

Kristian G Andersen

List of Publications by Citations

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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.

90
papers

10,062
citations

43
h-index

100
g-index

101
ext. papers

13,227
ext. citations

26.1
avg, IF

6.99
L-index

#	Paper	IF	Citations
90	The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020 , 26, 450-452	50.5	2687
89	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014 , 345, 1369-72	33.3	847
88	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017 , 12, 1261-1276	18.8	529
87	Clinical illness and outcomes in patients with Ebola in Sierra Leone. <i>New England Journal of Medicine</i> , 2014 , 371, 2092-100	59.2	392
86	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019 , 20, 8	18.3	308
85	Identifying recent adaptations in large-scale genomic data. <i>Cell</i> , 2013 , 152, 703-13	56.2	259
84	Neuropilin-1 expression on regulatory T cells enhances their interactions with dendritic cells during antigen recognition. <i>Immunity</i> , 2008 , 28, 402-13	32.3	255
83	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017 , 546, 411-415	50.4	253
82	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
81	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
80	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016 , 165, 1519-1529	56.2	228
79	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015 , 161, 1516-26	56.2	210
78	The evolution of Ebola virus: Insights from the 2013-2016 epidemic. <i>Nature</i> , 2016 , 538, 193-200	50.4	185
77	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19	26.6	179
76	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015 , 162, 738-50	56.2	176
75	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020 , 369, 582-587	33.3	162
74	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016 , 167, 1088-1098.e6	56.2	135

73	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , 2021 , 184, 2587-2594.e7	56.2	132
72	Systematic Analysis of Monoclonal Antibodies against Ebola Virus GP Defines Features that Contribute to Protection. <i>Cell</i> , 2018 , 174, 938-952.e13	56.2	126
71	Lassa fever in post-conflict sierra leone. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2748	4.8	126
70	A Role for Fc Function in Therapeutic Monoclonal Antibody-Mediated Protection against Ebola Virus. <i>Cell Host and Microbe</i> , 2018 , 24, 221-233.e5	23.4	121
69	High-Definition Medicine. <i>Cell</i> , 2017 , 170, 828-843	56.2	114
68	Alloantigen-enhanced accumulation of CCR5+ T effector/regulatory T cells in the gravid uterus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 594-9	11.5	107
67	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. <i>Cell</i> , 2018 , 173, 443-455.e12	56.2	104
66	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021 , 184, 4848-4856	56.2	103
65	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016 , 7, 11544	17.4	99
64	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014 , 15, 519	18.3	97
63	COVID-19 testing: One size does not fit all. <i>Science</i> , 2021 , 371, 126-127	33.3	85
62	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , 2018 , 379, 1745-1753	59.2	82
61	Structures of Ebola virus GP and sGP in complex with therapeutic antibodies. <i>Nature Microbiology</i> , 2016 , 1, 16128	26.6	78
60	Correction: Lassa hemorrhagic fever in a late term pregnancy from northern Sierra Leone with a positive maternal outcome: case report. <i>Virology Journal</i> , 2011 , 8, 480	6.1	78
59	Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018 , 558, 180-182	50.4	77
58	Genome-wide scans provide evidence for positive selection of genes implicated in Lassa fever. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012 , 367, 868-77	5.8	73
57	Nomenclature- and database-compatible names for the two Ebola virus variants that emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014 , 6, 4760-99	6.2	70
56	Evaluation of the potential impact of Ebola virus genomic drift on the efficacy of sequence-based candidate therapeutics. <i>MBio</i> , 2015 , 6,	7.8	54

55	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019 , 25, 206-211	50.5	52
54	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. <i>Nature Communications</i> , 2018 , 9, 1624	17.4	50
53	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020 , 11, 5110	17.4	49
52	GB virus C coinfections in west African Ebola patients. <i>Journal of Virology</i> , 2015 , 89, 2425-9	6.6	47
51	Comparative Genomics Reveals Key Gain-of-Function Events in Foxp3 during Regulatory T Cell Evolution. <i>Frontiers in Immunology</i> , 2012 , 3, 113	8.4	46
50	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019 , 178, 1057-1071.e11	56.2	45
49	Filovirus RefSeq entries: evaluation and selection of filovirus type variants, type sequences, and names. <i>Viruses</i> , 2014 , 6, 3663-82	6.2	44
48	Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States 2021 ,		44
47	Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. <i>PLoS Pathogens</i> , 2019 , 15, e1008042	7.6	42
46	Lassa hemorrhagic fever in a late term pregnancy from northern Sierra Leone with a positive maternal outcome: case report. <i>Virology Journal</i> , 2011 , 8, 404	6.1	42
45	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018 , 172, 1160-1162	56.2	39
44	Analysis of CD8 T cell response during the 2013-2016 Ebola epidemic in West Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E7578-E7586	11.5	38
43	Discovery of novel rhabdoviruses in the blood of healthy individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003631	4.8	36
42	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016 , 166, 5-8	56.2	35
41	Experimental Evolution to Study Virus Emergence. <i>Cell</i> , 2017 , 169, 1-3	56.2	33
40	Ontogeny of the B- and T-cell response in a primary Zika virus infection of a dengue-naïve individual during the 2016 outbreak in Miami, FL. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0006000	4.8	31
39	Foxp3 expression is required for the induction of therapeutic tissue tolerance. <i>Journal of Immunology</i> , 2012 , 189, 3947-56	5.3	31
38	Multiple circulating infections can mimic the early stages of viral hemorrhagic fevers and possible human exposure to filoviruses in Sierra Leone prior to the 2014 outbreak. <i>Viral Immunology</i> , 2015 , 28, 19-31	1.7	29

37	The Regulatory T Cell Lineage Factor Foxp3 Regulates Gene Expression through Several Distinct Mechanisms Mostly Independent of Direct DNA Binding. <i>PLoS Genetics</i> , 2015 , 11, e1005251	6	27
36	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. <i>Scientific Reports</i> , 2018 , 8, 5939	4.9	26
35	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016 , 214, S110-S121	7	25
34	Epidemiology. Emerging disease or diagnosis?. <i>Science</i> , 2012 , 338, 750-2	33.3	23
33	Foxp3 interacts with c-Rel to mediate NF- κ B repression. <i>PLoS ONE</i> , 2011 , 6, e18670	3.7	23
32	LEF-1 negatively controls interleukin-4 expression through a proximal promoter regulatory element. <i>Journal of Biological Chemistry</i> , 2008 , 283, 22490-7	5.4	22
31	Specific immunosuppression with inducible Foxp3-transduced polyclonal T cells. <i>PLoS Biology</i> , 2008 , 6, e276	9.7	21
30	A Genomic Survey of SARS-CoV-2 Reveals Multiple Introductions into Northern California without a Predominant Lineage 2020 ,		21
29	Survivors of Ebola Virus Disease Develop Polyfunctional Antibody Responses. <i>Journal of Infectious Diseases</i> , 2020 , 221, 156-161	7	19
28	Ebola Virus Transmission Initiated by Relapse of Systemic Ebola Virus Disease. <i>New England Journal of Medicine</i> , 2021 , 384, 1240-1247	59.2	16
27	High crossreactivity of human T cell responses between Lassa virus lineages. <i>PLoS Pathogens</i> , 2020 , 16, e1008352	7.6	10
26	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar		7
25	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020 , 11, 5620	17.4	7
24	A Fc engineering approach to define functional humoral correlates of immunity against Ebola virus. <i>Immunity</i> , 2021 , 54, 815-828.e5	32.3	7
23	Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations		6
22	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples		6
21	Ebola vaccine-induced protection in nonhuman primates correlates with antibody specificity and Fc-mediated effects. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	6
20	A laboratory in your pocket. <i>Lancet, The</i> , 2016 , 388, 1875	40	6

19	Identification of Common CD8 T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. <i>Journal of Virology</i> , 2020 , 94,	6.6	6
18	Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences". <i>Science</i> , 2016 , 353, 658	33.3	5
17	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study 2020 ,		5
16	Two Sides of a Coin: a Zika Virus Mutation Selected in Pregnant Rhesus Macaques Promotes Fetal Infection in Mice but at a Cost of Reduced Fitness in Nonpregnant Macaques and Diminished Transmissibility by Vectors. <i>Journal of Virology</i> , 2020 , 94,	6.6	4
15	Reporter Assays for Ebola Virus Nucleoprotein Oligomerization, Virion-Like Particle Budding, and Minigenome Activity Reveal the Importance of Nucleoprotein Amino Acid Position 111. <i>Viruses</i> , 2020 , 12,	6.2	3
14	Cross-Reactive Antibodies to SARS-CoV-2 and MERS-CoV in Pre-COVID-19 Blood Samples from Sierra Leoneans. <i>Viruses</i> , 2021 , 13,	6.2	3
13	Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. <i>Nature Medicine</i> , 2021 , 27, 710-716	50.5	3
12	Emergence of an early SARS-CoV-2 epidemic in the United States 2021 ,		3
11	Genetic characterization of the Zika virus epidemic in the US Virgin Islands		2
10	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021 , 184, 4939-4952.e15	56.2	2
9	Lassa Virus Genetics. <i>Current Topics in Microbiology and Immunology</i> , 2020 , 1	3.3	1
8	Navigating the Zika panic. <i>F1000Research</i> , 2016 , 5, 1914	3.6	1
7	Wastewater sequencing uncovers early, cryptic SARS-CoV-2 variant transmission. 2022 ,		1
6	Activation rather than Foxp3 expression determines that TGF- β -induced regulatory T cells out-compete naive T cells in dendritic cell clustering. <i>European Journal of Immunology</i> , 2012 , 42, 1436-48 ^{6.1}	6.1	0
5	Inter-individual variation in objective measure of reactivity following COVID-19 vaccination via smartwatches and fitness bands.. <i>Npj Digital Medicine</i> , 2022 , 5, 49	15.7	0
4	High crossreactivity of human T cell responses between Lassa virus lineages 2020 , 16, e1008352		
3	High crossreactivity of human T cell responses between Lassa virus lineages 2020 , 16, e1008352		
2	High crossreactivity of human T cell responses between Lassa virus lineages 2020 , 16, e1008352		

- 1 High crossreactivity of human T cell responses between Lassa virus lineages **2020**, 16, e1008352