122.	2.1	24
53	Spread of Measles Virus D4-Hamburg, Europe, 2008–2011. Emerging Infectious Diseases, 2011, 17, 1396-1401.	4.3	65
54	T Lymphocytes Promote the Antiviral and Inflammatory Responses of Airway Epithelial Cells. PLoS ONE, 2011, 6, e26293.	2.5	6

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#	Article	IF	CITATIONS
55	Rhinovirus Genome Evolution during Experimental Human Infection. PLoS ONE, 2010, 5, e10588.	2.5	48
56	New Molecular Detection Tools Adapted to Emerging Rhinoviruses and Enteroviruses. Journal of Clinical Microbiology, 2009, 47, 1742-1749.	3.9	77
57	New Respiratory Enterovirus and Recombinant Rhinoviruses among Circulating Picornaviruses. Emerging Infectious Diseases, 2009, 15, 719-726.	4.3	130
58	Simultaneous detection of parainfluenza viruses 1 and 3 by real-time reverse transcription-polymerase chain reaction. Journal of Virological Methods, 2009, 156, 166-168.	2.1	13
59	The <i>cis</i> -acting replication elements define human enterovirus and rhinovirus species. Rna, 2008, 14, 1568-1578.	3.5	51
60	Further characterization of a paramyxovirus transcription initiation signal: search for required nucleotides upstream and importance of the N phase context. Journal of General Virology, 2007, 88, 1555-1564.	2.9	5
61	New complete genome sequences of human rhinoviruses shed light on their phylogeny and genomic features. BMC Genomics, 2007, 8, 224.	2.8	63
62	Transcribing paramyxovirus RNA polymerase engages the template at its 3′ extremity. Journal of General Virology, 2006, 87, 665-672.	2.9	11
63	Nature of a paramyxovirus replication promoter influences a nearby transcription signal. Journal of General Virology, 2005, 86, 171-180.	2.9	15
64	Reconstruction of transmission chains of SARS-CoV-2 amidst multiple outbreaks in a geriatric acute-care hospital: a combined retrospective epidemiological and genomic study. ELife, 0, 11, .	6.0	8